

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 12:42:18 ; Search time 424 Seconds  
(without alignments)  
12691.144 Million cell updates/sec

Title: US-10-030-271-1  
Perfect score: 909  
Sequence: 1 atggcgcgtaccgcggcgtcac.....tcagtrgtgatgagcgtcac 909

Scoring table: OLGCO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: geneeqn19808:\*
- 2: geneeqn19908:\*
- 3: geneeqn20008:\*
- 4: geneeqn20018:\*
- 5: geneeqn20028:\*
- 6: geneeqn20038:\*
- 7: geneeqn20048:\*
- 8: geneeqn20058:\*
- 9: geneeqn20068:\*
- 10: geneeqn20078:\*
- 11: geneeqn20088:\*
- 12: geneeqn20098:\*
- 13: geneeqn20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	909	5	AAE27407 Human apo
2	909	100.0	1883	5	AAE27408 Human apo
3	858	94.4	981	10	ADC79259 Human DED
4	858	94.4	1230	6	ABA94362 Human APR
5	858	94.4	1524	6	AAH40080 Human DED
6	858	94.4	1924	6	AAH59062 Human DED
7	858	94.4	1979	12	AAH59062 Human DED
8	858	94.4	2045	3	AAH59062 Human DED
9	858	94.4	2045	3	AAH59062 Human DED
10	768	84.5	2044	3	AAH59062 Human DED
11	538	59.2	1966	6	AAH59062 Human DED
12	531	58.4	1570	4	AAH59062 Human DED
13	334	36.7	626	4	AAH59062 Human DED
14	281	30.9	1067	4	AAH59062 Human DED
15	281	30.9	1067	4	AAH59062 Human DED
16	281	30.9	1067	4	AAH59062 Human DED
17	281	30.9	1067	4	AAH59062 Human DED
18	277	30.5	11084	12	AAH59062 Human DED
19	252	27.7	303	6	AAH59062 Human DED
20	252	27.7	303	6	AAH59062 Human DED

21	187	20.6	1084	6	ABL39692 Human NS
22	187	20.6	1106	6	ABL39693 Human NS
23	177	19.5	603	5	AAE93937 Primer BP
24	151	16.6	451	9	ACH41209 Human foe
25	106	10.6	484	9	ACH25056 Human adu
26	25	2.8	25	10	ADC79263 Human DED
27	22	2.4	838	5	ADL44878 Human ova
28	21	2.3	323	5	ADL39650 Human ova
29	20	2.2	21	5	AAE27413 Human apo
30	20	2.2	23	5	AAE27416 Human apo
31	20	2.2	2610	9	ACC59397 Microbial
32	20	2.2	2673	11	ABD04389 Pseudomon
33	20	2.2	2715	11	ABD04082 Pseudomon
34	20	2.2	2814	11	ABD04271 Pseudomon
35	19	2.1	360	10	ADH78561 35 amino
36	19	2.1	579	13	ADH52281 Novel can
37	19	2.1	606	5	AAH52281 Human ARP
38	19	2.1	943	6	ABH70016 CDNA enco
39	19	2.1	943	9	ADA01379 Human PRO
40	19	2.1	943	9	ADA43808 Human CDN
41	19	2.1	943	9	ADA43576 Human CDN
42	19	2.1	943	9	ADA01251 Human PRO
43	19	2.1	943	9	ADA01135 Human CDN
44	19	2.1	943	9	ADA43632 Human CDN
45	19	2.1	943	9	ADA06954 Human PRO
46	19	2.1	943	9	ADA08442 Novel hum
47	19	2.1	943	9	ADB99735 Human PRO
48	19	2.1	943	9	ADB87018 Human PRO
49	19	2.1	943	9	ADB66173 Human CDN
50	19	2.1	943	10	ADB99851 Human PRO
51	19	2.1	943	10	ADB99506 Novel hum
52	19	2.1	943	10	ADB66057 Human CDN
53	19	2.1	943	10	ADC23455 Human CDN
54	19	2.1	943	10	ADC25148 Human PRO
55	19	2.1	943	10	ADC04975 Human PRO
56	19	2.1	943	10	ADH11281 Human PRO
57	19	2.1	943	10	ADD88212 Human PRO
58	19	2.1	943	10	ADD95507 Human CDN
59	19	2.1	943	10	ADD06437 Human PRO
60	19	2.1	943	10	ADD88328 Human PRO
61	19	2.1	943	10	ADD88328 Human PRO
62	19	2.1	943	10	ADD90909 Human CDN
63	19	2.1	943	10	ADF99464 Human CDN
64	19	2.1	943	10	ADG06557 Human PRO
65	19	2.1	943	10	ADG05508 Human PRO
66	19	2.1	943	10	ADG82509 Human PRO
67	19	2.1	943	12	ADE51762 Human CDN
68	19	2.1	943	12	ADE51878 Human CDN
69	19	2.1	943	12	ADE37736 Human CDN
70	19	2.1	943	12	ADE37620 Human CDN
71	19	2.1	943	12	ADD95391 Human CDN
72	19	2.1	943	12	ADE38091 Human PRO
73	19	2.1	943	12	ADE76180 Human PRO
74	19	2.1	943	12	ADE39503 Human PRO
75	19	2.1	943	12	ADE04307 Human PRO
76	19	2.1	943	12	ADE39904 Human PRO
77	19	2.1	943	12	ADE19769 Human PRO
78	19	2.1	943	12	ADE77347 Human CDN
79	19	2.1	943	12	ADE65455 Human PRO
80	19	2.1	943	12	ADE76064 Human PRO
81	19	2.1	943	12	ADE37975 Human PRO
82	19	2.1	943	12	ADE64585 Human PRO
83	19	2.1	943	12	ADE38920 Human PRO
84	19	2.1	943	12	ADE51994 Human CDN
85	19	2.1	943	12	ADD91025 Human CDN
86	19	2.1	943	12	ADD91025 Human CDN
87	19	2.1	943	12	ADD91025 Human CDN
88	19	2.1	943	12	ADD91025 Human CDN
89	19	2.1	943	12	ADD91025 Human CDN
90	19	2.1	943	12	ADD91025 Human CDN
91	19	2.1	943	12	ADD91025 Human CDN
92	19	2.1	943	12	ADD91025 Human CDN
93	19	2.1	943	12	ADD91025 Human CDN

94	19	2.1	943	12	ADb19885	Human	PRO	C 167	18	2.0	527	9	AC116894	AC116894 DNA clone
95	19	2.1	943	12	ADb77463	Human	CDN	C 168	18	2.0	558	9	AC116892	AC116892 DNA clone
96	19	2.1	943	12	ADb65339	Human	PRO	C 169	18	2.0	598	9	AC116893	AC116893 DNA clone
97	19	2.1	943	12	ADb39387	Human	PRO	C 170	18	2.0	618	6	ABK73212	ABK73212 Bacillus
98	19	2.1	943	12	ADb38572	Human	CDN	C 171	18	2.0	628	9	AC116900	AC116900 DNA clone
99	19	2.1	943	12	ADG11125	Human	CDN	C 172	18	2.0	629	9	AC116902	AC116902 DNA clone
100	19	2.1	943	12	ADG11009	Human	CDN	C 173	18	2.0	632	9	AC116901	AC116901 DNA clone
101	19	2.1	943	12	ADH31537	Human	PRO	C 174	18	2.0	697	13	ADQ54233	ADQ54233 Novel can
102	19	2.1	943	12	ADH38785	Human	CDN	C 175	18	2.0	767	6	AB576791	AB576791 Frog embry
103	19	2.1	943	12	ADH29420	Human	CDN	C 176	18	2.0	809	6	ABQ33820	ABQ33820 Oligonuc1
104	19	2.1	943	12	ADH23723	Human	CDN	C 177	18	2.0	809	6	ABQ33821	ABQ33821 Oligonuc1
105	19	2.1	943	12	ADH27053	Human	CDN	C 178	18	2.0	918	4	AA554068	AA554068 Pseudomon
106	19	2.1	943	12	ADH38921	Novel	hum	C 179	18	2.0	918	4	ACA42159	ACA42159 Prokaryot
107	19	2.1	943	12	ADH26937	Human	CDN	C 180	18	2.0	918	12	ADQ25331	ADQ25331 P. aerugin
108	19	2.1	943	12	ADH38205	Novel	hum	C 181	18	2.0	918	12	ADQ25329	ADQ25329 P. aerugin
109	19	2.1	943	12	ADH38901	Human	CDN	C 182	18	2.0	927	8	ACA54525	ACA54525 Prokaryot
110	19	2.1	943	12	ADH38339	Human	CDN	C 183	18	2.0	1011	11	ABD14470	ABD14470 Pseudomon
111	19	2.1	943	12	ADH40214	Human	PRO	C 184	18	2.0	1056	3	AAZ49478	AAZ49478 Xylitol d
112	19	2.1	943	12	ADH40099	Human	PRO	C 185	18	2.0	1163	5	AA545101	AA545101 CDNA enco
113	19	2.1	943	12	ADH31421	Human	PRO	C 186	18	2.0	1179	12	ADM80103	ADM80103 Sphramycl
114	19	2.1	943	12	ADH29299	Human	CDN	C 187	18	2.0	1179	12	ADN97619	ADN97619 S. ambofac
115	19	2.1	943	12	ADH49514	Novel	hum	C 188	18	2.0	1258	5	AA545289	AA545289 CDNA enco
116	19	2.1	943	12	ADH49514	Novel	hum	C 189	18	2.0	1265	8	ACA42690	ACA42690 Prokaryot
117	19	2.1	943	12	ADH49833	Novel	hum	C 190	18	2.0	1273	2	AAK20428	AAK20428 Human sec
118	19	2.1	943	12	ADH52434	Novel	hum	C 191	18	2.0	1273	10	ADD90212	ADD90212 Novel hum
119	19	2.1	943	12	ADH52550	Novel	hum	C 192	18	2.0	1273	10	ADG90031	ADG90031 Human CDN
120	19	2.1	943	12	ADH58547	Novel	hum	C 193	18	2.0	1311	8	ACA26866	ACA26866 Prokaryot
121	19	2.1	943	12	ADH51862	Novel	hum	C 194	18	2.0	1314	5	AAH68574	AAH68574 Bordetell
122	19	2.1	943	12	ADH58423	Novel	hum	C 195	18	2.0	1355	5	AAH68574	AAH68574 Human pro
123	19	2.1	943	12	AD113620	Novel	hum	C 196	18	2.0	1388	12	ADQ68764	ADQ68764 Human tum
124	19	2.1	943	12	ADK00876	Human	PRO	C 197	18	2.0	1388	13	ADQ85685	ADQ85685 Human tum
125	19	2.1	943	12	ADL08617	Human	PRO	C 198	18	2.0	1409	5	AAc88080	AAc88080 Human FLB
126	19	2.1	1285	6	AB190412	Human	CDN	C 199	18	2.0	1412	11	ABD11817	ABD11817 Pseudomon
127	19	2.1	1742	6	AB211501	Human	pol	C 200	18	2.0	1439	13	ACN40506	ACN40506 Tumour-as
128	19	2.1	1742	12	ADMA4019	Novel	hum	C 201	18	2.0	1447	5	ABX71274	ABX71274 Human bra
129	19	2.1	1852	13	ADQ85413	Human	tum	C 202	18	2.0	1448	6	ABQ54670	ABQ54670 Human ova
130	19	2.1	1870	11	ADN95938	Human	BEC	C 203	18	2.0	1646	3	AAc76512	AAc76512 Human ORF
131	19	2.1	1870	13	ADP55303	Human	PRO	C 204	18	2.0	1695	11	ABD11715	ABD11715 Pseudomon
132	19	2.1	1871	12	ADM96334	Human	FLJ	C 205	18	2.0	1809	11	ABD14263	ABD14263 Pseudomon
133	19	2.1	2019	11	ABD07232	Pseudomon		C 206	18	2.0	1890	13	ABD33429	ABD33429 Human can
134	19	2.1	2247	4	AB129951	Drosophill		C 207	18	2.0	1899	6	ABZ11986	ABZ11986 Human pol
135	19	2.1	2417	5	ADM19574	Novel	hum	C 208	18	2.0	1899	12	ADMA4504	ADMA4504 Novel hum
136	19	2.1	2527	3	ADQ25121	Human	sof	C 209	18	2.0	1922	6	ABL68889	ABL68889 Kidney ca
137	19	2.1	2528	12	AAZ51797	Full leng		C 210	18	2.0	1922	6	ABL68628	ABL68628 Kidney ca
138	19	2.1	2528	10	ADb61984	Human	Bcl	C 211	18	2.0	1922	6	ABL70020	ABL70020 Pancreas
139	19	2.1	2533	10	ADb78552	575 amino		C 212	18	2.0	1922	6	ABL62350	ABL62350 Polon ade
140	19	2.1	2534	3	AAZ51804	Full leng		C 213	18	2.0	1922	6	ABL68275	ABL68275 Kidney ca
141	19	2.1	2534	10	ADb61991	Human	Bcl	C 214	18	2.0	1922	6	ABK64494	ABK64494 Human ben
142	19	2.1	2605	10	ADP69191	Human	MP5	C 215	18	2.0	1922	6	ABN95603	ABN95603 Gene #210
143	19	2.1	2605	13	ADG32699	Human	DNA	C 216	18	2.0	1922	8	ACA64898	ACA64898 Human mt1
144	19	2.1	2605	13	ADR25151	Breast ca		C 217	18	2.0	1922	9	AA157584	AA157584 Human met
145	19	2.1	2605	13	ADP24847	PRO polyp		C 218	18	2.0	1944	6	ABA93761	ABA93761 Human tes
146	19	2.1	2611	5	ADM19321	Novel hum		C 219	18	2.0	1953	12	ADP71877	ADP71877 Renal tox
147	19	2.1	2739	8	ADb70889	Rice gene		C 220	18	2.0	1970	10	ADC11957	ADC11957 Human nov
148	19	2.1	2748	11	ABD07169	Pseudomon		C 221	18	2.0	2005	10	AB142238	AB142238 Toxigenity
149	19	2.1	4756	4	AB103648	Drosophill		C 222	18	2.0	2283	12	ADQ64827	ADQ64827 Novel hum
150	19	2.1	5268	4	AB129950	Drosophill		C 223	18	2.0	2332	10	ADb63500	ADb63500 Human gen
151	19	2.1	5760	6	AB578661	M. echino		C 224	18	2.0	2332	10	ADb63500	ADb63500 Human gen
152	19	2.1	15462	4	AAK74459	Human imm		C 225	18	2.0	2376	11	ABD12137	ABD12137 Pseudomon
153	19	2.1	15462	5	ABBA21217	Human ner		C 226	18	2.0	2412	11	ADM03644	ADM03644 Human CDN
154	18	2.0	142	10	ADP38268	Synchronti		C 227	18	2.0	2569	12	ADQ17411	ADQ17411 Human sof
155	18	2.0	385	8	ABK35833	Bovine ES		C 228	18	2.0	2676	12	ADJ39546	ADJ39546 Plant CDN
156	18	2.0	393	8	ABX39164	Bovine ES		C 229	18	2.0	2745	8	ABZ20402	ABZ20402 Oncofoeta
157	18	2.0	426	3	ABX40466	Human sec		C 230	18	2.0	2745	12	ADQ22503	ADQ22503 Human sof
158	18	2.0	426	8	ABX42473	Bovine ES		C 231	18	2.0	2753	6	ABT03399	ABT03399 Ovary cel
159	18	2.0	435	4	AAK78370	Human imm		C 232	18	2.0	2997	12	ADP45491	ADP45491 Human KIR
160	18	2.0	442	9	AC116898	DNA clone		C 233	18	2.0	3016	6	ABZ11184	ABZ11184 Human pol
161	18	2.0	442	9	AC116896	DNA clone		C 234	18	2.0	3016	12	ADM43702	ADM43702 Novel hum
162	18	2.0	460	9	AC116904	DNA clone		C 235	18	2.0	3120	12	ADK33144	ADK33144 Human N-a
163	18	2.0	482	9	ACH44039	Human foe		C 236	18	2.0	3156	2	AAV18471	AAV18471 T-cell su
164	18	2.0	508	9	AC116899	DNA clone		C 237	18	2.0	3399	10	ADCS9315	ADCS9315 DNA encod
165	18	2.0	510	9	AC116897	DNA clone		C 238	18	2.0	3403	6	AB126595	AB126595 Drosophill
166	18	2.0	513	6	ABK78152	Bacillus		C 239	18	2.0	3414	6	ABT07557	ABT07557 Human bre



240	18	2.0	4989	8	AD054622	Aad54622 Human Mas	C 313	17	1.9	358	2	AAV86648	AAV86648 EST clone
241	18	2.0	5341	10	ADD29667	Add29667 Human tum	C 314	17	1.9	382	6	ABL82930	AbI82930 Human ova
C 242	18	2.0	5735	6	ABK94926	AbK94926 Human nov	C 315	17	1.9	386	6	ABL82848	AbI82848 Human ova
C 243	18	2.0	5735	6	ABK94980	AbK94980 Human nov	C 316	17	1.9	389	12	ADK13892	AdI13892 Murine PS
C 244	18	2.0	5768	6	ABL61797	AbI61797 COLon ade	C 317	17	1.9	394	6	ABV94914	AbV94914 Human pan
C 245	18	2.0	6032	10	ADG71667	AdG71667 Chlamydom	C 318	17	1.9	396	9	AD060082	Ad060082 Soybean v
C 246	18	2.0	6222	4	ABL26974	AbI26974 Drosophill	C 319	17	1.9	405	12	ADP64240	ADP64240 Soybean c
C 247	18	2.0	7612	13	ADH84505	AdH84505 Aspergill	C 320	17	1.9	406	11	ABD09167	ABD09167 Pseudomon
C 248	18	2.0	7826	12	AD022140	AdD22140 Human sof	C 321	17	1.9	410	12	ADP64035	ADP64035 Maize car
C 249	18	2.0	9873	4	AAK89905	AaK89905 Human dig	C 322	17	1.9	419	3	AAK52656	AAK52656 Arabidops
C 250	18	2.0	9973	4	AAJ35986	AaI35986 Human mus	C 323	17	1.9	422	8	AB218661	Ab218661 Group ITI
C 251	18	2.0	9973	8	ABX58974	AbX58974 CDNA enco	C 324	17	1.9	425	12	ADP64030	ADP64030 Maize car
C 252	18	2.0	9973	12	ADJ29724	AdJ29724 Human mus	C 325	17	1.9	430	12	ADP64026	ADP64026 Maize car
C 253	18	2.0	12851	10	ADG71668	AdG71668 Chlamydom	C 326	17	1.9	432	2	AAV69391	AAV69391 H. confor
C 254	18	2.0	30943	12	ADN97550	AdN97550 S ambotac	C 327	17	1.9	437	11	ABD14652	ABD14652 Pseudomon
C 255	18	2.0	30943	12	ADN97550	AdN97550 S ambotac	C 328	17	1.9	437	8	ABK37295	ABK37295 Bovine RS
C 256	18	2.0	32229	13	ADR67012	AdR67012 Human can	C 329	17	1.9	444	8	ABK91608	ABK91608 Murine ge
C 257	18	2.0	35026	3	AAA64890	Aaa64890 Bordetell	C 330	17	1.9	449	9	ACH40180	ACH40180 Human fce
C 258	18	2.0	52211	11	ACN44892	AcN44892 Mouse gen	C 331	17	1.9	450	6	ABL87323	ABL87323 Human ova
C 259	18	2.0	68732	13	ABD33428	AbD33428 Human can	C 332	17	1.9	458	4	AAI85286	AAI85286 Human pol
C 260	18	2.0	89873	13	ABD32846	AbD32846 Mouse can	C 333	17	1.9	458	4	AAI86353	AAI86353 Human pol
C 261	18	2.0	105219	11	ACN44286	AcN44286 Human gen	C 334	17	1.9	459	8	ACA54500	ACA54500 Prokaryot
C 262	18	2.0	128600	6	ABK83461	AbK83461 Human CDN	C 335	17	1.9	465	4	AAI16090	AAI16090 Probe #60
C 263	18	2.0	176594	6	ABD33387	AbD33387 Murine ca	C 336	17	1.9	465	4	ABA58643	ABA58643 Human fce
C 264	18	2.0	326014	6	ABK89296	AbK89296 Human gen	C 337	17	1.9	465	4	AAI38318	AAI38318 Probe #70
C 265	18	2.0	340449	8	AAI52198	AaI52198 Human kin	C 338	17	1.9	465	4	ABA27635	ABA27635 Probe #61
C 266	18	2.0	340449	8	AAI52198	AaI52198 Human sec	C 339	17	1.9	465	4	AAK32491	AAK32491 Human bon
C 267	17	1.9	60	6	ABN59247	AbN59247 Human epl	C 340	17	1.9	465	4	AAK06775	AAK06775 Human bra
C 268	17	1.9	141	6	AB212551	Ab212551 Arabidops	C 341	17	1.9	465	4	ABK32199	ABK32199 Human liv
C 269	17	1.9	141	6	ABK83922	AbK83922 Human gen	C 342	17	1.9	465	6	ABK07276	ABK07276 Human gen
C 270	17	1.9	158	3	ACH91070	AcH91070 Human sec	C 343	17	1.9	473	4	AAI90094	AAI90094 Human pol
C 271	17	1.9	164	12	ACH91070	AcH91070 Human gen	C 344	17	1.9	477	3	AAK55129	AAK55129 Arabidops
C 272	17	1.9	164	12	ADP64007	AdP64007 Maize car	C 345	17	1.9	477	4	ABL25519	ABL25519 Drosophill
C 273	17	1.9	166	6	ABN79237	AbN79237 Human gly	C 346	17	1.9	479	9	ACH27184	ACH27184 Human adu
C 274	17	1.9	202	12	ADP64037	AdP64037 Maize car	C 347	17	1.9	483	9	ACH27861	ACH27861 Human adu
C 275	17	1.9	222	12	ADK43201	AdK43201 Human pro	C 348	17	1.9	495	9	ACH34100	ACH34100 Human end
C 276	17	1.9	232	7	ADK67042	AdK67042 Corn seed	C 349	17	1.9	497	13	ACH05313	ACH05313 Novel can
C 277	17	1.9	241	6	ABN18672	AbN18672 Human ORF	C 350	17	1.9	515	5	AAK21950	AAK21950 Human col
C 278	17	1.9	246	6	ADK60064	AdK60064 Soybean v	C 351	17	1.9	523	4	AAH06261	AAH06261 Human CDN
C 279	17	1.9	246	12	ADP64144	AdP64144 Soybean c	C 352	17	1.9	528	11	ABD08387	ABD08387 Pseudomon
C 280	17	1.9	255	9	ADK60058	AdK60058 Soybean v	C 353	17	1.9	531	12	ACH70593	ACH70593 Human gen
C 281	17	1.9	255	12	ADP64138	AdP64138 Soybean c	C 354	17	1.9	533	9	ACH23692	ACH23692 Human adu
C 282	17	1.9	257	6	ABL79682	AbI79682 Human ova	C 355	17	1.9	572	9	ACH40027	ACH40027 Human fce
C 283	17	1.9	259	9	ADK60054	AdK60054 Soybean v	C 356	17	1.9	572	9	ACH40053	ACH40053 Human fce
C 284	17	1.9	259	12	ADP64134	AdP64134 Soybean c	C 357	17	1.9	582	12	ACH70221	ACH70221 Human gen
C 285	17	1.9	266	9	ADK60051	AdK60051 Soybean v	C 358	17	1.9	586	12	ACH77370	ACH77370 Human gen
C 286	17	1.9	266	12	ADP64131	AdP64131 Soybean c	C 359	17	1.9	588	12	ACH77377	ACH77377 Human gen
C 287	17	1.9	278	11	ADT94498	AdT94498 Corn can	C 360	17	1.9	591	12	ADO00355	ADO00355 Novel hum
C 288	17	1.9	280	10	ABX83021	AbX83021 Corn ear-	C 361	17	1.9	591	12	ADN98786	ADN98786 Novel hum
C 289	17	1.9	283	12	ADP64032	AdP64032 Maize car	C 362	17	1.9	606	5	ABV57788	ABV57788 Human pro
C 290	17	1.9	287	9	ADK60055	AdK60055 Soybean v	C 363	17	1.9	651	13	ADK56232	ADK56232 Novel can
C 291	17	1.9	287	12	ADP64135	AdP64135 Soybean c	C 364	17	1.9	652	6	ABQ43193	ABQ43193 Oligonuci
C 292	17	1.9	290	9	ADK60052	AdK60052 Soybean v	C 365	17	1.9	652	6	ABQ43192	ABQ43192 Oligonuci
C 293	17	1.9	290	12	ADP64132	AdP64132 Soybean c	C 366	17	1.9	669	6	AAH05181	AAH05181 Human CDN
C 294	17	1.9	296	6	ADK60053	AdK60053 Soybean v	C 367	17	1.9	696	12	ADL81748	ADL81748 P. aerugi
C 295	17	1.9	296	12	ADP64133	AdP64133 Soybean c	C 368	17	1.9	713	6	ABK76957	ABK76957 Frog embri
C 296	17	1.9	299	12	ADP63896	AdP63896 Maize car	C 369	17	1.9	716	13	ADR26096	ADR26096 Breast ca
C 297	17	1.9	318	12	ADJ44361	AdJ44361 Plant CDN	C 370	17	1.9	727	4	AAI97835	AAI97835 Human neu
C 298	17	1.9	332	12	ADP63895	AdP63895 Maize car	C 371	17	1.9	735	10	ADK55838	ADK55838 Plant DNA
C 299	17	1.9	347	4	AAI25298	AaI25298 Probe #15	C 372	17	1.9	758	6	ABK77298	ABK77298 Frog embri
C 300	17	1.9	347	4	ABA71220	AbA71220 Human fce	C 373	17	1.9	769	10	ADD34431	ADD34431 Mouse mit
C 301	17	1.9	347	4	AAI51454	AaI51454 Probe #20	C 374	17	1.9	780	4	ABLI1313	ABLI1313 Drosophill
C 302	17	1.9	347	4	ABA37529	AbA37529 Probe #15	C 375	17	1.9	822	10	ADDI6673	ADDI6673 DNA (SegI
C 303	17	1.9	347	4	AAK45513	AaK45513 Human bon	C 376	17	1.9	858	8	ADA70840	ADA70840 Rice gene
C 304	17	1.9	347	4	AAK19519	AaK19519 Human bra	C 377	17	1.9	872	6	ABK34512	ABK34512 Human CDN
C 305	17	1.9	347	4	ABK45199	AbK45199 Human liv	C 378	17	1.9	875	6	AAFI5034	AAFI5034 Trichoder
C 306	17	1.9	348	6	ABK19781	AbK19781 Human gen	C 379	17	1.9	912	10	ADH48573	ADH48573 O-acetyl
C 307	17	1.9	348	10	ADK55845	AdK55845 Human gen	C 380	17	1.9	912	10	ADH48575	ADH48575 Experimen
C 308	17	1.9	351	6	ABO85820	AbO85820 Human gen	C 381	17	1.9	933	13	ADSI4773	ADSI4773 Pseudomon
C 309	17	1.9	351	6	ABO85820	AbO85820 Arabidops	C 382	17	1.9	962	4	AAH32213	AAH32213 Human olf
C 310	17	1.9	352	3	AAK44118	AaK44118 Arabidops	C 383	17	1.9	962	4	ADDI7518	ADDI7518 DNA (SegI
C 311	17	1.9	354	11	ABD13946	AbD13946 Pseudomon	C 384	17	1.9	962	10	ADK58212	ADK58212 Plant DNA
C 312	17	1.9	354	12	ACH84293	ACH84293 Human gen	C 385	17	1.9	962	10	ADK57482	ADK57482 Plant DNA

386	17	1.9	962	11	ADM45007	Insect re	C 459	17	1.9	1686	8	ABX56030	Abx56030 M. echino
387	17	1.9	969	11	ABD10237	Pseudomon	C 460	17	1.9	1711	10	ADD13642	Add13642 C. glutam
388	17	1.9	983	12	ACH87261	Human gen	C 461	17	1.9	1717	3	AACT78069	Aac78069 Human can
389	17	1.9	1008	11	ABD10349	Pseudomon	C 462	17	1.9	1730	3	AAA26383	Aaa26383 Human sec
390	17	1.9	1011	2	AAK65962	Human tum	C 463	17	1.9	1730	12	ADL171444	Adl171444 Novel hum
391	17	1.9	1012	4	AA559715	Propionib	C 464	17	1.9	1742	6	AA562540	Aaa62540 CDNA sequ
392	17	1.9	1012	8	ACR64644	Propionib	C 465	17	1.9	1752	6	AB154835	Abi54835 Levam lru
393	17	1.9	1020	12	ADJ43382	Plant CDN	C 466	17	1.9	1766	5	AAAD04277	Aad04277 Short for
394	17	1.9	1045	2	AAV74137	Human FLA	C 467	17	1.9	1766	5	AAAD04276	Aad04276 Short for
395	17	1.9	1045	6	AAD43203	Human FLA	C 468	17	1.9	1830	4	AAH15765	Aah15765 Human CDN
C 396	17	1.9	1050	3	AAA53949	ORF8 sequ	C 469	17	1.9	1840	5	AA585767	Aaa85767 DNA encod
C 397	17	1.9	1050	6	AA143629	Rhodococc	C 470	17	1.9	1875	10	ADA53225	Ada53225 Human cod
C 398	17	1.9	1050	6	ABK51847	R. erythr	C 471	17	1.9	1879	5	AAAD04274	Aad04274 Long form
C 400	17	1.9	1056	6	ADJ27248	Rhodococc	C 472	17	1.9	1879	5	AAAD04275	Aad04275 Long form
C 401	17	1.9	1056	6	ADJ31760	Coen. lbov	C 473	17	1.9	1888	13	ACN43748	Acn43748 Human dia
C 402	17	1.9	1107	11	ABD00807	Klebsiell	C 474	17	1.9	1894	13	ACN43747	Acn43747 Human dia
C 403	17	1.9	1114	4	AAE71205	Corynebac	C 475	17	1.9	1908	8	ACA53411	Ac53411 Prokaryot
C 404	17	1.9	1116	5	ADB83240	Human CDN	C 476	17	1.9	1927	2	AAO47841	Aaa47841 Flavonoid
C 405	17	1.9	1137	5	AA587537	DNA encod	C 477	17	1.9	1935	12	ADL70564	Adl70564 Cervical
C 406	17	1.9	1137	5	AA587536	DNA encod	C 478	17	1.9	1951	6	AA562304	Aaa62304 CDNA sequ
C 407	17	1.9	1139	3	AAZ43923	Human DED	C 479	17	1.9	1973	1	AAAN91045	Aan91045 Gene enco
C 408	17	1.9	1142	3	AAZ43924	Murine DE	C 480	17	1.9	1974	8	ACC42477	Acc42477 Murine C1
C 409	17	1.9	1200	5	AA585037	DNA encod	C 481	17	1.9	1978	13	ACN43745	Acn43745 Human dia
C 410	17	1.9	1200	6	AAV74138	Mouse FLA	C 482	17	1.9	2000	6	AB199444	Abi99444 Mouse lbc
C 411	17	1.9	1236	10	ADP94930	Human gen	C 483	17	1.9	2005	2	AAQ71303	Aaq71303 Mouse otc
C 412	17	1.9	1253	3	AACT5178	Zea maye	C 484	17	1.9	2010	8	ABX17536	Abx17536 Human SNP
C 413	17	1.9	1253	2	AAQ70661	SCFV pRAS	C 485	17	1.9	2014	13	ADQ38799	Adq38799 Human SNP
C 414	17	1.9	1273	2	AAQ74636	Aspergill	C 486	17	1.9	2044	13	ADS48703	Ads48703 Bacterial
C 415	17	1.9	1279	8	ACC50966	Human bla	C 487	17	1.9	2067	8	ACA27186	Ac27186 Prokaryot
C 416	17	1.9	1279	8	ACC50999	Human bla	C 488	17	1.9	2079	5	ABV24761	Abv24761 Human pro
C 417	17	1.9	1279	11	ADN38839	Cancer/an	C 489	17	1.9	2085	8	ACA40672	Ac40672 Prokaryot
C 418	17	1.9	1279	12	ADM87422	Human EST	C 490	17	1.9	2100	5	AAE98725	Aae98725 Human lat
C 419	17	1.9	1296	2	AAQ70660	SCFV pRAS	C 491	17	1.9	2100	12	ADL70562	Adl70562 Cervical
C 420	17	1.9	1307	6	AAIC46525	Zea maye	C 492	17	1.9	2127	4	ABL11312	Ab11312 Drosophill
C 421	17	1.9	1312	6	AB199926	Rat mucoc	C 493	17	1.9	2136	11	ABD14485	Abd14485 Pseudomon
C 422	17	1.9	1316	6	AB876373	CDNA enco	C 494	17	1.9	2180	12	ADL70566	Adl70566 Cervical
C 423	17	1.9	1316	8	ACP12835	Human cer	C 495	17	1.9	2187	11	ABD08438	Abd08438 Pseudomon
C 424	17	1.9	1316	12	ADJ75173	Marker ge	C 496	17	1.9	2212	13	ACN38839	Acn38839 Tumour-as
C 425	17	1.9	1316	12	ADJ75293	Marker ge	C 497	17	1.9	2220	10	ADB63585	Adb63585 Human CDN
C 426	17	1.9	1332	8	ADA70436	Rice gene	C 498	17	1.9	2232	12	ADO20098	Ado20098 Human PRO
C 427	17	1.9	1340	4	ABLO9137	Drosophill	C 499	17	1.9	2239	13	ADO87327	Ado87327 Human tum
C 428	17	1.9	1344	4	AC98034	Human col	C 500	17	1.9	2261	6	AAH14367	Aah14367 Human CDN
C 429	17	1.9	1353	11	ABD09111	Pseudomon	C 501	17	1.9	2261	4	ABK46133	Abk46133 CDNA enco
C 430	17	1.9	1356	2	AAQ70659	SCFV pRAS	C 502	17	1.9	2308	11	ADM03580	Adm03580 Human CDN
C 431	17	1.9	1359	12	ADO42037	Human cel	C 503	17	1.9	2347	5	AA588827	Aaa88827 DNA encod
C 432	17	1.9	1361	3	AA588832	Maize ste	C 504	17	1.9	2367	2	AAV44448	Aav44448 Mycobacte
C 433	17	1.9	1379	2	AAQ08978	Mouse ade	C 505	17	1.9	2367	2	AAV64557	Aav64557 M. tuberc
C 434	17	1.9	1385	3	AAAC48022	Zea maye	C 506	17	1.9	2367	2	AAZ19146	Aaz19146 M. tuberc
C 435	17	1.9	1397	12	ADM80821	Human CAD	C 507	17	1.9	2367	2	AAZ19358	Aaz19358 M. tuberc
C 436	17	1.9	1398	13	ADT66719	Rat 26S p	C 508	17	1.9	2373	12	ADM86938	Adm86938 Human pro
C 437	17	1.9	1417	12	ADJ62811	Human CDN	C 509	17	1.9	2381	8	ABX55998	Abx55998 Gene enco
C 438	17	1.9	1417	12	ADJ62812	Human CDN	C 510	17	1.9	2406	11	ABD14099	Abd14099 Pseudomon
C 439	17	1.9	1432	8	AAAC48011	Zea maye	C 511	17	1.9	2413	4	AAI60272	Aai60272 Human pol
C 440	17	1.9	1458	8	ACA32203	Prokaryot	C 512	17	1.9	2419	4	ABL25542	Ab125542 Drosophill
C 441	17	1.9	1471	4	AAI58912	Human pol	C 513	17	1.9	2460	2	AAV44303	Aav44303 Human sec
C 442	17	1.9	1488	8	ACA27255	Prokaryot	C 514	17	1.9	2460	5	AAE98477	Aae98477 Human gen
C 443	17	1.9	1518	4	AA501474	Human sec	C 515	17	1.9	2496	2	AAQ80750	Aaq80750 T. flavus
C 444	17	1.9	1518	10	ADP94924	Thermus f	C 516	17	1.9	2496	2	AAV65780	Aav65780 Thermus f
C 445	17	1.9	1523	10	ADA52444	Human gen	C 517	17	1.9	2496	2	AAV63401	Aav63401 DNA sequ
C 446	17	1.9	1536	4	AAE61016	P. putida	C 518	17	1.9	2496	6	ADES3382	Ade3382 T. flavus
C 447	17	1.9	1550	2	AAAT09256	Human ara	C 519	17	1.9	2496	7	AD192601	Ad192601 T. flavus
C 448	17	1.9	1551	2	AAAI19627	Arthrobac	C 520	17	1.9	2496	9	ADBI6311	Adbi6311 DNA encod
C 449	17	1.9	1581	6	AAH66268	C. glutami	C 521	17	1.9	2496	9	ACF05365	Acf05365 Thermus i
C 450	17	1.9	1628	6	AA559913	Novel hum	C 522	17	1.9	2496	9	ACF05366	Acf05366 Thermus i
C 451	17	1.9	1629	8	AAAF71204	Corynebac	C 523	17	1.9	2496	9	ACF05364	Acf05364 Thermus i
C 452	17	1.9	1656	8	ACA43651	Prokaryot	C 524	17	1.9	2496	9	ACF05363	Acf05363 Thermus i
C 453	17	1.9	1662	6	AAK63616	Rat sequ	C 525	17	1.9	2511	11	ABD10528	Abd10528 Pseudomon
C 454	17	1.9	1662	10	ADBS5257	Toxicity-	C 526	17	1.9	2512	5	AAAD07667	Aad07667 Human sec
C 455	17	1.9	1662	10	ADBS5937	Primary x	C 527	17	1.9	2525	2	AAV02016	Aav02016 DNA encod
C 456	17	1.9	1662	12	ABT42496	Toxicity	C 528	17	1.9	2527	2	AAZ00313	Aaz00313 Human tum
C 457	17	1.9	1662	12	ADP73011	Renal tox	C 529	17	1.9	2536	10	ADP94952	Adp94952 Human gen
C 458	17	1.9	1680	10	ACF68722	Phototrab	C 530	17	1.9	2537	4	AAK52190	Aak52190 Human pol
							C 531	17	1.9	2538	2	AAK21398	Aak21398 Central f

C 532	17	1.9	2542	6	ABL63691	Abi63691 Breast ca	605	17	1.9	3930	3	AAZ44744	Aaz44744 Human KLI
C 533	17	1.9	2542	6	ABL67221	Abi67221 Thyroid c	606	17	1.9	3930	5	ADD08139	ADD08139 Human kin
C 534	17	1.9	2550	4	AAFP5640	AAFP5640 Human cel	607	17	1.9	3930	8	ABS57217	ABS57217 Human kin
C 535	17	1.9	2575	2	AAH85781	AAH85781 Human Mic	608	17	1.9	3930	10	ADG63389	ADG63389 Human CDN
C 536	17	1.9	2575	5	AA158486	AA158486 Human pol	609	17	1.9	3954	3	AACT5733	AACT5733 Human ORF
C 537	17	1.9	2575	5	ADQ98701	ADQ98701 DNA encod	610	17	1.9	4638	10	AD102662	AD102662 Human CDN
C 538	17	1.9	2575	9	ADB48461	ADB48461 Novel hum	611	17	1.9	4722	12	ADQ85612	ADQ85612 Human tum
C 539	17	1.9	2587	12	AD063163	ADQ63163 Novel hum	612	17	1.9	4722	12	AD084694	ADQ84694 Human tum
C 540	17	1.9	2592	2	AAZ41355	AAZ41355 Human nor	613	17	1.9	4722	13	ADQ83469	ADQ83469 Human tum
C 541	17	1.9	2602	11	ACN43022	ACN43022 Human dia	614	17	1.9	4722	13	ADQ84235	ADQ84235 Human tum
C 542	17	1.9	2616	11	ABD14247	ABD14247 Pseudomon	615	17	1.9	4722	13	ADQ86713	ADQ86713 Human tum
C 543	17	1.9	2629	13	ACN43021	ACN43021 Human dia	616	17	1.9	4744	6	ABN96962	ABN96962 Gene #346
C 544	17	1.9	2649	10	ADL13617	ADL13617 Osteoartrh	617	17	1.9	4950	6	ABK83470	ABK83470 Human CDN
C 545	17	1.9	2692	10	ADL13618	ADL13618 Osteoartrh	618	17	1.9	4950	6	ABK13302	ABK13302 DNA encod
C 546	17	1.9	2736	4	ABL25518	ABL25518 Drosophill	619	17	1.9	4950	13	ACN40396	ACN40396 Tumour-as
C 547	17	1.9	2756	4	ABL12176	ABL12176 Drosophill	620	17	1.9	4950	13	ADR52806	ADR52806 Drug ther
C 548	17	1.9	2793	13	ADS64243	ADS64243 Bacterial	621	17	1.9	4993	10	ADP74197	ADP74197 Human nov
C 549	17	1.9	2793	13	ADS63868	ADS63868 Bacterial	622	17	1.9	5075	12	ADP04059	ADP04059 Human col
C 550	17	1.9	2803	12	ADQ22316	ADQ22316 Human sof	623	17	1.9	5372	8	ABX10239	ABX10239 Human CDN
C 551	17	1.9	2804	3	AAFP21915	AAFP21915 Human bre	624	17	1.9	5385	6	ABL99888	ABL99888 Human sec
C 552	17	1.9	2825	4	ABL16532	ABL16532 Drosophill	625	17	1.9	5408	13	ADS09831	ADS09831 Human the
C 553	17	1.9	2836	10	ADA53209	ADA53209 Human cod	626	17	1.9	5429	4	ABL12170	ABL12170 Drosophill
C 554	17	1.9	2850	8	ACA44145	ACA44145 Prokaryot	627	17	1.9	5434	4	ABS67750	ABS67750 Human int
C 555	17	1.9	2859	13	ADS63497	ADS63497 Bacterial	628	17	1.9	5569	5	ABV24840	ABV24840 Human ova
C 556	17	1.9	2875	8	ABX70971	ABX70971 Novel hum	629	17	1.9	5570	5	ADP81684	ADP81684 Leukaemia
C 557	17	1.9	2886	10	ACD19394	ACD19394 CDNA enco	630	17	1.9	5682	10	ADP81684	ADP81684 Leukaemia
C 558	17	1.9	2897	12	ADQ85666	ADQ85666 Human tum	631	17	1.9	5733	13	ACN39104	ACN39104 Tumour-as
C 559	17	1.9	2897	13	ADQ83578	ADQ83578 Human tum	632	17	1.9	6040	4	AA106077	AA106077 Human rep
C 560	17	1.9	2909	10	ADG93394	ADG93394 Maize lrp	633	17	1.9	6040	4	ABL98642	ABL98642 Human tes
C 561	17	1.9	2970	6	ABS67320	ABS67320 Breast gp	634	17	1.9	6044	4	AA106074	AA106074 Human rep
C 562	17	1.9	2973	8	ACFP34508	ACFP34508 Gene enco	635	17	1.9	6044	4	AA106076	AA106076 Human rep
C 563	17	1.9	2973	10	ACD19393	ACD19393 CDNA enco	636	17	1.9	6044	4	ABL98639	ABL98639 Human tes
C 564	17	1.9	2973	12	ADQ96263	ADQ96263 T cell ac	637	17	1.9	6044	4	ABL98641	ABL98641 Human tes
C 565	17	1.9	2984	6	ABA01095	ABA01095 Brevibact	638	17	1.9	6044	4	AA546715	AA546715 Tumour su
C 566	17	1.9	3001	4	AAH88439	AAH88439 CNS disor	639	17	1.9	6083	4	ACC46588	ACC46588 Human dlt
C 567	17	1.9	3001	4	AAH15723	AAH15723 Human CDN	640	17	1.9	6324	8	ABL26680	ABL26680 Drosophill
C 568	17	1.9	3048	4	AB118019	AB118019 Drosophill	641	17	1.9	6621	4	ABK83783	ABK83783 Human CDN
C 569	17	1.9	3129	13	ADT43898	ADT43898 Bacterial	642	17	1.9	6765	6	ADS99929	ADS99929 Human ape
C 570	17	1.9	3148	12	ADK43180	ADK43180 Human PTP	643	17	1.9	6765	12	ADP13354	ADP13354 Renal cel
C 571	17	1.9	3167	6	ABK34683	ABK34683 Human CDN	644	17	1.9	6765	12	ADP13354	ADP13354 Renal cel
C 572	17	1.9	3171	4	ABL26681	ABL26681 Drosophill	645	17	1.9	6797	4	ABL18018	ABL18018 Drosophill
C 573	17	1.9	3187	8	ABZ35872	ABZ35872 Human sec	646	17	1.9	7186	8	ACC46573	ACC46573 Human dlt
C 574	17	1.9	3203	10	ADBC62175	ADBC62175 Human CDN	647	17	1.9	7373	4	AA541749	AA541749 Genomic s
C 575	17	1.9	3211	4	AAH34203	AAH34203 Human col	648	17	1.9	7373	4	ABA06810	ABA06810 Human gen
C 576	17	1.9	3244	10	AAD49459	AAD49459 Human yes	649	17	1.9	7373	6	ABV84147	ABV84147 Human pol
C 577	17	1.9	3279	12	ADK43402	ADK43402 Human PTP	650	17	1.9	7655	10	ADC27428	ADC27428 CDNA enco
C 578	17	1.9	3345	13	ACN43026	ACN43026 Human dia	651	17	1.9	8443	10	ADC27428	ADC27428 CDNA enco
C 579	17	1.9	3420	10	ADC73044	ADC73044 Triametes	652	17	1.9	8880	4	AAK83253	AAK83253 Human imm
C 580	17	1.9	3431	8	ABZ34816	ABZ34816 Coding se	653	17	1.9	10835	4	AA559527	AA559527 Propionib
C 581	17	1.9	3431	13	ACN37667	ACN37667 Tumour-as	654	17	1.9	10835	8	ACFP64456	ACFP64456 Propionib
C 582	17	1.9	3448	4	ABL09136	ABL09136 Drosophill	655	17	1.9	10976	13	ABD32650	ABD32650 Human can
C 583	17	1.9	3480	10	ADC73046	ADC73046 Triametes	656	17	1.9	11796	8	ABX10231	ABX10231 Human CDN
C 584	17	1.9	3483	13	ACN43025	ACN43025 Human dia	657	17	1.9	11796	10	ADG39785	ADG39785 Human CDN
C 585	17	1.9	3517	12	ADJ67698	ADJ67698 KifLC DNA	658	17	1.9	12508	3	AAAS3941	AAAS3941 12.5 kb p
C 586	17	1.9	3517	12	ADJ67696	ADJ67696 KifLC DNA	659	17	1.9	12508	6	AAAD27240	AAAD27240 Rhodococc
C 587	17	1.9	3517	12	ADJ67695	ADJ67695 KifLC DNA	660	17	1.9	12523	6	AA143619	AA143619 Rhodococc
C 588	17	1.9	3518	12	ADJ67697	ADJ67697 KifLC DNA	661	17	1.9	12523	6	ABK51837	ABK51837 Rhodococc
C 589	17	1.9	3518	12	ADJ67699	ADJ67699 KifLC DNA	662	17	1.9	14044	4	AAFP54793	AAFP54793 Nucleotid
C 590	17	1.9	3540	13	ADSA45801	ADSA45801 Bacteri	663	17	1.9	17606	5	AAFP83655	AAFP83655 Human COL
C 591	17	1.9	3546	13	ACN43024	ACN43024 Human dia	664	17	1.9	17606	5	AA521772	AA521772 Human gen
C 592	17	1.9	3573	13	ACN43023	ACN43023 Human dia	665	17	1.9	20158	10	ADL13614	ADL13614 Osteoartrh
C 593	17	1.9	3615	12	ACAS6656	ACAS6656 Human big	666	17	1.9	20158	4	AAK82721	AAK82721 Human imm
C 594	17	1.9	3615	12	AD156452	AD156452 Human pro	667	17	1.9	21635	11	ACN44628	ACN44628 Mouse gen
C 595	17	1.9	3615	12	ADK43194	ADK43194 Human pol	668	17	1.9	23024	4	AAFP25499	AAFP25499 Nucleotid
C 596	17	1.9	3630	13	ADQ85894	ADQ85894 Human tum	669	17	1.9	33351	12	ADQ59404	ADQ59404 Human can
C 597	17	1.9	3630	13	ADQ84819	ADQ84819 Human tum	670	17	1.9	33023	6	ABN96853	ABN96853 Gene #315
C 598	17	1.9	3642	5	ABD33170	ABD33170 Murine ca	671	17	1.9	33023	12	ADP13378	ADP13378 Renal cel
C 599	17	1.9	3642	5	AA858083	AA858083 DNA encod	672	17	1.9	33023	13	ADT93877	ADT93877 Non-small
C 600	17	1.9	3643	12	ADK43401	ADK43401 Human PTP	673	17	1.9	35183	13	ABD33355	ABD33355 Murine ca
C 601	17	1.9	3779	13	ADQ86756	ADQ86756 Full leng	674	17	1.9	42000	3	AAAP63349	AAAP63349 Streptom
C 602	17	1.9	3781	12	ADQ87056	ADQ87056 Human tum	675	17	1.9	43712	12	ADQ18757	ADQ18757 Human sof
C 603	17	1.9	3781	12	ADQ85867	ADQ85867 Human tum	676	17	1.9	45993	6	AAAD36070	AAAD36070 Human liv
C 604	17	1.9	3781	13	ACN40680	ACN40680 Tumour-as	677	17	1.9	48037	4	AAK84729	AAK84729 Human imm

678	17	1.9	48037	4	AAK85983	751	16	1.8	150	6	ABL01772	Abi01772 Human MSH
679	17	1.9	48045	4	AAK84730	752	16	1.8	150	12	ADP43117	Adp43117 MSH2 exon
680	17	1.9	48045	4	AAK85984	753	16	1.8	173	8	ABX52457	Abx52457 Bovine ES
681	17	1.9	55998	9	ADA02975	754	16	1.8	183	12	ACH85312	Ach85312 Human gen
682	17	1.9	55998	10	ADB72713	755	16	1.8	186	9	ACH03443	Ach03443 Human lat
683	17	1.9	55998	10	ADC85455	756	16	1.8	192	5	AAS65862	Aas65862 DNA encod
684	17	1.9	55998	12	ADM74570	757	16	1.8	201	13	ADS41306	Ads41306 Human aut
685	17	1.9	58857	3	AAH58471	758	16	1.8	201	13	ADS41305	Ads41305 Human aut
686	17	1.9	63164	13	AAH63348	759	16	1.8	201	13	ADS40308	Ads40308 Human aut
687	17	1.9	63164	13	ABD33426	760	16	1.8	216	4	ABA72518	Ab72518 Human foe
688	17	1.9	67212	10	AAA08954	761	16	1.8	216	4	AAI52931	AAI52931 Probe #21
689	17	1.9	69770	10	ADC86870	762	16	1.8	216	4	AAK47095	AAK47095 Human bon
690	17	1.9	70782	12	ADO59147	763	16	1.8	216	4	AAK20942	AAK20942 Human bra
691	17	1.9	70782	12	ADO59147	764	16	1.8	216	4	ABS46855	ABS46855 Human liv
692	17	1.9	75252	11	ACN44450	765	16	1.8	216	6	ABS21325	ABS21325 Human gen
693	17	1.9	80959	8	AAI51405	766	16	1.8	220	2	AAO20723	AAO20723 B. hermsli
694	17	1.9	84830	12	ADL81732	767	16	1.8	227	2	AAH85309	Aah85309 Human sin
695	17	1.9	87464	11	ACN44788	768	16	1.8	227	4	AAI27044	AAI27044 Probe #16
696	17	1.9	94001	13	ADJ33491	769	16	1.8	227	4	ABA75314	ABA75314 Human foe
697	17	1.9	102790	13	ABD33649	770	16	1.8	227	4	AAI55878	AAI55878 Probe #24
698	17	1.9	103464	13	ABD33278	771	16	1.8	227	4	ABA39964	ABA39964 Probe #18
699	17	1.9	107280	13	ABD33169	772	16	1.8	227	4	AAK49947	AAK49947 Human bon
700	17	1.9	110000	2	AAV30458_3	773	16	1.8	227	4	AAK23869	AAK23869 Human bra
701	17	1.9	110000	2	AAV30459_3	774	16	1.8	228	8	ABX47690	ABX47690 Human liv
702	17	1.9	110000	4	AAI99682_27	775	16	1.8	232	12	ADP64130	ADP64130 Soybean v
703	17	1.9	110000	4	AAI99682_27	776	16	1.8	232	12	ADP64130	ADP64130 Soybean v
704	17	1.9	110000	4	AAI99683_27	777	16	1.8	241	10	ACA55485	ACA55485 Human sig
705	17	1.9	110000	4	AAI99683_27	778	16	1.8	241	12	ADIS5281	Adis5281 Human pol
706	17	1.9	110000	10	ACF67367_15	779	16	1.8	242	9	ADA60057	Ada60057 Soybean v
707	17	1.9	110000	11	ADM27081_00	780	16	1.8	242	9	ADA60063	Ada60063 Soybean v
708	17	1.9	123219	4	AAH88703	781	16	1.8	242	12	ADP64143	Adp64143 Soybean c
709	17	1.9	138627	12	ADQ97183	782	16	1.8	246	12	ADP64140	Adp64140 Soybean c
710	17	1.9	176001	12	ADK43203	783	16	1.8	246	12	AAK57464	AAK57464 Human imm
711	17	1.9	186739	12	ADK43195	784	16	1.8	246	9	ADA60060	Ada60060 Soybean v
712	17	1.9	200000	12	ADQ47190	785	16	1.8	246	9	ADA60059	Ada60059 Soybean v
713	17	1.9	226475	9	AAH58279	786	16	1.8	246	12	ADP64139	Adp64139 Soybean c
714	17	1.9	249878	10	ACPF65381	787	16	1.8	246	12	ADP64140	Adp64140 Soybean c
715	17	1.9	272022	12	ADQ97126	788	16	1.8	248	6	ABN76668	ABN76668 Human ORF
716	17	1.9	330973	11	ACN44846	789	16	1.8	248	9	ADA60062	Ada60062 Soybean v
717	17	1.9	334462	10	ADQ24763	790	16	1.8	248	12	ADP64142	Adp64142 Soybean c
718	17	1.9	337022	12	ADQ59416	791	16	1.8	249	12	ADA60065	Ada60065 Soybean v
719	17	1.9	349980	5	AAH68527	792	16	1.8	249	9	ADA60065	Ada60065 Soybean v
720	17	1.9	349980	5	AAH68528	793	16	1.8	253	3	AAK32443	Aac32443 Human bec
721	16	1.8	16	6	AAH40092	794	16	1.8	255	6	ABL37449	Abi37449 Human col
722	16	1.8	16	6	AAH59074	795	16	1.8	255	6	ABL36911	Abi36911 Human col
723	16	1.8	16	17	AAA22755	796	16	1.8	258	12	ADQ21814	Adq21814 Human bof
724	16	1.8	16	20	ABZ98661	797	16	1.8	258	12	ADQ21814	Adq21814 Human bof
725	16	1.8	16	20	ABZ98661	798	16	1.8	264	9	ABN15934	ABN15934 Human ORF
726	16	1.8	16	20	ADJ60540	799	16	1.8	266	12	ADP64141	Adp64141 Soybean c
727	16	1.8	16	20	ADK43355	800	16	1.8	266	12	ADP64141	Adp64141 Soybean c
728	16	1.8	16	20	ADK43233	801	16	1.8	273	10	ACD97961	ACD97961 Human col
729	16	1.8	16	20	ADQ46029	802	16	1.8	274	12	ADP63916	Adp63916 Maize cat
730	16	1.8	16	23	ABN83374	803	16	1.8	276	8	ACA26440	ACA26440 Prokaryot
731	16	1.8	16	25	ACC47832	804	16	1.8	276	11	ABD16447	Abd16447 Pseudomon
732	16	1.8	16	29	ABK83200	805	16	1.8	281	9	ADA60056	Ada60056 Soybean v
733	16	1.8	16	41	ADG16991	806	16	1.8	281	9	ADA60056	Ada60056 Soybean v
734	16	1.8	16	47	AAH86394	807	16	1.8	291	12	ADP64136	Adp64136 Soybean c
735	16	1.8	16	60	ABN38637	808	16	1.8	291	6	ABO91162	ABO91162 M. capauli
736	16	1.8	16	65	ABN27987	809	16	1.8	295	7	ADS68892	Ads68892 Corn seed
737	16	1.8	16	65	ABN58427	810	16	1.8	297	11	ABD16005	Abd16005 Pseudomon
738	16	1.8	16	66	ABN58427	811	16	1.8	299	6	ABN22757	ABN22757 Human ORF
739	16	1.8	16	66	AAO49187	812	16	1.8	304	2	AAQ60270	AAQ60270 Human bra
740	16	1.8	16	66	ABN58427	813	16	1.8	305	2	AAV52943	AAV52943 Human UNC
741	16	1.8	16	80	ADM95586	814	16	1.8	309	6	ABL74370	ABL74370 Corn tabs
742	16	1.8	16	90	ADM95586	815	16	1.8	314	4	AAA96834	AAA96834 Nucleotid
743	16	1.8	16	91	ACG91112	816	16	1.8	314	5	AAK89803	AAK89803 Human BAT
744	16	1.8	16	92	ACG91112	817	16	1.8	314	5	ABK89237	ABK89237 Human BAT
745	16	1.8	16	121	AAH80371	818	16	1.8	314	12	ADH35220	Adh35220 Human mut
746	16	1.8	16	121	AAH80370	819	16	1.8	315	4	AAA31619	AAA31619 Plant mic
747	16	1.8	16	121	ADQ71305	820	16	1.8	315	4	ABL23727	ABL23727 Drosophili
748	16	1.8	16	144	ABL59553	821	16	1.8	317	2	AAO61187	AAO61187 Human bra
749	16	1.8	16	146	AAH36098	822	16	1.8	321	11	ABD16329	Abd16329 Pseudomon
750	16	1.8	150	2	AAQ93939	823	16	1.8	332	10	ADH85087	Adh85087 Farnesyl

824	16	1.8	348	6	ABN23094	Abn23094 Human ORF	C 897	16	1.8	508	9	ACH18628	Ach18628 Human adu
825	16	1.8	360	3	AAC09023	Aac09023 Human sec	C 898	16	1.8	510	2	AAC47652	Aac47652 Arabidops
C 826	16	1.8	361	8	ABX37223	Abx37223 Bovine ES	C 899	16	1.8	513	3	AAx98247	Aax98247 Nucleotid
C 827	16	1.8	364	8	ABX1546	Abx1546 CDNA encd	C 900	16	1.8	514	11	ACN80427	Acn80427 Breast ca
828	16	1.8	374	4	AA125184	AA125184 Probe #15	C 901	16	1.8	515	12	ACH69777	Ach69777 Human gen
829	16	1.8	374	4	ABx70956	Abx70956 Human foe	C 902	16	1.8	525	9	ACH18501	Ach18501 Human adu
830	16	1.8	374	4	AA151147	AA151147 Probe #19	C 903	16	1.8	525	10	ADBS5684	Adbs5684 Toxicity-
831	16	1.8	374	4	ABx37382	Abx37382 Probe #15	C 904	16	1.8	529	10	ACH71556	Ach71556 Human sec
832	16	1.8	374	4	AAK45194	AAK45194 Human bon	C 905	16	1.8	530	12	ACH71556	Ach71556 Human gen
833	16	1.8	374	4	AAK19226	AAK19226 Human bra	C 906	16	1.8	533	10	ABX57454	Abx57454 Arabidops
834	16	1.8	374	4	ABx44866	Abx44866 Human liv	C 907	16	1.8	535	6	ABx69544	Abx69544 Novel mur
C 835	16	1.8	374	4	ABx19444	Abx19444 Human gen	C 908	16	1.8	535	12	ACH68059	Ach68059 Human gen
C 836	16	1.8	375	13	ADT44415	Adt44415 Bacterial	C 909	16	1.8	537	11	ABD17566	Abd17566 Pseudomon
C 837	16	1.8	383	6	ABx88199	Abx88199 Human col	C 910	16	1.8	538	5	AD169273	Ad169273 Human ova
C 838	16	1.8	391	8	ABx35794	Abx35794 Bovine ES	C 911	16	1.8	538	5	AD175619	Ad175619 Human ova
C 839	16	1.8	393	4	AA110228	AA110228 Human bre	C 912	16	1.8	538	12	ACH70226	Ach70226 Human gen
C 840	16	1.8	399	12	ADP93186	Adp93186 Cotton ex	C 913	16	1.8	540	12	ADM80058	Adm80058 Spirampci
C 841	16	1.8	400	5	ABV33317	Abv33317 Human pro	C 914	16	1.8	540	12	ADN97574	Adn97574 S ambotac
C 842	16	1.8	400	5	ABV42240	Abv42240 Human pro	C 915	16	1.8	544	13	ADS18530	Ads18530 Human MRP
C 843	16	1.8	400	8	ABx40316	Abx40316 Bovine ES	C 916	16	1.8	545	12	ACH78377	Ach78377 Human gen
C 844	16	1.8	410	5	AAx67584	AAx67584 Novel hum	C 917	16	1.8	545	11	ABD12467	Abd12467 Pseudomon
C 845	16	1.8	412	4	AAx527086	AAx527086 CDNA encd	C 918	16	1.8	552	12	ACH89579	Ach89579 Human gen
C 846	16	1.8	412	4	AAK58371	AAK58371 Human lim	C 919	16	1.8	553	4	AAx44710	Aax44710 Human ful
C 847	16	1.8	412	10	ABx43490	Abx43490 DNA encd	C 920	16	1.8	555	12	ACH67155	Ach67155 Human gen
C 848	16	1.8	412	10	ADB93264	Adb93264 Human CDN	C 921	16	1.8	556	4	AA117849	AA117849 Probe #77
C 849	16	1.8	412	12	AD153877	Ad153877 CDNA encd	C 922	16	1.8	556	4	ABA62804	Abx62804 Human foe
C 850	16	1.8	417	10	ADH28961	Adh28961 Human chr	C 923	16	1.8	556	4	AA142820	AA142820 Probe #11
C 851	16	1.8	423	4	AAK57725	AAK57725 Human lim	C 924	16	1.8	556	4	ABA30094	Abx30094 Probe #85
C 852	16	1.8	423	3	ACH14533	Ach14533 Human adu	C 925	16	1.8	556	4	AAK17007	AAK17007 Human bon
C 853	16	1.8	424	3	AAC02693	Aac02693 Human sec	C 926	16	1.8	556	4	AAK11204	AAK11204 Human bra
C 854	16	1.8	424	3	AAA89681	AAA89681 Mouse Exo	C 927	16	1.8	556	4	ABx36689	Abx36689 Human liv
C 855	16	1.8	426	3	AAA89682	AAA89682 Mouse Exo	C 928	16	1.8	559	13	ADS62161	Ads62161 Bacterial
C 856	16	1.8	429	6	AB189486	Ab189486 Human pol	C 929	16	1.8	560	10	ADJ72426	Adj72426 DNA Seq I
C 857	16	1.8	429	6	ABx48348	Abx48348 Bovine ES	C 930	16	1.8	561	10	ADJ92290	Adj92290 Mouse hai
C 858	16	1.8	442	5	ABV12172	Abv12172 Human pro	C 931	16	1.8	562	6	ABO56954	Abx56954 Human col
C 859	16	1.8	444	8	ABx41536	Abx41536 Bovine ES	C 932	16	1.8	563	10	ACD94817	AcD94817 Human col
C 860	16	1.8	444	11	ABD00840	ABD00840 K1ebs1e11	C 933	16	1.8	564	5	ADL40855	Adl40855 Human ova
C 861	16	1.8	447	5	ADL38910	Adl38910 Human ova	C 934	16	1.8	566	4	AAx27472	AAx27472 CDNA encd
C 862	16	1.8	450	3	AAC02173	Aac02173 Human sec	C 935	16	1.8	566	10	ADB93650	Adb93650 Human CDN
C 863	16	1.8	454	3	AAc41478	Aac41478 Zee maye	C 936	16	1.8	566	10	ABT40376	ABT40376 Toxicity
C 864	16	1.8	455	3	ABV46106	Abv46106 Human pro	C 937	16	1.8	566	12	ACH70093	Ach70093 Human gen
C 865	16	1.8	456	6	ABx45904	Abx45904 CDNA encd	C 938	16	1.8	566	12	ACH69990	Ach69990 Human gen
C 866	16	1.8	459	9	ACH27308	Ach27308 Human adu	C 939	16	1.8	567	3	AAx08041	Aax08041 Fusarim
C 867	16	1.8	462	5	AAx87821	AAx87821 DNA encd	C 940	16	1.8	569	4	AA118832	AA118832 Probe #87
C 868	16	1.8	462	5	AAx03003	AAx03003 Human pro	C 941	16	1.8	569	4	ABA63830	Abx63830 Human foe
C 869	16	1.8	465	5	AAx74705	AAx74705 DNA encd	C 942	16	1.8	569	4	AA143955	AA143955 Probe #12
C 870	16	1.8	465	8	ABx00879	ABx00879 Somacosta	C 943	16	1.8	569	4	ABx31011	Abx31011 Probe #94
C 871	16	1.8	465	10	ABx258928	ABx258928 Human som	C 944	16	1.8	569	4	AAK38060	AAK38060 Human bon
C 872	16	1.8	468	6	ABx45064	ABx45064 CDNA encd	C 945	16	1.8	569	4	AAK12341	AAK12341 Human bra
C 873	16	1.8	468	6	ABN73893	Abn73893 Bovine em	C 946	16	1.8	569	6	ABx12067	ABx12067 Human gen
C 874	16	1.8	468	9	ACH12973	Ach12973 Human adu	C 947	16	1.8	571	10	ABx56935	ABx56935 Arabidops
C 875	16	1.8	469	9	ACH16876	Ach16876 Human adu	C 948	16	1.8	573	11	ACH91587	Ach91587 Pseudomon
C 876	16	1.8	471	6	AB193396	Ab193396 Arabidops	C 949	16	1.8	573	12	ACH77412	Ach77412 Human gen
C 877	16	1.8	471	6	ACH35175	Ach35175 Human end	C 950	16	1.8	578	12	ACH77412	Ach77412 Human gen
C 878	16	1.8	471	9	ACH36314	Ach36314 Human end	C 951	16	1.8	579	11	ABD02989	ABD02989 Pseudomon
C 879	16	1.8	471	11	ABD17275	ABD17275 Pseudomon	C 952	16	1.8	579	11	ABD07528	ABD07528 Pseudomon
C 880	16	1.8	473	4	AAx26332	AAx26332 Human cdn	C 953	16	1.8	580	5	ABV58878	ABV58878 Human pro
C 881	16	1.8	473	8	ABx73673	ABx73673 Human nov	C 954	16	1.8	580	4	ABx59977	ABx59977 Human foe
C 882	16	1.8	474	9	ACH32532	Ach32532 Human end	C 955	16	1.8	583	4	AA139650	AA139650 Probe #85
C 883	16	1.8	474	12	ACH83927	Ach83927 Human gen	C 956	16	1.8	583	4	AAK34127	AAK34127 Human bon
C 884	16	1.8	475	9	ACH43718	Ach43718 Human foe	C 957	16	1.8	583	4	AAK08248	AAK08248 Human bra
C 885	16	1.8	477	12	ADJ44735	Adj44735 Plant CDN	C 958	16	1.8	583	3	ABx31925	ABx31925 Human liv
C 886	16	1.8	478	4	AAx98682	AAx98682 Human EST	C 959	16	1.8	583	6	ABx08891	ABx08891 Human gen
C 887	16	1.8	484	9	ACH39852	Ach39852 Human foe	C 960	16	1.8	584	3	AAx09173	AAx09173 Human pen
C 888	16	1.8	486	9	AAx05720	AAx05720 Human sec	C 961	16	1.8	585	11	ABD06024	ABD06024 Pseudomon
C 889	16	1.8	486	11	ACH99971	Ach99971 K1ebs1e11	C 962	16	1.8	587	6	ABx62827	ABx62827 Rat seque
C 890	16	1.8	490	9	ACH44274	Ach44274 Human foe	C 963	16	1.8	587	10	ADBS6789	ADBS6789 Toxicity-
C 891	16	1.8	492	11	ABD16297	ABD16297 Pseudomon	C 964	16	1.8	587	12	ACH69640	Ach69640 Human gen
C 892	16	1.8	500	6	ABN62652	ABN62652 Human can	C 965	16	1.8	587	12	ADP72121	ADP72121 Renal tox
C 893	16	1.8	505	10	ADBS1554	ADBS1554 Arabidops	C 966	16	1.8	588	4	AAx31178	AAx31178 Human dia
C 894	16	1.8	506	2	AAV02884	AAV02884 Human HMG	C 967	16	1.8	588	6	ABx71795	ABx71795 Human dit
C 895	16	1.8	507	6	ABT07257	ABT07257 Human CpG	C 968	16	1.8	591	11	ABD08032	ABD08032 Pseudomon
C 896	16	1.8	507	11	ABD05999	ABD05999 Pseudomon	C 969	16	1.8	591	13	ADQ51836	ADQ51836 Novel can

C 970	16	1.8	592	3	AAFI1381	Aafi1381 Aspergill1
971	16	1.8	593	5	AA505448	Aa505448 Mammalian
972	16	1.8	597	5	AAH78212	Aah78212 Nucleoid
973	16	1.8	597	5	AA505467	Aa505467 Mammalian
974	16	1.8	597	5	ABT23375	Abt23375 Breast ca
975	16	1.8	598	13	ACN53714	Acn53714 Coton an
976	16	1.8	601	10	ADK58253	Adk58253 Plant DNA
977	16	1.8	603	6	ADQ57137	Adq57137 Human col
978	16	1.8	603	13	ADQ56284	Adq56284 Novel can
979	16	1.8	606	2	AAV71928	Aav71928 MOR1 iso
980	16	1.8	606	2	AAV71929	Aav71929 MOR1 iso
981	16	1.8	606	6	ADQ54671	Adq54671 Human ova
982	16	1.8	606	10	ADK5837	Adk5837 Plant DNA
983	16	1.8	607	10	ADB49764	Adb49764 Primary r
984	16	1.8	607	13	ADQ57026	Adq57026 Novel can
C 985	16	1.8	608	10	ADK55977	Adk55977 Plant DNA
986	16	1.8	609	13	ADQ53001	Adq53001 Novel can
C 987	16	1.8	609	13	ADT44525	Adt44525 Bacterial
988	16	1.8	611	10	ADD1687	Add1687 DNA (Seqi
C 989	16	1.8	611	10	AAQ91084	Aaq91084 Human her
990	16	1.8	615	2	AAH22905	Aah22905 Codon opt
991	16	1.8	615	10	ADK41226	Adk41226 CHO expre
C 992	16	1.8	615	11	ABD17930	Abd17930 Pseudomon
C 993	16	1.8	621	4	AAH06272	Aah06272 Human CDN
C 994	16	1.8	622	10	ADCT2543	Adc72543 DNA Seq I
995	16	1.8	624	11	ABD05800	Abd05800 Pseudomon
996	16	1.8	626	10	ADD16690	Add16690 DNA (Seqi
997	16	1.8	627	2	AAV71930	Aav71930 MOR1 iso
998	16	1.8	635	13	ADQ79142	Adq79142 Novel can
999	16	1.8	636	11	ABD06775	Abd06775 Pseudomon
C1000	16	1.8	639	11	ABD14656	Abd14656 Pseudomon

## ALIGNMENTS

RESULT 1  
AAF27407  
ID AAF27407 standard; cDNA; 909 BP.

XX AAF27407;

DT 24-APR-2001 (first entry)

XX Human apoptosis-associated factor NT2RM1000558 partial cDNA, SEQ ID NO:1.

DE Human apoptosis-associated factor; NT2RM1000558; death effector domain;

KW DEB; Caspase family cleavage domain; pro-apoptotic; drug screening;

KM cell proliferation; ischemic disease; chronic viral disease; ss.

XX Homo sapiens.

OS

XX WO200104300-A1.

PN

XX 18-JAN-2001.

PD

XX 06-JUL-2000; 2000WO-JP004516.

XX 08-JUL-1999; 99JP-00194179.

XX 18-OCT-1999; 99US-0159566P.

XX (HELI-) HELIX RES INST.

XX Oca T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;

XX WPI: 2001-1138348/14.

XX P-PSDB; AAB60386.

XX Polynucleotide encoding an apoptosis-associated factor protein with death

PT effector domain and caspase family-cleavage domain, useful in regulating

XX diseases with cell proliferation.

PS Claim 1; Page 41-43; 53pp; Japanese.

XX The invention relates to a novel human apoptosis-associated factor  
CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death  
CC effector domain (DED) and a caspase family cleavage domain and is capable  
CC of inducing apoptosis in cells. The invention also relates to nucleic  
CC acids encoding the protein (AAF27407, AAF27408); variants of the protein  
CC (particularly dominant negative variants); vectors and host cells  
CC comprising a nucleic acid which encodes an apoptosis-associated factor  
CC of the invention; the recombinant production of the protein; an antibody  
CC against the protein; and methods of screening for compounds which can  
CC regulate apoptosis. The apoptosis-related factor is useful in regulating  
CC diseases associated with cell proliferation and in screening drug  
CC candidates e.g., for regulating cell proliferation or cell death in  
CC ischaemic diseases and chronic viral diseases. The present sequence  
CC represents cDNA encoding a substantial proportion of the human apoptosis-  
CC associated factor NT2RM1000558

Sequence 909 BP; 139 A; 284 C; 332 G; 154 T; 0 U; 0 Other;

Query Match 100.0%; Score 909; DB 5; Length 909;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCGCTATCGGCTGACCCCGCCGCTGCGAGAGATGAGTCTGACTAC	60
DB	1	ATGCGCTATCGGCTGACCCCGCCGCTGCGAGAGATGAGTCTGACTAC	60
QY	61	TACGGAGTCTGCTTCAACCGATGTTGAGGTGGGCGGCACTGACCGAGTGC	120
DB	61	TACGGAGTCTGCTTCAACCGATGTTGAGGTGGGCGGCACTGACCGAGTGC	120
QY	121	GAGCTGAGCTCTGAGCTTCTGCTGATGAGCTCTGAGCGCGCGAGGCTTAC	180
DB	121	GAGCTGAGCTCTGAGCTTCTGCTGATGAGCTCTGAGCGCGCGAGGCTTAC	180
QY	181	CGGCGCCGACCGGCTTCTGCTGAGCTGAGCGCGCGGCTGAGCGCGGCTGAG	240
DB	181	CGGCGCCGACCGGCTTCTGCTGAGCTGAGCGCGCGGCTGAGCGCGGCTGAG	240
QY	241	AGCAACCTGCGGCTGCTGAGGCACTCTGAGCGGCTGAGCGCGGCTGAGCGG	300
DB	241	AGCAACCTGCGGCTGCTGAGGCACTCTGAGCGGCTGAGCGCGGCTGAGCGG	300
QY	301	CACCTGCGGCGCAAGCGCGCGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG	360
DB	301	CACCTGCGGCGCAAGCGCGCGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG	360
QY	361	AGCTCTTCAAG	420
DB	361	AGCTCTTCAAG	420
QY	421	AATCTCAG	480
DB	421	AATCTCAG	480
QY	481	CGGCGCGCGCGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540
DB	481	CGGCGCGCGCGCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540
QY	541	CAGCAGTCAAG	600
DB	541	CAGCAGTCAAG	600
QY	601	CGGCTTGAAG	660
DB	601	CGGCTTGAAG	660
QY	661	CGGCGCGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
DB	661	CGGCGCGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	720
QY	721	TCAAGGAGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780
DB	721	TCAAGGAGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	780



Db 721 TCAAGGACCTGGCTGTGTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780  
Qy 781 GCTTCTGGGGGAGTACTGATGTCGCGCCCTGTCGAGAGCCCTGCGGCGCTGTTCTCG 840  
Db 781 GCTTCTGGGGGAGTACTGATGTCGCGCCCTGTCGAGAGCCCTGCGGCGCTGTTCTCG 840  
Qy 841 ACTGAGGCTTCGAGAGGCTGTGGGCGGAGGCTGTCGCTGCTGTCAGTGTGAT 900  
Db 841 ACTGAGGCTTCGAGAGGCTGTGGGCGGAGGCTGTCGCTGCTGTCAGTGTGAT 900  
Qy 901 GAGGCTGAC 909  
Db 901 GAGGCTGAC 909  
RESULT 2  
ID AAF27408 standard; cDNA; 1883 BP.  
AC AAF27408;  
XX 24-APR-2001 (first entry)  
DT Human apoptosis-associated factor NT3RM1000558 cDNA, SEQ ID NO:3.  
DE Human apoptosis-associated factor; NT3RM1000558; death effector domain;  
KW DBD; caspase family cleavage domain; pro-apoptotic; drug screening;  
KM cell proliferation; ischemic disease; chronic viral disease; ss.  
XX Homo sapiens.  
OS  
XX MO200104300-A1.  
PN 18-JAN-2001.  
XX 06-JUL-2000; 2000MO-JP004516.  
PF 08-JUL-1999; 99JUP-00194179.  
PR 18-OCT-1999; 99JUP-01595862.  
XX (HELI-) HELIX RES INST.  
PA Ota T, Isegai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;  
PI WPI, 2001-138348/14.  
DR P-PDB; AAB60387.  
XX Polynucleotide encoding an apoptosis-associated factor protein with death  
PT effector domain and caspase family-cleavage domain, useful in regulating  
PT diseases with cell proliferation.  
XX  
PS Claim 3; Page 44-47; 53pp; Japanese.  
XX  
XX The invention relates to a novel human apoptosis-associated factor  
CC (AAB60386, AAB60387), designated NT3RM1000558, which contains a death  
CC effector domain (DED) and a caspase family cleavage domain and is capable  
CC of inducing apoptosis in cells. The invention also relates to nucleic  
CC acids encoding the protein (AA27407, AA27408); variants of the protein  
CC (particularly dominant negative variants); vectors and host cells  
CC comprising a nucleic acid which encodes an apoptosis-associated factor  
CC of the invention; the recombinant production of the protein; an antibody  
CC against the protein; and methods of screening for compounds which can  
CC regulate apoptosis. The apoptosis-related factor is useful in regulating  
CC diseases associated with cell proliferation and in screening drug  
CC candidates e.g., for regulating cell proliferation or cell death in  
CC ischemic diseases and chronic viral diseases. The present sequence  
CC represents a full-length cDNA encoding the human apoptosis-associated  
CC factor NT3RM1000558  
XX  
SQ Sequence 1883 BP; 343 A; 595 C; 588 G; 357 T; 0 U; 0 Other;  
Query Match 100.0%; Score 909; DB 5; Length 1883;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCGCATCCGGGTGACCCCGGCGCGCTGCTGGAGAGAGATGATGCTGACATAC 60  
Db 124 ATGGCGCATCCGGGTGACCCCGGCGCGCTGCTGGAGAGAGATGATGCTGACATAC 183  
Qy 61 TACGGAGTCTGTGCTTCACTGATGTTGAGAGTGTGGCGGCAATGACCAAGTGC 120  
Db 184 TACGGAGTCTGTGCTTCACTGATGTTGAGAGTGTGGCGGCAATGACCAAGTGC 243  
Qy 121 GAGCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
Db 244 GAGCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303  
Qy 181 CGGGCCCGAGCGGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 304 CGGGCCCGAGCGGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363  
Qy 241 AGCAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Db 364 AGCAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423  
Qy 301 CACTGCGCGGAGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
Db 424 CACTGCGCGGAGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 483  
Qy 361 AGCTTTTAAAGAGACAGAGGTAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
Db 484 AGCTTTTAAAGAGACAGAGGTAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543  
Qy 421 AATTCTCAGACAGGCTCAGTGGAGACAGAGCTTCCCGCAACCAACGAGCGGCGAGT 480  
Db 544 AATTCTCAGACAGGCTCAGTGGAGACAGAGCTTCCCGCAACCAACGAGCGGCGAGT 603  
Qy 481 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 604 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663  
Qy 541 CAGCAGTCAAGAGCCCGCAGACCTTCTGTAAGGCAAGTGAAGTGAAGTGAAGTGA 600  
Db 664 CAGCAGTCAAGAGCCCGCAGACCTTCTGTAAGGCAAGTGAAGTGAAGTGAAGTGA 723  
Qy 601 CGGGTTCAGACAGAGTACTGTCAGAGATGAGCCAGCTTGGAGCAGAGCGGCTGATC 660  
Db 724 CGGGTTCAGACAGAGTACTGTCAGAGATGAGCCAGCTTGGAGCAGAGCGGCTGATC 783  
Qy 661 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 784 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843  
Qy 721 TCAAGGACCTGGCTGTGTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780  
Db 844 TCAAGGACCTGGCTGTGTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 903  
Qy 781 GCTTCTGGGGGAGTACTGATGTCGCGCCCTGTCGAGAGCCCTGCGGCGCTGTTCTCG 840  
Db 904 GCTTCTGGGGGAGTACTGATGTCGCGCCCTGTCGAGAGCCCTGCGGCGCTGTTCTCG 963  
Qy 841 ACTGAGGCTTCGAGAGGCTGTGGGCGGAGGCTGTCGCTGCTGTCAGTGTGAT 900  
Db 964 ACTGAGGCTTCGAGAGGCTGTGGGCGGAGGCTGTCGCTGCTGTCAGTGTGAT 1023  
Qy 901 GAGGCTGAC 909  
Db 1024 GAGGCTGAC 1032  
RESULT 3  
ID ADC79259 standard; cDNA; 981 BP.  
AC ADC79259;  
XX ADC79259;  
XX



DT 01-JAN-2004 (first entry)

XX Human DEDD2 encoding cDNA SEQ ID NO:1.

XX human; death effector domains containing DNA-binding protein;

XX DED-containing DNA-binding protein; DEDD2; cell death; gene therapy;

KW cytostatic; cancer; chronic myeloid leukaemia; gene; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 1..981

FT /tag= a

FT /product= "DEDD2"

XX MO2003054195-A1.

XX 03-JUL-2003.

XX 20-DEC-2002; 2002MO-JP013371.

XX 20-DEC-2001; 2001JP-00387854.

XX 18-JUL-2002; 2002JP-00209458.

XX (MORG ) MORINAGA MILK IND CO LTD.

XX Suzu S, Hageshita H, Nomaguchi K, Yamada M, Hayasawa H;

XX WPI; 2003-569246/53.

XX P-PSDB; ADC79260.

XX DNA encoding cell death proteins for treatment of kidney, large intestine

XX and prostate cancers and leukemia.

XX Claim 2; Page 18-20; 26pp; Japanese.

XX The present sequence encodes a human death effector domains (DED)

XX containing DNA-binding protein (DEDD) protein, designated DEDD2, that

XX causes cell death. Also described: (1) primer and probe for investigation

XX of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has

XX cytostatic activity. DEDD2 can be used in the diagnosis and treatment of

XX cancers of the kidney, large intestine and prostate, and acute and

XX chronic myeloid leukaemia.

XX Sequence 981 BP; 151 A; 303 C; 363 G; 164 T; 0 U; 0 Other;

XX

Query Match 94.4%; Score 858; DB 10; Length 981;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTGACCCCGGCGCTGCTGGAGAGAGATGAGTGCCTGACTAC 60

DB 1 ATGGCGCTATCCGGGTGACCCCGGCGCTGCTGGAGAGAGATGAGTGCCTGACTAC 60

QY 61 TACGGGAGCTGCTGCTTACCGTATGTTTCAGAGTGTGTGGGCGGCACTGACGAGTTC 120

DB 61 TACGGGAGCTGCTGCTTACCGTATGTTTCAGAGTGTGTGGGCGGCACTGACGAGTTC 120

QY 121 GAGCTGAGCTCTGCGCTTTCTGCTGATGAGGCTCTGGGCGCGGAGGCTTAGCC 180

DB 121 GAGCTGAGCTCTGCGCTTTCTGCTGATGAGGCTCTGGGCGCGGAGGCTTAGCC 180

QY 181 CGGCGCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGCGAGTGCAG 240

DB 181 CGGCGCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGCGAGTGCAG 240

QY 241 AGCAACCTGCGGCTGCTGGGCACTCTGCGCGTGTGGCGCCGCAAGACTGCTGCGG 300

DB 241 AGCAACCTGCGGCTGCTGGGCACTCTGCGCGTGTGGCGCCGCAAGACTGCTGCGG 300

QY 301 CACCTGGCGCGCAAGCGCGCGCGGCGAGTGTCTCAGAAAGCTATAGCTATGCACTCC 360

DB 301 CACCTGGCGCGCAAGCGCGCGCGGCGAGTGTCTCAGAAAGCTATAGCTATGCACTCC 360

QY 361 AGCTCTCAAGAGAGACAGAGGTAAGTCCGCTGCGCAGTCAAGAGTTCGCA 420

DB 361 AGCTCTCAAGAGAGACAGAGGTAAGTCCGCTGCGCAGTCAAGAGTTCGCA 420

QY 421 AATTTCAGCAGAGGTCAAGTGGAGACAGGCTCCCCCAACCAAGCGGAGCGGAGT 480

DB 421 AATTTCAGCAGAGGTCAAGTGGAGACAGGCTCCCCCAACCAAGCGGAGCGGAGT 480

QY 481 CGGGCGCGGCGAGTGTGTGCGAGACGGGCGGAGAGGGGCGCGACCGCAACCCAG 540

DB 481 CGGGCGCGGCGAGTGTGTGCGAGACGGGCGGAGAGGGGCGCGACCGCAACCCAG 540

QY 541 CAGCAGTCAAGACCCCGCAGACCTTCTCTGAGGCAAGTGAACCTGTGATCCGCGTC 600

DB 541 CAGCAGTCAAGACCCCGCAGACCTTCTCTGAGGCAAGTGAACCTGTGATCCGCGTC 600

QY 601 CGGGTTCAAGCAGAGTACTGCGAGCATGGGCGAGCTTGGAGCAGGGCGTGCATCCCG 660

DB 601 CGGGTTCAAGCAGAGTACTGCGAGCATGGGCGAGCTTGGAGCAGGGCGTGCATCCCG 660

QY 661 CGGCCCCAGGCGCTGGGCGGCGAGCTGGAAGTGTGGGCGAGGCCAGCGAGTGTGCGC 720

DB 661 CGGCCCCAGGCGCTGGGCGGCGAGCTGGAAGTGTGGGCGAGGCCAGCGAGTGTGCGC 720

QY 721 TCAAGGACCTGGGCTGTGTGTGTGACATCAAGTTCAGAGCTCTCTATCTGGAC 780

DB 721 TCAAGGACCTGGGCTGTGTGTGTGACATCAAGTTCAGAGCTCTCTATCTGGAC 780

QY 781 GCCTTTGGGCGGACTACTAGTGGCGGCGCTGCTGCAAGGCGCTCGGGGCGTGTCTTG 840

DB 781 GCCTTTGGGCGGACTACTAGTGGCGGCGCTGCTGCAAGGCGCTCGGGGCGTGTCTTG 840

QY 841 ACTGAGGCGCTGCGGAGGCTGTGGGCGGAGGCGTGTGCGCTGCTGATGATGAT 900

DB 841 ACTGAGGCGCTGCGGAGGCTGTGGGCGGAGGCGTGTGCGCTGCTGATGATGAT 900

QY 901 GAGGCTGAC 909

DB 901 GAGGCTGAC 909

RESULT 4

ABA94362

ID ABA94362 standard; DNA; 1230 BP.

XX

XX ABA94362;

XX

DT 26-MAR-2002 (first entry)

XX

XX Human APRG polypeptide (Incyte ID. 3102521CD1) encoding cDNA.

XX

XX APRG; apoptosis regulator; cytosstatic; antiatherosclerotic; osteopathic;

XX antiarteriosclerotic; hepatotropic; antiposrotic; antelmintic; human;

XX antiallergic; antineuric; antiaschematic; antithyroid; anti-HIV; cancer;

XX antiinflammatory; antidiabetic; antipout; nephrotropic; ophthalmological;

XX immunosuppressive; dermatological; antitumor; antineumatic; fungicide;

XX antiarthritic; antibacterial; virucide; antiparasitic; protozoicide;

XX tranquilizer; vulnerary; gynecological; vasotropic; gene therapy; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 127..1107

FT /tag= a

FT /product= "APRG polypeptide"

XX MO200192527-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001MO-US017581.

XX



PD 23-MAY-2002.  
XX 15-NOV-2001; 2001WO-US044844.  
XX 17-NOV-2000; 2000US-00715893.  
XX 29-JUN-2001; 2001US-0301889P.  
XX (BURN-) BURNHAM INST.  
XX  
XX Reed JC, Goddik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
PI Stenner-Liewen F;  
XX WPI: 2002-500222/53.  
XX P-PSDB: AAE24860.  
XX  
XX New polypeptide comprising a death domain or death effector domain,  
PT useful for discovery of drugs that suppress infection, inflammation,  
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
XX  
XX Claim 19; Page 184-186; 209pp; English.

XX The invention relates to an isolated polypeptide comprising a death  
XX domain (DD), death effector domain (DED) or NB-ARC domain. The invention  
XX is useful for identifying a binding agent, preferably a protein or a drug  
XX that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC  
XX domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or  
XX NIDD (NGFR-intersecting Death Domain), with a candidate binding agent and  
XX detecting the association of the domain and the candidate binding agent,  
XX by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or  
XX chemical crosslinking, nuclear magnetic resonance (NMR), mass  
XX spectroscopy (MS) and FPA. The invention is useful for modulating the  
XX level of a cell process such as cell proliferation, cell adhesion, cell  
XX stress responses, responses to microbial infection and B cell  
XX immunoglobulin class switching, in particular apoptosis within a cell.  
XX Antibody specifically reactive with CTDD DD of C. trachomatis, C.  
XX muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the  
XX CTDD DD protein is useful for detecting a Chlamydia infection. The  
XX invention is useful for modulating the activity of oncogenic proteins,  
XX for treating a pathology caused by the oncogenic proteins and for  
XX treating bacterial infections by modulating the activity of bacterial  
XX proteins. The protein and antibody specific for it are useful for  
XX discovery of drugs that suppress infection, inflammation, allergy,  
XX sepsis, autoimmunity, allograft rejection and other diseases. The protein  
XX is useful for treating immune-based pathologies, pathologies associated  
XX with cell division, inflammatory diseases such as sepsis, fibrosis,  
XX arthritis, graft versus host disease. The invention is used in antisense  
XX therapy and gene therapy. The present sequence is human DED4 gene  
XX  
XX  
XX Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;

Query Match 94.4%; Score 858; DB 6; Length 1924;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCGTATCCGGGTCGACCCCGGCGTGGGAGGAGAGTGGCTGACAC 60  
DB 91 ATGGCGCTATCCGGGTCGACCCCGGCGTGGGAGGAGAGTGGCTGACAC 150  
QY 61 TACGGGATGCTGTGCTTCCACCGTATGTTTCGAGGTGTGGGCGCACTGACGAGTGC 120  
DB 151 TACGGGATGCTGTGCTTCCACCGTATGTTTCGAGGTGTGGGCGCACTGACGAGTGC 210  
QY 121 GAGCTGAGAGCTCTGCGCTTTTCTGCTGATGAGGCTCTCGGCGCCGCGAGGCTTACCC 180  
DB 211 GAGCTGAGAGCTCTGCGCTTTTCTGCTGATGAGGCTCTCGGCGCCGCGAGGCTTACCC 270  
QY 181 CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCGCAGTCCGAG 240  
DB 271 CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCGCAGTCCGAG 330  
QY 241 AGCAACTGCTGCGGCTGCTGCTGCGGCACTCTGCGCGCTGCTGCGCCGACGACTGTGCGG 300  
DB 331 AGCAACTGCTGCGGCTGCTGCTGCGGCACTCTGCGCGCTGCTGCGCCGACGACTGTGCGG 390

QY 301 CACTGCGCGCAGACGGGCGCGCGCACTGTCTCCAGAACGCTATAGTATGCACTCC 360  
DB 391 CACTGCGCGCGCAGACGGGCGCGCGCACTGTCTCCAGAACGCTATAGTATGCACTCC 450  
QY 361 AGCTCTTAAAGAGAGACAGAGGTAGTACGTCGGCTGGCGCTCGGCACTCAAGACTTCTGCA 420  
DB 451 AGCTCTTAAAGAGAGACAGAGGTAGTACGTCGGCTGGCGCTCGGCACTCAAGACTTCTGCA 510  
QY 421 AATTCTCAGCAGGGCTCAGTGGGAGACAGAGCTCCCCCAACCAAGCGGCGAGCGAGT 480  
DB 511 AATTCTCAGCAGGGCTCAGTGGGAGACAGAGCTCCCCCAACCAAGCGGCGAGCGAGT 570  
QY 481 CGGGGCGCGCGCAGTGTGTGTGTCAGACGCGCGCGAGAGGCGGCCAGCGCACCCGAG 540  
DB 571 CGGGGCGCGCGCAGTGTGTGTGTCAGACGCGCGCGAGAGGCGGCCAGCGCACCCGAG 630  
QY 541 CAGAGTGAAGACCGCGCAGACCTTCCCTGTAAGGCAAGTGAATCTGATCCGGCTC 600  
DB 631 CAGAGTGAAGACCGCGCAGACCTTCCCTGTAAGGCAAGTGAATCTGATCCGGCTC 690  
QY 601 CGGGTTGAGAGAGTACTGCGACATGAGCGCAGCTTGGAGCAGGCGGTGCAATCCCGG 660  
DB 691 CGGGTTGAGAGAGTACTGCGACATGAGCGCAGCTTGGAGCAGGCGGTGCAATCCCGG 750  
QY 661 CGGCCCCAGGCGCTGCGCGCGCAGCTGAGCGTGTGGGCGAGCCAGCGAGTCTGCGC 720  
DB 751 CGGCCCCAGGCGCTGCGCGCGCAGCTGAGCGTGTGGGCGAGCCAGCGAGTCTGCGC 810  
QY 721 TCAAGGAGACCTGGGCTGTGTGTGTTGACATCAAGTTCAGAGCTCTCTATCTGAGC 780  
DB 811 TCAAGGAGACCTGGGCTGTGTGTGTTGACATCAAGTTCAGAGCTCTCTATCTGAGC 870  
QY 781 GCTTCTGCGGCGCACTAGTGTGCGCCCTGTGTCAGGCGCTGCGGCGGTGCTCTG 840  
DB 871 GCTTCTGCGGCGCACTAGTGTGCGCCCTGTGTCAGGCGCTGCGGCGGTGCTCTG 930  
QY 841 ACTGAGGCGCTTGCAGAGAGCTGTGCGCGCGGAGGCTGTTGCTGCTGCTGATGTGAT 900  
DB 931 ACTGAGGCGCTTGCAGAGAGCTGTGCGCGCGGAGGCTGTTGCTGCTGCTGATGTGAT 990  
QY 901 GAGGCTGAC 909  
DB 991 GAGGCTGAC 999

RESULT 6  
AADS9062  
ID AADS9062 standard; cDNA; 1924 BP.

XX AADS9062;  
XX 18-DEC-2003 (first entry)  
XX  
XX Human DED4 full length gene.

XX Human, death Domain; DD; death effector domain; DED; cell proliferation;  
XX Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;  
XX neural growth factor receptor-interacting domain; cell adhesion;  
XX vasotrophic; microbial infection; inflammation; allograft rejection; CTDD;  
XX cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;  
XX apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;  
XX neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;  
XX keloid; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 91..1044

FT /tag= a

FT /product= "Human DED4 protein"

FT /note= "No stop codon"

FT /partial

```

FT misc_signal 157..222
FT /*tag= b
FT /note= "Nuclear localisation sequence"
XX
XX US2003049702-A1.
XX
XX 13-MAR-2003.
XX
XX 15-NOV-2001; 2001US-00001254.
XX
XX 17-NOV-2000; 2000US-00715893.
XX 17-NOV-2000; 2000US-0367360P.
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (REED/ REED J C.
XX (GODZ/ GODZIK A.
XX (PAWL/ PAWLOWSKI K.
XX (FIOR/ FIORENTINO L.
XX (LEBS/ LEE S H.
XX (ROTH/ ROTH W.
XX (STEN/ STENNER-LIEWEN F.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
XX Stenner-Liewen F;
XX
XX MPI; 2002-500222/53.
XX P-PsDB; AAE38903.
XX
XX New polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19; Page 42-44; 99pp; English.
XX
XX The present invention provides novel death domain (DD) and death effector
XX domain (DED) proteins and nucleic acids encoding them. The invention also
XX provides death domain containing protein such as Chlamydia trachomatis
XX death domain containing protein (CTDP) DD and neural growth factor
XX receptor-interacting death domain (NIDD) DD. The invention is useful for
XX identifying a binding agent (e.g. protein or drug) that binds a DD, DED
XX or NB-ARC domain from DAP3, IRAK4, CTDP, DED4 or NIDD with a candidate
XX binding agent and identifying an effective agent (e.g. protein or drug)
XX that modulates the association of a DD, DED or NB-ARC domain with protein
XX that binds the DD, DED or NB-ARC domain. The invention is also useful for
XX modulating the level of cell process such as apoptosis, cell adhesion,
XX cell proliferation, cell stress responses, responses to microbial
XX infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC
XX domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
XX useful for discovery of drugs that suppress infection, autoimmunity,
XX inflammation, allergy, allograft rejection, sepsis and other diseases.
XX DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
XX autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
XX hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
XX inflammatory hyperplasia and smooth muscle cell proliferation in arteries
XX following balloon angioplasty (restenosis). The invention is also used in
XX antibody therapy and gene therapy. The present sequence is human DED4
XX full length gene. The DED4 gene is located on chromosome 19
XX
XX Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;
SQ

```

```

Db 211 GAGCTGAGACTCTTGCCCTTCTGCTGATAGAGCTCTGCGCGCCGCGAGGCTTAAGCC 270
Qy 181 CGGGCCCGACCGGCTGAGACTCTGCTGAGAGAGCCCGCGGCGAGTGGCGGAG 240
Db 271 CGGGCCCGACCGGCTGAGACTCTGCTGAGAGAGCCCGCGGCGAGTGGCGGAG 330
Qy 241 AGCAACTGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 331 AGCAACTGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390
Qy 301 CACCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 391 CACCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
Qy 361 AGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 451 AGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
Qy 421 AATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 511 AATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
Qy 481 CGGGCCCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 571 CGGGCCCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
Qy 541 CAGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 631 CAGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
Qy 601 CGGGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 691 CGGGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
Qy 661 CGGGCCCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 751 CGGGCCCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
Qy 721 TCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 811 TCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
Qy 781 GCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 871 GCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
Qy 841 ACTGAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 931 ACTGAGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
Qy 901 GAGGCTGAC 909
Db 991 GAGGCTGAC 999

```

RESULT 7  
 AD086891  
 ID AD086891 standard; cDNA; 1979 BP.  
 AC AD086891;  
 XX  
 XX 07-OCT-2004 (first entry)  
 XX  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3766.  
 XX human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.  
 OS Homo sapiens.  
 XX  
 XX WO2004060270-A2.  
 XX

PD 22-JUL-2004.  
XX 15-OCT-2003; 2003WO-US029126.  
XX 18-OCT-2002; 2002US-0418988P.  
XX (GERTH ) GENENTECH INC.  
XX (WUTD/) WU T D.  
XX (ZHOU/) ZHOU Y.  
XX Wu TD, Zhou Y;  
XX WPI: 2004-534300/51.  
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
XX preventing or treating cell proliferative disorders such as cancer.  
XX Claim 1, SEQ ID NO 3766; 5504pp; English.  
XX  
XX The present invention describes an isolated tumour-associated antigenic  
XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
XX sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
XX (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
XX sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
XX (c). Also described: (1) an expression vector comprising the above  
XX nucleic acid; (2) a host cell comprising the above expression vector; (3)  
XX a process for producing a polypeptide; (4) an isolated polypeptide  
XX comprising: (a) an amino acid sequence encoded by any of the above  
XX nucleic acid sequences; (b) an amino acid sequence encoded by the full-  
XX length coding region of the above nucleotide sequences; or (c) a sequence  
XX having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
XX comprising the above polypeptide fused to a heterologous polypeptide; (6)  
XX an isolated antibody that binds to the above polypeptide; (7) a process  
XX for producing the antibody; (8) an isolated oligopeptide that binds to  
XX the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
XX binding organic molecule that binds to the above polypeptide; (10) a  
XX composition of matter comprising the above (chimeric) polypeptide,  
XX antibody, oligopeptide or TAT binding organic molecule, in combination  
XX with a carrier; (11) an article of manufacture comprising a container and  
XX the composition of matter contained within the container; (12) methods of  
XX inhibiting the growth of a cell that expresses the above protein, where  
XX the growth of the cell is at least in part dependent upon a growth  
XX potentiating effect of the above protein; (13) a method of  
XX therapeutically treating a mammal having a cancerous tumour comprising  
XX cells that express the above protein; (14) a method of determining the  
XX presence of a protein in a sample suspected of containing the protein  
XX described above; (15) methods of diagnosing the presence of a tumour in a  
XX mammal; (16) a method for treating or preventing a cell proliferative  
XX disorder associated with increased expression or activity of the above  
XX protein; and (17) a method of binding an antibody, oligopeptide or  
XX organic molecule to a cell that expresses the protein described above.  
XX The TAT sequences have cytostatic activities, and can be used in gene  
XX therapy. The composition and methods are useful for diagnosing,  
XX preventing or treating cancer. The composition is also used for preparing  
XX a medicament for the therapeutic treatment or diagnostic detection of a  
XX cell proliferative disorder or cancer. The present sequence represents a  
XX human TAT CDNA sequence from the present invention.  
XX  
XX Sequence 1979 BP; 365 A; 617 C; 627 G; 370 T; 0 U; 0 Other;  
XX  
XX Query Match 94.4%; Score 858; DB 12; Length 1979;  
XX Best Local Similarity 99.9%; Pred. No. 0;  
XX Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGGGCTATCGGATCGACCCCGGCGCTGGGAGAGAGATGCTGAGTAC 60  
DB 161 ATGGGCTATCGGATCGACCCCGGCGCTGGGAGAGAGATGCTGAGTAC 220  
QY 61 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGTGGCGGCAACGACGATGC 120  
DB 221 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGTGGCGGCAACGACGATGC 280  
QY 121 GAGCTGAGAGCTCTGCGCTTTCTGCTGATGAGGCTCTCGGCGCCGCGAGGCTTAGCC 180

DB 281 GAGCTGAGAGCTCTGCGCTTTCTGCTGATAGAGGCTCTGCGCGCCGAGGCTTAGCC 340  
QY 181 CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGAGTGAAGCCCGCGGCGAGTGCAGAG 240  
DB 341 CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGAGTGAAGCCCGCGGCGAGTGCAGAG 400  
QY 241 AGCAACCTGCGGCTGCTGCGGCAACTCTGCGCGTGTGAGCCCGCAGACCTGTCGCG 300  
DB 401 AGCAACCTGCGGCTGCTGCGGCAACTCTGCGCGTGTGAGCCCGCAGACCTGTCGCG 460  
QY 301 CACCTGCGCGCAAGCGGCGCGGCGCACTGCTCCAGAACGCTATAGTACCTCC 360  
DB 461 CACCTGCGCGCAAGCGGCGCGGCGCACTGCTCCAGAACGCTATAGTACCTCC 520  
QY 361 AGCTTTTAAAGAGAGACAGAGGATAGTCCGCTGCGCGCTCGGAGTCAAGAGTTCGCA 420  
DB 521 AGCTTTTAAAGAGAGACAGAGGATAGTCCGCTGCGCGCTCGGAGTCAAGAGTTCGCA 580  
QY 421 AATTCTGAGCAGGCTCACTGAGAGACAGGCTCCCGCCCAACCAAGCGGCGAGT 480  
DB 581 AATTCTGAGCAGGCTCACTGAGAGACAGGCTCCCGCCCAACCAAGCGGCGAGT 640  
QY 481 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 641 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 700  
QY 541 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAGGCAAAAGTCACTGATCATCCGCTC 600  
DB 701 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAGGCAAAAGTCACTGATCATCCGCTC 760  
QY 601 CGGGTTCAGAGAGTACTGAGAGATGAGGCACTGCTTGAAGAGAGGCGTGCATCCCGG 660  
DB 761 CGGGTTCAGAGAGTACTGAGAGATGAGGCACTGCTTGAAGAGAGGCGTGCATCCCGG 820  
QY 661 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
DB 821 CGGGCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 880  
QY 721 TCAAGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
DB 881 TCAAGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940  
QY 781 GCTTTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 941 GCTTTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000  
QY 841 ACTGAGGCTTGCAGAGAGGCTGTGGGCGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTG 900  
DB 1001 ACTGAGGCTTGCAGAGAGGCTGTGGGCGGAGGCTGTGCTGCTGCTGCTGCTGCTGCTG 1060  
QY 901 GAGGCTGAC 909  
DB 1061 GAGGCTGAC 1069  
XX  
XX RESULT 8  
XX ID AAA95790 standard; cDNA; 2045 BP.  
XX AAA95790;  
XX 28-FEB-2001 (first entry)  
XX  
XX Apoptosis related gene 1 clone H1DOK36.  
XX  
XX Cytostatic; antiinflammatory; immunosuppressive; antiisclerotic; cardiant;  
XX vitrucidal; anti-AIDS; vasotrophic; anti-ischaemic; antiparkinsonian; B6;  
XX anti-Alzheimer; gene therapy; human; apoptosis; fusion protein; cancer;  
XX colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;  
XX autoimmune disorder; multiple sclerosis; viral infection.  
XX  
XX Homo sapiens.  
XX OS

XX W020056752-A2.  
 XX 28-SEP-2000.  
 XX 15-MAR-2000; 2000WO-US006642.  
 XX 24-MAR-1999; 99US-0126018P.  
 XX 17-JUN-1999; 99US-0139638P.  
 XX 18-AUG-1999; 99US-0149449P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Ruben SM, Ni J, Young PA;  
 XX WPI, 2000-587660/55.  
 XX P-PSDB; AAB15551.  
 DR Nucleic acids encoding human apoptosis associated protein, useful for the  
 PT prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's  
 PT disease, inflammation and ischemic injury.  
 PS Claim 1; Page 244-245; 273pp; English.

CC The invention relates to the isolation of genes encoding 9 human  
 CC apoptosis-related proteins. The nucleotide sequences AAB95790-A95798  
 CC encode the human apoptosis related proteins AAB15551-B15559. The genes  
 CC can be used to generate fusion proteins by linking to the gene for the  
 CC human immunoglobulin G Fc (199 Fc) portion (AAB95799) for increasing the  
 CC stability of the fusion protein as compared to the human protein only.  
 CC The gene and encoded protein may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate apoptosis associated  
 CC protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,  
 CC melanomas and lymphomas), inflammation, autoimmune disorders (e.g.  
 CC multiple sclerosis) and viral infections (e.g. herpes)

CC Sequence 2045 BP; 457 A; 620 C; 604 G; 364 T; 0 U; 0 Other;

Query Match 94.4%; Score 858; DB 3; Length 2045;

Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGCGCTATCCGCGGTGACCCCGGCGCTGCTGGAGAGAGATGATGCTGACATAC 60  
 DB 121 ATGCGCTATCCGCGGTGACCCCGGCGCTGCTGGAGAGAGATGATGCTGACATAC 180  
 QY 61 TACGGGATCTGTGCTTCAACCGTATGTTGAGCTGTGGCGCGCACTGACCGATGC 120  
 DB 181 TACGGGATCTGTGCTTCAACCGTATGTTGAGCTGTGGCGCGCACTGACCGATGC 240  
 QY 121 GAGCTGAGACTCTGCGCTTTTGTGCTGATGAGAGCTCTGGGCGCGCGGAGGCTTAC 180  
 DB 241 GAGCTGAGACTCTGCGCTTTTGTGCTGATGAGAGCTCTGGGCGCGCGGAGGCTTAC 300  
 QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGAGTGGCGGAG 240  
 DB 301 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGAGTGGCGGAG 360  
 QY 241 AGCAACTGTGCTGTGGGCAATCTCTGCGCTGTGGCGCGGAGGCTTACCGG 300  
 DB 361 AGCAACTGTGCTGTGGGCAATCTCTGCGCTGTGGCGCGGAGGCTTACCGG 420  
 QY 301 CACCTGGCGGCAAGGCGCGCGCGGAGGCTCTCAAGACGATAGCTATGACATCC 360  
 DB 421 CACCTGGCGGCAAGGCGCGCGCGGAGGCTCTCAAGACGATAGCTATGACATCC 480  
 QY 361 AGCTTTCAAGAGAGCAGAGGATGCTGCTGTGCGCTGTGCGAGTCAAGCACTTCTGA 420  
 DB 481 AGCTTTCAAGAGAGCAGAGGATGCTGCTGTGCGCTGTGCGAGTCAAGCACTTCTGA 540  
 QY 421 AATTTTCAGAGAGGTCAGTGGAGAGACAGGCTCCCGCCCAACCAAGGCGGAGGAGT 480  
 DB 541 AATTTTCAGAGAGGTCAGTGGAGAGACAGGCTCCCGCCCAACCAAGGCGGAGGAGT 600

QY 481 CGGGCCCGGAGCGGCTGAGTGTGCTCAGACGAGCGGCGGAGAGGAGGCCCCAGCGCACCCGAG 540  
 DB 601 CGGGCCCGGAGCGGCTGAGTGTGCTCAGACGAGCGGCGGAGAGGAGGCCCCAGCGCACCCGAG 660  
 QY 541 CAGCAGTACAGAGCCCGGAGACCTTCTCTGAAAGCAAGTGAACCTGTGACATCCGGCTC 600  
 DB 661 CAGCAGTACAGAGCCCGGAGACCTTCTCTGAAAGCAAGTGAACCTGTGACATCCGGCTC 720  
 QY 601 CGGGTTTCAGAGAGTACTGTGAGAGATAGGCGCCAGGCTTGAGAGAGGCGTGCATCCGG 660  
 DB 721 CGGGTTTCAGAGAGTACTGTGAGAGATAGGCGCCAGGCTTGAGAGAGGCGTGCATCCGG 780  
 QY 661 CGGGCCCGGAGCGGCTGAGGCGGAGGCTGAGACGCTGTTGGGACAGGCCAGTGTGCGC 720  
 DB 781 CGGGCCCGGAGCGGCTGAGGCGGAGGCTGAGACGCTGTTGGGACAGGCCAGTGTGCGC 840  
 QY 721 TCAGAGGACCTGAGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780  
 DB 841 TCAGAGGACCTGAGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 900  
 QY 781 GCTTCTGAGGAGACTTACCTGAGTGGCGCCCTGCTGACAGGCCCTGCGGGCGGTTCCTG 840  
 DB 901 GCTTCTGAGGAGACTTACCTGAGTGGCGCCCTGCTGACAGGCCCTGCGGGCGGTTCCTG 960  
 QY 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGATGTGAT 900  
 DB 961 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGATGTGAT 1020  
 QY 901 GAGGCTGAC 909  
 DB 1021 GAGGCTGAC 1029

RESULT 9  
 AAH33283  
 ID AAH33283 standard; cDNA; 2045 BP.

XX AAH33283;

XX 03-SEP-2001 (first entry)

DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.

KM Human; colon cancer; colon cancer antigen; diagnosis; detection;

KM colorectal carcinoma; ss.

OS Homo sapiens.

PN W0200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US026524.

XX 29-SEP-1999; 99US-0157137P.

PR 03-NOV-1999; 99US-0163280P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX WPI, 2001-235357/24.

DR P-PSDB; AAG73852.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers.

PS Claim 1; Page 2451; 9803pp; English.

CC AAH33943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
 CC proteins are collectively known as colon cancer antigens. The colon







Query Match	84.5%	Score 768;	DB 3;	Length 2044;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 818; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	ATGGGCGCTATCCGGGATCGAACCCCGGCGCCGGTCTGGGAGAGAGATATGATGCTCGACCTAC	60
Dp	121	ATGGGCGCTATCCGGGATCGAACCCCGGCGCCGGTCTGGGAGAGAGATATGATGCTCGACCTAC	180
QY	61	TACGGGATGCTGTGCTTCCTACCGTATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC	120
Dp	181	TACGGGATGCTGTGCTTCCTACCGTATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC	240
QY	121	GAGCTGGAGCTCCCTGGCCCTTTTGTGCTGGAATGAGCGCTCTGGGCGCCGCGCGAGCTTAAGC	180
Dp	241	GAGCTGGAGCTCTGAGCCTTTTGTGCTGGAATGAGCGCTCTGGGCGCCGCGAGCTTAAGC	300
QY	181	CGGGCCCCAGCGGCGCTAGAGCTCTGCTGGAGCTTGAAGCGCGCGGGAGATGTCGGCGAG	240
Dp	301	CGGGCCCCAGCGGCGCTAGAGCTCTGCTGGAGCTTGAAGCGCGCGGGAGATGTCGAAGAG	360
QY	241	AGCAACTGTGGCTGTGGGGGCAACTCTGTGGCGGTGCTGGCCGCGCACTGTGTCCG	300
Dp	361	AGCAACTGTGGCTGTGGGGGCAACTCTGTGGCGGTGCTGGCCGCGCACTGTGTCCG	420
QY	301	CACCTGGGCGCGCAACCGGGCGCGGCGCAAGTGTCTCCAGAAAGCTATAGCTATGCGACCTCC	360
Dp	421	CACCTGGGCGCGCAACCGGGCGCGGCGCAAGTGTCTCCAGAAAGCTATAGCTATGCGACCTCC	480
QY	361	AGCTTTCAAAAGAGGACAGAGGGGTAGCTCCGTGCGCGTCTGGGAGTCAAGCAGTTCTGCA	420
Dp	481	AGCTTTCAAAAGAGGACAGAGGGGTAGCTCCGTGCGCGTCTGGGAGTCAAGCAGTTCTGCA	540
QY	421	AATTTCTCAGCAGGGGTCAGTGGGAGACAGGCTCCCGCCCAACCAAGCGCGCGCGAGT	480
Dp	541	AATTTCTCAGCAGGGGTCAGTGGGAGACAGGCTCCCGCCCAACCAAGCGCGCGCGAGT	600
QY	481	CGGGGCGGGCCCAAGTGTGTGTGTCGAGCGGCGCGGAGAGGGGCCCCAGCGCGCACCCGAG	540
Dp	601	CGGGGCGGGCCCAAGTGTGTGTGTCGAGCGGCGCGGAGAGGGGCCCCAGCGCGCACCCGAG	660
QY	541	CAGCAGTCAGAGCCCGGCCAGACCTTCTCTGAAAGCAAAAGTGACTTGTGACATCCGGCTTC	600
Dp	661	CAGCAGTCAGAGCCCGGCCAGACCTTCTCTGAAAGCAAAAGTGACTTGTGACATCCGGCTTC	720
QY	601	CGGGTTTCGAGCAGAGTACTGCGACATGTGGGCCAGCTTGGAGCAGGGCGTGTGACATCCCG	660
Dp	721	CGGGTTTCGAGCAGAGTACTGCGACATGTGGGCCAGCTTGGAGCAGGGCGTGTGACATCCCG	780
QY	661	CGGGCCCAAGGCGCTGGCGCGCGGCGAGCTGACGTGTGTTGGGAGGCGCACCGCAGTGTGCGC	720
Dp	781	CGGGCCCAAGGCGCTGGCGCGCGGCGAGCTGACGTGTGTTGGGAGGCGCACCGCAGTGTGCGC	840
QY	721	TCAAGGAGACTGTGGCTCTGTGTGTTGTGACATCAAGTTCTCAGAGCTCTTCTATCTGAGC	780
Dp	841	TCAAGGAGACTGTGGCTCTGTGTGTTGTGACATCAAGTTCTCAGAGCTCTTCTATCTGAGC	900
QY	781	GCTTCTGTGGGCGACTACTGAGTGGCGGCTGTGTGAC	819
Dp	901	GCTTCTGTGGGCGACTACTGAGTGGCGGCTGTGTGAC	939

RESULT 11  
AAS62603  
ID AAS62603 standard; cDNA, 1966 BP.  
XX  
AC AAS62603;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE cDNA sequence #390 encoding novel human secreted protein.  
DE  
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
XX

KW immune deficiency disorder; blood disorder; inflammatory disorder  
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
KW immunosuppressive; antirheumatic; ss.

OS	Homo sapiens.
XX	
PN	WO20017291-A2.
XX	
PD	18-OCT-2001.
XX	
PF	29-MAR-2001; 2001WO-US010485.
XX	
PR	06-APR-2000; 2000US-0195604P.
XX	
PA	(GENY ) GENETICS INST INC.
XX	
P1	Wong GG, Clark HF, Rechei K, Agostino MJ, Howes SH, Resnick RJ,
P1	Gulukota K, Graham JR;
XX	
DR	WPI; 2002-010900/01.
XX	
PT	New polynucleotides encoding secreted proteins useful for treating e.g.
PT	asthma, HIV and Crohn's disease.
XX	
PS	Claim 1; Page 280; 391pp; English.

CC The present invention relates to the isolation of novel cDNA sequences  
CC which encode human secreted proteins. The cDNA sequences have been  
CC derived from a variety of human tissues. The invention also provides a  
CC method for producing proteins from these polynucleotide sequences. The  
CC proteins are useful for identifying compounds that modulate their  
CC activity and production, and the cell is also useful for identifying  
CC compounds that modulate expression of the polynucleotide sequences  
CC encoding the secreted proteins. The sequences of the invention are useful  
CC for treating diseases such as hyperproliferative disorders (e.g. cancer),  
CC immune deficiency disorders (e.g. severe combined immunodeficiency  
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders  
CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and  
CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of  
CC the invention are also useful in gene therapy. AAG6211-AAG62838  
CC represent the cDNA sequences of the invention that encode for novel human  
CC secreted proteins  
CC  
CC  
SQ Sequence 1966 BP, 356 A, 618 C, 614 G, 378 T, 0 U, 0 Other;

Query Match	59.2%	Score 538	DB 6;	Length 1966;
Best Local Similarity	99.8%	Pred: No.	2.9e-236;	
Matches 568; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

Qy	1	ATGGGCGTATCCGGGTCACACCCGGCCCCGTCCTGGGAAGAGGAATGAGTCCCTGAGACTAC	60
Db	50	ATGGGCGTATCCGGGTCACACCCGGCCCCGTCCTGGGAAGAGGAATGAGTCCCTGAGACTAC	1080
Qy	61	TACGGGATGCTGTCCGCTTACCGTATGTTGAGAGTGTGGGCGGGCAACTGACCCGAGTGC	120
Db	110	TACGGGATGCTGTCCGCTTACCGTATGTTGAGAGTGTGGGCGGGCAACTGACCCGAGTGC	165
Qy	121	GAGCTGAGACTTCCTGAGCCCTTTCTGTGATGAGGACTCTGAGCGCGCCGGAGGCTTAGCC	180
Db	170	GAGCTGAGACTTCCTGAGCCCTTTCTGTGATGAGGACTCTGAGCGCGCCGGAGGCTTAGCC	228
Qy	181	CGGGCCCGCAGCGGCGCTTAGAGCTCTGTCTGAGAGCTGGAAGCGCGCGGCGAGTGGCGGAG	240
Db	230	CGGGCCCGCAGCGGCGCTTAGAGCTCTGTCTGAGAGCTGGAAGCGCGCGGCGAGTGGCGGAG	288
Qy	241	AGCAACCTGCGGCTGTGGGGGCAACTCTGAGCGGTCGTGGCCCGCGCAGCACTGCTGCGG	300
Db	290	AGCAACCTGCGGCTGTGGGGGCAACTCTGAGCGGTCGTGGCCCGCGCAGCACTGCTGCGG	348
Qy	301	CACCTGAGCGCGAAGCGGCGCGGCGCAGTGTCTCCAGAACGCTATAGCTATGCACTCC	360
Db	350	CACCTGAGCGCGAAGCGGCGCGGCGCAGTGTCTCCAGAACGCTATAGCTATGCACTCC	408

Accession	Gene	Protein	Length	Source	Species	Organism	Strain	Accession	Gene	Protein	Length	Source	Species	Organism	Strain	
AY	361	AGCTCTTCAAAAGAGGACAGAGGGTACTGCGCGTGGCGAGTCAACAGTTCGCA	42	Human	Human	Human	Human	AY	361	AGCTCTTCAAAAGAGGACAGAGGGTACTGCGCGTGGCGAGTCAACAGTTCGCA	42	Human	Human	Human	Human	
DB	410	AGCTTTCAAAAGAGGACAGAGGGTACTGCGCGTGGCGAGTCAACAGTTCGCA	46	Human	Human	Human	Human	DB	410	AGCTTTCAAAAGAGGACAGAGGGTACTGCGCGTGGCGAGTCAACAGTTCGCA	46	Human	Human	Human	Human	
OY	421	AATTTCTCAGCAGGCGTTCAGTGGGAGACAGGCTCCCTCCCAACCAAGCGGCGAGT	48	Human	Human	Human	Human	OY	421	AATTTCTCAGCAGGCGTTCAGTGGGAGACAGGCTCCCTCCCAACCAAGCGGCGAGT	48	Human	Human	Human	Human	
DB	470	AATTTCTCAGCAGGCGTTCAGTGGGAGACAGGCTCCCTCCCAACCAAGCGGCGAGT	52	Human	Human	Human	Human	DB	470	AATTTCTCAGCAGGCGTTCAGTGGGAGACAGGCTCCCTCCCAACCAAGCGGCGAGT	52	Human	Human	Human	Human	
OY	481	CGGGGCGGGCCCAAGTGTGTGTGTCAGACGCGCGGAGAGGGGCGCCAGTCCGAC	54	Human	Human	Human	Human	OY	481	CGGGGCGGGCCCAAGTGTGTGTGTCAGACGCGCGGAGAGGGGCGCCAGTCCGAC	54	Human	Human	Human	Human	
DB	530	CGGGGCGGGCCCAAGTGTGTGTGTCAGACGCGCGGAGAGGGGCGCCAGTCCGAC	58	Human	Human	Human	Human	DB	530	CGGGGCGGGCCCAAGTGTGTGTGTCAGACGCGCGGAGAGGGGCGCCAGTCCGAC	58	Human	Human	Human	Human	
OY	541	CAGCAGTCAGAGCCCGCCAGACCTTCCTCTGAAAGGCAAGTGACTGTG	58	Human	Human	Human	Human	OY	541	CAGCAGTCAGAGCCCGCCAGACCTTCCTCTGAAAGGCAAGTGACTGTG	58	Human	Human	Human	Human	
DB	550	CAGCAGTCAGAGCCCGCCAGACCTTCCTCTGAAAGGCAAGTGACTGTG	63	Human	Human	Human	Human	DB	550	CAGCAGTCAGAGCCCGCCAGACCTTCCTCTGAAAGGCAAGTGACTGTG	63	Human	Human	Human	Human	
RESULT 12								RESULT 12								
AAH99646								AAH99646								
XX	AAH99646	standard; cDNA; 1570 BP.						XX	AAH99646	standard; cDNA; 1570 BP.						
AC	AAH99646;							AC	AAH99646;							
XX	16-OCT-2001 (first entry)							XX	16-OCT-2001 (first entry)							
DT	Human protein encoding cDNA sequence SEQ ID NO:481.							DT	Human protein encoding cDNA sequence SEQ ID NO:481.							
XX	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;							XX	Human; cancer; ulcer; HIV infection; human immunodeficiency virus;							
KW	antiinflammatory; antipneumatic; antiarthritic; immunosuppressive;							KW	antiinflammatory; antipneumatic; antiarthritic; immunosuppressive;							
KW	antibacterial; endocrine; cardiac; central nervous system; viricide;							KW	antibacterial; endocrine; cardiac; central nervous system; viricide;							
KW	anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;							KW	anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;							
KW	antaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema;							KW	antaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema;							
KW	dermatological; antiallergic; antiaesthetic; antidabetic; cyostatic;							KW	dermatological; antiallergic; antiaesthetic; antidabetic; cyostatic;							
KW	neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;							KW	neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;							
KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;							KW	immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;							
KW	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;							KW	antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;							
KW	cardiac dysfunction; neuropathic disorder; cardiac anaphylaxis; autoimmunity;							KW	cardiac dysfunction; neuropathic disorder; cardiac anaphylaxis; autoimmunity;							
KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;							KW	genetic disease; haematopoietic disorder; platelet disorder; asthma;							
KW	thrombocytopenia; osteoporosis; severe combined immunodeficiency;							KW	thrombocytopenia; osteoporosis; severe combined immunodeficiency;							
KW	allergic rhinitis; diabetes; multiple sclerosis; depression;							KW	allergic rhinitis; diabetes; multiple sclerosis; depression;							
KW	Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;							KW	Alzheimer's disease; Parkinson's disease;							

CC	antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
CC	antidiabetic; cytoskeletal; neuroprotective; antidepressant; nootropic;
CC	antiParkinsonian; and immunostimulant. The proteins and polynucleotides
CC	encoding them can be used in gene therapy, antisense therapy and vaccine
CC	production. The proteins and polynucleotides are useful for screening for
CC	agonists or antagonists of a protein and for the treatment and diagnosis
CC	of disorders associated with the activity of a protein e.g. inflammation,
CC	rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC	neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC	infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC	anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC	osteoporosis, severe combined immunodeficiency, eczema, allergic
CC	rinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC	Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC	neurological disorders
SQ	Sequence 1570 BP; 311 A; 488 C; 466 G; 305 T; 0 U; 0 Other;
XX	
XX	
Query Match	58.4%; Score 531; DB 4; Length 1570;
Best Local Similarity	99.8%; Pied. No. 4,7e-233;
Matches 581; Conservative	0; Mismatches 1; Indels 0; Gaps 0
OY	328 GTGTCTTCAGAAAGCGTATAGCTATGACGCCTCCAGCTCTTTCAAAAGACAGAGGGTAGC 387
DB	76 GTGTCTTCAGAAAGCGTATAGCTATGACGCCTCCAGCTCTTTCAAAAGACAGAGGGTAGC 135
OY	388 TGCCGCTGCCCGTCGGCAGTCAAGCAGATTCTGCAAAATTCTCAGCAGAGGTCAGTGAGACA 447
DB	136 TGCCGCTGCCCGTCGGCAGTCAAGCAGATTCTGCAAAATTCTCAGCAGAGGTCAGTGAGACA 195
OY	448 GGCTTCCCCCAAACCAAGCGGACGAGGGGAGTCGGGGCCGGCCCAATGATGTGTCCAGA 507
DB	196 GGCTTCCCCCAAACCAAGCGGACGAGGGGAGTCGGGGCCGGCCCAATGATGTGTCCAAA 255
OY	508 CGGCGCGGAGAGGGGGCCCCAAGCCGACCCCAGACAGCATGACAGCCCGCACACTTCC 567
DB	256 CGGCGCGGAGAGGGGGCCCCAAGCCGACCCCAGACAGCATGACAGCCCGCACACTTCC 315
OY	568 TCTGAAGGCAAAAGTACCTGTGACATCCGGGCTCCGGGTTTCAGCAGAGTACTGCGAGCAT 627
DB	316 TCTGAAGGCAAAAGTACCTGTGACATCCGGGCTCCGGGTTTCAGCAGAGTACTGCGAGCAT 375
OY	628 GGGCCAGCGCTTGGACAGAGGGGCTGGCATCCGGCGGGCCCCAAGCGCTTGGCGGAGCTG 687
DB	376 GGGCCAGCGCTTGGACAGAGGGGCTGGCATCCGGCGGGCCCCAAGCGCTTGGCGGAGCTG 435
OY	688 GACGCTGTTTGGGACAGGCGCACCGCAGTGTGGGCTCTCAAGGGACCTTGGGCTCTGTGGTTGT 747
DB	436 GACGCTGTTTGGGACAGGCGCACCGCAGTGTGGGCTCTCAAGGGACCTTGGGCTCTGTGGTTGT 495
OY	748 GACATCAAGTTCTCAGAGCTCTCCTATCTGAGACGCGCTTCTGGGGGCACTAACCTGAGTGC 807
DB	496 GACATCAAGTTCTCAGAGCTCTCCTATCTGAGACGCGCTTCTGGGGGCACTAACCTGAGTGC 555
OY	808 GCCCTGCTGCAGGCGCTTCGGGGCGGTGTTCTTGACTGAGGCCCTTCGAGAGGCTGTGGGC 867
DB	556 GCCCTGCTGCAGGCGCTTCGGGGCGGTGTTCTTGACTGAGGCCCTTCGAGAGGCTGTGGGC 615
OY	868 CGGAGGCGTGTTCGCTGCTGCTGATGATGATGATGAGGCTGAC 909
DB	616 CGGAGGCGTGTTCGCTGCTGCTGATGATGATGATGAGGCTGAC 657
RESULT 13	
AAH07925	ID AAH07925 standard; cDNA; 626 BP.
XX	AAH07925;
XX	AC
XX	DT 26-JUN-2001 (first entry)
DE	Human cDNA clone (5'-primer) SEQ ID NO:4760.





DB 571 AATTCTCAGCAGG 584

Search completed: February 12, 2005, 13:53:46  
Job time : 484 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 13:34:28 ; Search time 2502 Seconds  
(without alignments)  
13829.105 Million cell updates/sec

Title: US-10-030-271-1  
Perfect score: 909  
Sequence: 1 atggcgcacccgcggtcgac.....tcagtgatgagcgacgac 909

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hrc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_est8:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	858	94.4	1053	3	CR604307 full-length
2	858	94.4	1860	3	CR593642 full-length
3	858	94.4	1866	3	CR619301 full-length
4	858	94.4	1894	3	CR625070 full-length
5	607	66.8	1090	3	BM920838 AGENCOURT
6	586	64.5	800	4	BG685173 AGENCOURT
7	582	64.0	634	4	B1907024 603064980
8	582	64.0	905	4	B1910528 603068215
9	582	64.0	927	4	BG251151 602364954
10	582	64.0	947	4	B1910416 603068087
11	582	64.0	1062	5	BM908148 AGENCOURT
12	582	64.0	1131	2	BE907425 601500161
13	582	64.0	1510	3	CR599685 full-length
14	582	64.0	1586	3	CR590827 full-length
15	558	61.4	1089	5	BM925969 AGENCOURT
16	532	58.5	655	7	CK429257 0134512.Y
17	531	58.4	644	7	CK373290 170004241
18	531	58.4	993	4	BM559141 AGENCOURT
19	531	58.4	1051	5	BQ073197 AGENCOURT
20	531	58.4	1161	5	BQ902131 AGENCOURT
21	521	57.3	569	5	BP306442 BP306442
22	515	56.7	793	2	BE883568 601508040
23	508	55.9	654	2	BE391120 601286078
24	506	55.7	506	2	BF655646 602119860

25	502	55.2	678	7	CN373294	CN373294 170005999
26	500	55.0	731	5	BQ923358	BQ923358 AGENCOURT
27	480	52.8	783	5	BU602002	BU602002 AGENCOURT
28	476	52.4	718	4	B1117988	B1117988 602867244
29	471	51.8	671	7	CN373287	CN373287 170004251
30	458	50.4	577	7	CN373291	CN373291 170004250
31	454	49.9	991	5	BQ956773	BQ956773 AGENCOURT
32	453	49.8	832	4	BI827768	BI827768 603075430
33	450	49.5	1028	5	BM928759	BM928759 AGENCOURT
34	450	49.5	1033	5	BM922715	BM922715 AGENCOURT
35	446	49.1	586	5	BP343733	BP343733 BP343733
36	446	49.1	780	6	CB994488	CB994488 AGENCOURT
37	442	48.6	831	6	CB992627	CB992627 AGENCOURT
38	440	48.4	1042	5	BQ072022	BQ072022 AGENCOURT
39	435	47.9	931	5	BX381775	BX381775 BX381775
40	432	47.5	580	5	BP211545	BP211545 BP211545
41	429	47.2	583	5	BP305292	BP305292 BP305292
42	427	47.0	817	6	CB990003	CB990003 AGENCOURT
43	426	46.9	891	5	BK458265	BK458265 BX458265
44	417	45.9	938	5	BU507654	BU507654 AGENCOURT
45	415	45.7	1151	5	BQ947706	BQ947706 AGENCOURT
46	410	45.1	837	4	BM547754	BM547754 AGENCOURT
47	407	44.8	1233	4	BP253687	BP253687 BP253687
48	403	44.3	582	5	BP253687	BP253687 BP253687
49	393	43.2	402	7	CN373296	CN373296 170005999
50	388	42.7	50	2	AN245758	AN245758 2822785..5
51	387	42.6	826	6	CB991766	CB991766 AGENCOURT
52	385	42.4	582	5	BP360582	BP360582 BP360582
53	385	42.4	1428	5	BM906070	BM906070 AGENCOURT
54	384	42.2	680	4	BG340752	BG340752 602462347
55	383	42.1	576	4	BM126446	BM126446 1F06C09.Y
56	381	41.9	583	5	BP352691	BP352691 BP352691
57	380	41.8	495	7	CR746989	CR746989 K-EST0113
58	380	41.8	567	6	CB154807	CB154807 K-EST0212
59	378	41.6	527	4	BM837565	BM837565 K-EST0113
60	375	41.3	643	7	CN373297	CN373297 170006000
61	372	40.9	586	5	BP254070	BP254070 BP254070
62	372	40.9	1313	5	BQ709748	BQ709748 AGENCOURT
63	368	40.5	657	7	CN373295	CN373295 170006000
64	368	40.5	1043	5	BU180173	BU180173 AGENCOURT
65	367	40.4	824	6	CB989607	CB989607 AGENCOURT
66	362	39.8	583	5	BP304786	BP304786 BP304786
67	353	38.8	690	4	BG706385	BG706385 202669711
68	349	38.4	574	7	CK819032	CK819032 1F06C09.Y
69	349	38.4	842	4	BI752583	BI752583 603028419
70	344	37.8	842	4	BP333294	BP333294 BP333294
71	343	37.7	878	4	BI756130	BI756130 603030029
72	340	37.4	479	7	CN373293	CN373293 170006000
73	334	36.7	474	4	BM700298	BM700298 UI-E-DW1-
74	325	35.8	415	7	CN373288	CN373288 170005326
75	325	35.2	465	6	CB153442	CB153442 K-EST0210
76	300	33.0	799	4	BG681575	BG681575 60628062
77	299	32.9	924	7	CN373289	CN373289 170006000
78	297	32.7	686	7	BG57042	BG57042 602710464
79	286	31.5	561	7	CN373292	CN373292 170004705
80	285	31.4	546	4	BM849284	BM849284 K-EST0129
81	285	31.4	549	4	BM853352	BM853352 K-EST0134
82	285	31.4	623	4	BG819012	BG819012 602781053
83	275	30.3	496	4	BG180215	BG180215 602329820
84	268	29.5	522	4	BM147424	BM147424 TCAAP1011
85	266	29.3	1046	5	BK342837	BK342837 7F65604.X
86	262	28.8	583	2	BE856624	BE856624 7F65604.X
87	262	28.8	587	5	BP306585	BP306585 BP306585
88	262	28.8	1481	5	BQ071492	BQ071492 AGENCOURT
89	254	27.9	421	6	CB153158	CB153158 K-EST0210
90	235	25.9	872	4	CB107743	CB107743 K-EST0147
91	235	25.9	872	4	BI253561	BI253561 603175851
92	235	25.9	872	4	BI757389	BI757389 603029320
93	230	25.3	532	2	BM837877	BM837877 K-EST0114
94	219	24.1	823	2	BE785785	BE785785 601478567
95	216	23.8	855	2	BE797255	BE797255 601507614
96	210	23.1	1021	5	BK384448	BK384448 BX384448
97	209	23.0	951	5	BK375652	BK375652 BX375652



98	204	22.4	993	4	BC766140	BC766140	602738347	171	31	3.4	884	4	BT151137
99	188	20.7	762	4	BT600659	BT600659	603247545	172	30	3.3	161	2	AW794030
100	173	19.0	924	5	BK442929	BK442929	60442929	173	30	3.3	496	2	BP041764
101	172	18.9	756	1	AL562850	AL562850	60562850	174	30	3.3	650	6	CB557769
102	169	18.6	951	4	BG122215	BG122215	602349767	175	30	3.3	821	7	CK598082
103	166	18.3	635	2	BF339818	BF339818	602038823	176	29	3.2	333	5	BY348107
104	165	18.2	570	5	BP370313	BP370313	60370313	177	29	3.2	340	5	BY351863
105	163	17.9	340	4	BM149931	BM149931	TCAP3011	178	29	3.2	344	5	BY184868
106	154	16.9	358	4	BM706675	BM706675	UI-E-CO-	179	29	3.2	346	6	CB693072
107	154	16.9	371	4	BM706666	BM706666	UI-E-CO-	180	29	3.2	346	6	BY348272
108	148	16.3	276	6	CB130725	CB130725	K-EST0180	181	29	3.2	351	5	BY353184
109	146	16.1	904	5	BK328274	BK328274	BK328274	182	29	3.2	373	2	BB844365
110	145	16.0	763	4	BT520263	BT520263	603071122	183	29	3.2	379	2	BY023438
111	144	15.8	702	4	BG393347	BG393347	602411571	184	29	3.2	463	5	BY255034
112	143	15.7	469	5	BQ361597	BQ361597	RC4-OT024	185	29	3.2	474	5	BY255034
113	142	15.6	1192	5	BT190812	BT190812	AGENCOCURT	186	29	3.2	476	2	AW227145
114	143	14.6	1129	5	BK372293	BK372293	BK372293	187	29	3.2	543	2	AW227145
115	133	14.6	1267	5	BM625194	BM625194	AGENCOCURT	188	29	3.2	645	5	BO109330
116	129	14.2	642	2	BE781207	BE781207	601469135	189	29	3.2	679	4	BC696319
117	127	14.0	981	4	BM008603	BM008603	603618247	190	29	3.2	779	7	CK464017
118	120	13.2	874	1	AL519410	AL519410	AL519410	191	29	3.2	792	7	CO393836
119	119	13.2	200	2	BE242821	BE242821	TCAP1E21	192	29	3.2	802	4	BI649594
120	111	12.2	244	4	BM695503	BM695503	UI-E-CO-	193	29	3.2	900	6	CB589155
121	111	12.2	1146	2	BE870610	BE870610	601447719	194	28	3.1	240	5	CR185950
122	104	11.4	304	1	AA090354	AA090354	Y0170.8eq	195	27	3.0	361	4	BR837318
123	90	9.9	1123	5	BQ230921	BQ230921	AGENCOCURT	196	25	2.8	334	4	AM158134
124	89	9.8	217	1	AA218681	AA218681	zq96908.x	197	25	2.8	404	2	AM159003
125	88	9.7	356	4	BM149218	BM149218	TCAP2011	198	25	2.8	525	8	BR860059
126	88	9.7	504	5	BK374863	BK374863	BK374863	199	25	2.8	771	7	CK803280
127	88	9.7	1091	5	BM374729	BM374729	BM374729	200	25	2.8	775	7	CV117797
128	84	9.2	224	4	BM150154	BM150154	TCAP5011	201	25	2.8	835	7	CN328654
129	79	8.7	553	8	AQ171450	AQ171450	HS_3073_A	202	25	2.8	948	6	CD254010
130	77	8.5	816	4	BT171166	BT171166	603052476	203	25	2.8	1051	5	BK354590
131	77	8.5	915	2	BF695740	BF695740	601852476	204	25	2.8	1061	5	BK374728
132	65	7.2	466	1	AA725300	AA725300	MYE4045.M	205	23	2.5	386	6	CB806813
133	61	6.2	122	2	BF174916	BF174916	602023718	206	23	2.5	419	6	CB799420
134	56	6.2	622	2	BP233168	BP233168	BY747525	207	23	2.5	539	1	AL925092
135	56	6.2	760	6	BY47525	BY47525	Forward.B	208	23	2.5	632	4	BM534241
136	56	6.2	898	5	BQ951680	BQ951680	AGENCOCURT	209	23	2.5	638	6	CA334090
137	56	6.2	1017	3	AK011713	AK011713	Mus.muscu	210	23	2.5	650	6	CD596064
138	56	6.2	1199	3	AK089096	AK089096	Mus.muscu	211	23	2.5	684	7	CN083958
139	55	6.1	653	1	AU296471	AU296471	AU296471	212	23	2.5	811	7	CP661528
140	55	6.1	820	5	BP158001	BP158001	BP158001	213	22	2.4	1079	9	CI021177
141	55	5.9	618	4	BG404101	BG404101	602420009	214	22	2.4	331	5	BY347412
142	54	5.9	1166	5	BK342836	BK342836	60342836	215	22	2.4	422	1	AA511237
143	52	5.7	1025	6	BY101117	BY101117	Mus.muscu	216	22	2.4	982	4	BG419147
144	51	5.6	1027	6	BK384908	BK384908	60384908	217	21	2.3	251	2	BB606071
145	50	5.5	1641	3	AK010701	AK010701	Mus.muscu	218	21	2.3	334	7	CP649266
146	50	5.5	555	6	CD471681	CD471681	Leukose.4	219	21	2.3	362	5	BP147125
147	44	4.8	706	7	CK837899	CK837899	4063095.B	220	21	2.3	373	5	BY195304
148	41	4.5	1017	6	BY10940	BY10940	PM2-UM005	221	21	2.3	459	9	CG289307
149	41	4.4	187	4	BI048697	BI048697	UI-H-BT3-	222	21	2.3	527	9	CG289316
150	40	4.4	383	2	AM449244	AM449244	UI-H-BT3-	223	21	2.3	622	5	BP150734
151	40	4.4	674	4	BT108561	BT108561	602895012	224	21	2.3	622	5	BP150734
152	38	4.2	763	4	BB641783	BB641783	AGENCOCURT	225	21	2.3	736	6	CB647590
153	38	4.2	925	5	BQ894996	BQ894996	Mus.muscu	226	21	2.3	819	9	CG339398
154	38	4.2	4598	3	AK043908	AK043908	AGENCOCURT	227	21	2.3	855	9	CG339398
155	38	4.2	935	5	BT151149	BT151149	602916901	228	21	2.3	945	9	CG298032
156	37	4.1	836	4	BK458264	BK458264	BK458264	229	21	2.3	189	1	AI576572
157	36	4.0	993	5	BK381774	BK381774	BK381774	230	20	2.2	197	1	BE096391
158	36	4.0	1008	5	BK375651	BK375651	150948.MA	231	20	2.2	231	2	BE096761
159	35	3.9	462	2	BE666984	BE666984	217308.MA	232	20	2.2	288	2	BE095960
160	35	3.9	545	2	BE809924	BE809924	4122243.B	233	20	2.2	295	1	AI576594
161	35	3.9	593	7	CN787982	CN787982	4056539.B	234	20	2.2	327	2	BE096550
162	35	3.9	634	7	CK832751	CK832751	4056973.B	235	20	2.2	339	1	AI577932
163	35	3.9	859	2	BF241187	BF241187	601880059	236	20	2.2	345	2	AM533372
164	35	3.6	859	2	BF241187	BF241187	601880059	237	20	2.2	349	2	AM533231
165	33	3.5	378	5	BO824818	BO824818	LY234818	238	20	2.2	355	4	BM286915
166	32	3.5	537	5	BO828297	BO828297	LY612304	239	20	2.2	360	1	AI574869
167	32	3.5	650	7	CV106762	CV106762	AGENCOCURT	240	20	2.2	361	1	AM528910
168	32	3.5	735	7	CK031162	CK031162	AGENCOCURT	241	20	2.2	377	1	AI602034
169	32	3.5	735	7	CK838175	CK838175	4063565.B	242	20	2.2	432	1	AI574862
170	31	3.4	657	7	CK838175	CK838175	4063565.B	243	20	2.2	432	1	AI574862

244	20	2.2	439	2	AM533057	AM533057	UI-R-BUO-	C 317	19	2.1	459	8	A2047947	A2047947	LMJFV1.1
245	20	2.2	442	2	AM533745	AM533745	UI-R-BUO-	318	19	2.1	477	4	B1822296	B1822296	603036434
246	20	2.2	449	1	A1112094	A1112094	UI-R-YO-m	319	19	2.1	478	1	AL926032	AL926032	
247	20	2.2	450	1	A1577948	A1577948	UI-R-GO-u	320	19	2.1	484	4	B1391929	B1391929	pgp1n.pko
248	20	2.2	451	2	AM533656	AM533656	UI-R-BUO-	321	19	2.1	488	9	CL440459	CL440459	GLab-did
249	20	2.2	452	2	AM530308	AM530308	UI-R-BUO-	322	19	2.1	499	4	B1759835	B1759835	603045826
250	20	2.2	463	2	BE096598	BE096598	UI-R-BUO-	323	19	2.1	499	6	CB405935	CB405935	OSTR05785
251	20	2.2	465	2	BF651114	BF651114	UI-R-BUO-	324	19	2.1	501	2	BF178254	BF178254	601807785
252	20	2.2	470	2	BE096557	BE096557	UI-R-BUO-	325	19	2.1	503	9	CL440458	CL440458	GLab-did
253	20	2.2	473	1	A1578239	A1578239	UI-R-GO-u	326	19	2.1	505	2	BE328699	BE328699	h16gco4.x
254	20	2.2	474	2	AM533477	AM533477	UI-R-BUO-	327	19	2.1	506	6	CD550200	CD550200	B0308C09-
255	20	2.2	482	2	BF776323	BF776323	287090 MA	328	19	2.1	507	6	CB364185	CB364185	ZF001-P00
256	20	2.2	496	2	BE681718	BE681718	179470 MA	329	19	2.1	513	2	BE391525	BE391525	601285055
257	20	2.2	531	1	A1575156	A1575156	UI-R-GO-u	330	19	2.1	513	7	CN666076	CN666076	A0835B03-
258	20	2.2	532	4	BM256051	BM256051	518311 MA	331	19	2.1	515	5	BO318938	BO318938	QVO-CT058
259	20	2.2	533	4	BE096048	BE096048	UI-R-BUO-	332	19	2.1	521	7	CV055136	CV055136	BNE117C2
260	20	2.2	538	2	BF076755	BF076755	226489 MA	333	19	2.1	522	2	BE031003	BE031003	129328 MA
261	20	2.2	543	2	AM533294	AM533294	UI-R-BUO-	334	19	2.1	529	8	A2261067	A2261067	RPCT-23-1
262	20	2.2	543	4	BI538575	BI538575	433967 MA	335	19	2.1	534	1	AJ677224	AJ677224	AJ677224
263	20	2.2	549	6	CA144377	CA144377	SCRLV102	336	19	2.1	534	4	AU279585	AU279585	AU279585
264	20	2.2	598	6	CB654257	CB654257	OSUNEC0E	337	19	2.1	539	4	AO506300	AO506300	1E16F04.Y
265	20	2.2	607	6	CA137330	CA137330	SCAGRT203	338	19	2.1	539	8	AO506300	AO506300	RPCT-11-2
266	20	2.2	623	6	CB578521	CB578521	AMGNNUC:N	339	19	2.1	540	2	BE514595	BE514595	UI-H-BM1-
267	20	2.2	627	6	CD452572	CD452572	WHEL113.C	340	19	2.1	546	2	BE391977	BE391977	601285006
268	20	2.2	646	6	CA295799	CA295799	SCRLV102	341	19	2.1	553	6	CA194960	CA194960	SCAGSBI08
269	20	2.2	659	7	CF303451	CF303451	ABP1--02-	342	19	2.1	554	4	BM129247	BM129247	1E19601.Y
270	20	2.2	663	6	CA142052	CA142052	SCMCR208	343	19	2.1	556	5	BO566244	BO566244	G155604.Y
271	20	2.2	675	4	BI532559	BI532559	1024122H1	344	19	2.1	566	1	AT141157	AT141157	W919F07.X
272	20	2.2	684	7	CK978639	CK978639	4110322.B	345	19	2.1	571	4	BI908845	BI908845	603066419
273	20	2.2	706	7	CO885829	CO885829	BoVGen.14	346	19	2.1	571	8	B2359915	B2359915	1d84A10.B
274	20	2.2	727	6	CA245277	CA245277	SCBFL507	347	19	2.1	574	7	CN664706	CN664706	A0816F05-
275	20	2.2	744	7	CK215269	CK215269	FGAS02722	348	19	2.1	579	5	BO786882	BO786882	1151A04.X
276	20	2.2	768	6	CD452443	CD452443	WHE1104.B	349	19	2.1	595	8	CN702477	CN702477	E0462H03-
277	20	2.2	777	2	BF306627	BF306627	60188882	350	19	2.1	596	2	BE584360	BE584360	5-7H-HA.P
278	20	2.2	786	8	BZ803349	BZ803349	PJFEM93TB	351	19	2.1	597	7	BP279067	BP279067	UI-M-HQO-
279	20	2.2	793	8	CC350221	CC350221	COQAR07TV	352	19	2.1	604	7	CN532131	CN532131	UI-M-HQO-
280	20	2.2	797	2	BE737843	BE737843	601572476	353	19	2.1	608	5	BP279067	BP279067	hW46607.Y
281	20	2.2	801	6	CB658148	CB658148	OSUNE13P	354	19	2.1	608	7	CN484409	CN484409	hW46607.Y
282	20	2.2	817	6	CB668061	CB668061	OSUNE13L	355	19	2.1	609	4	BM170531	BM170531	B1170531
283	20	2.2	849	6	CB668017	CB668017	OSUNE13K	356	19	2.1	611	8	BM331280	BM331280	CH230-125
284	20	2.2	853	7	CK952982	CK952982	4092551.B	357	19	2.1	616	5	BP238569	BP238569	BP238569
285	20	2.2	866	8	BZ803354	BZ803354	PJFEM93TD	358	19	2.1	617	5	BP279044	BP279044	BP279044
286	20	2.2	908	7	CK952473	CK952473	6092167.B	359	19	2.1	623	7	CN355179	CN355179	170005999
287	20	2.2	957	4	BM046431	BM046431	603626461	360	19	2.1	623	7	CF863839	CF863839	PEZS008XG
288	20	2.2	1051	1	AL547355	AL547355	AL547355	361	19	2.1	628	7	CV026354	CV026354	4266.Fu11
289	20	2.2	1067	9	CNS0453F	AL274884	Teltraodon	362	19	2.1	630	7	CF844514	CF844514	PSH8028XG
290	20	2.2	1256	6	CD558654	CD558654	AGENCOURT	363	19	2.1	632	7	CF539030	CF539030	UI-M-G10-
291	20	2.2	1334	5	BO391316	BO391316	AGENCOURT	364	19	2.1	634	7	CN355178	CN355178	170005999
292	20	2.2	1369	6	CA131149	CA131149	SCBFR106	365	19	2.1	639	7	CN527995	CN527995	UI-M-HQO-
293	20	2.2	1511	3	AK013072	AK013072	Mus muscu	366	19	2.1	651	4	BI764859	BI764859	603047148
294	19	2.1	143	2	BP376237	BP376237	CNO-TN003	367	19	2.1	654	7	CK316994	CK316994	SRB02020A2
295	19	2.1	177	9	CE690180	CE690180	t1gr-g8a-	368	19	2.1	655	4	BI487097	BI487097	RE70607.5
296	19	2.1	214	8	AQ937975	AQ937975	NB6-730R	369	19	2.1	659	4	BI14210	BI14210	603182186
297	19	2.1	232	1	AI981180	AI981180	Patc.DK004	370	19	2.1	662	6	CA160342	CA160342	SCJFR23CO
298	19	2.1	253	9	CL217227	CL217227	ZMMBB040	371	19	2.1	675	7	CN460483	CN460483	UI-M-HB0-
299	19	2.1	284	7	CF649582	CF649582	3530.1.72	372	19	2.1	677	7	CN355181	CN355181	328769210
300	19	2.1	286	7	CF862927	CF862927	PEZS005Xr	373	19	2.1	678	8	AO779723	AO779723	HS.5571.B
301	19	2.1	290	2	BE760046	BE760046	an.0165.A	374	19	2.1	679	7	CN355177	CN355177	170005831
302	19	2.1	300	1	AU098867	AU098867	AU098867	375	19	2.1	680	6	CA385282	CA385282	666182.NC
303	19	2.1	300	5	BO345968	BO345968	PM3-NT031	376	19	2.1	681	9	AY406899	AY406899	Homo.sapi
304	19	2.1	313	4	BG729532	BG729532	FG85H10.Y	377	19	2.1	688	9	CC757271	CC757271	ZMMBB014
305	19	2.1	327	6	CB676471	CB676471	OSUNE12M	378	19	2.1	691	4	BI368003	BI368003	RE53901.5
306	19	2.1	329	7	CR464086	CR464086	CA464086	379	19	2.1	693	4	BI579622	BI579622	Bu579622
307	19	2.1	353	6	CA126736	CA126736	SCVPLN100	380	19	2.1	698	5	BUD55262	BUD55262	UI-M-P00-
308	19	2.1	371	4	BI027080	BI027080	CM3-MT029	381	19	2.1	698	5	BUD53177	BUD53177	1112104H0
309	19	2.1	377	8	B30709	B30709	HS-1003-A1-	382	19	2.1	710	6	CA171228	CA171228	SCRUSBI06
310	19	2.1	390	4	AI001904	AI001904	OC42B09.6	383	19	2.1	711	5	BUT08512	BUT08512	UI-M-F10-
311	19	2.1	399	4	BG897441	BG897441	HOA13-1-B	384	19	2.1	713	4	BJ166947	BJ166947	Bu166947
312	19	2.1	408	4	BM784583	BM784583	AL544361	385	19	2.1	715	9	CE003425	CE003425	t1gr-g8a-
313	19	2.1	415	4	AL544361	AL544361	AL544361	386	19	2.1	716	7	CF862041	CF862041	PEZS001XK
314	19	2.1	424	5	BY307673	BY307673	BY307673	387	19	2.1	724	7	CF520199	CF520199	AGENCOURT
315	19	2.1	432	1	AI94967	AI94967	b807605.Y	388	19	2.1	736	2	BE409341	BE409341	601330993
316	19	2.1	436	9	AY406900	AY406900	Pan.trogl	389	19	2.1	737	2	BE563801	BE563801	601335415

390	19	2.1	752	7	CF948639	UI-M-HUO-
391	19	2.1	753	4	BG769028	602742963
392	19	2.1	759	4	AG030724	Pan tlog1
393	19	2.1	766	9	AG581668	Mus muscu
394	19	2.1	768	5	BX355175	BX355175
395	19	2.1	777	7	CK306757	SB02035A1
396	19	2.1	794	7	CN157609	CN157609
397	19	2.1	797	7	CN328875	CN328875
398	19	2.1	799	6	CB997025	CB997025
399	19	2.1	813	9	AL548800	AL548800
400	19	2.1	830	6	CF994215	CF994215
401	19	2.1	834	6	CA496393	CA496393
402	19	2.1	834	6	AG314176	AG314176
403	19	2.1	839	5	BUS09596	Mus muscu
404	19	2.1	842	4	BG763628	BG763628
405	19	2.1	844	7	CF243159	CF243159
406	19	2.1	845	8	BZ148659	BZ148659
407	19	2.1	847	4	BG296749	BG296749
408	19	2.1	850	4	BG919487	BG919487
409	19	2.1	851	1	AL549056	AL549056
410	19	2.1	852	6	CA787600	CA787600
411	19	2.1	861	9	CG432941	CG432941
412	19	2.1	866	9	CG671800	CG671800
413	19	2.1	867	5	BQ427693	BQ427693
414	19	2.1	871	1	AL528945	AL528945
415	19	2.1	872	4	BG539339	BG539339
416	19	2.1	874	8	BZ530271	BZ530271
417	19	2.1	884	9	CG836312	CG836312
418	19	2.1	886	5	BU929064	BU929064
419	19	2.1	886	6	CD557530	CD557530
420	19	2.1	886	5	BX383398	BX383398
421	19	2.1	900	6	CB994477	CB994477
422	19	2.1	918	4	BG770258	BG770258
423	19	2.1	923	5	BU148611	BU148611
424	19	2.1	924	5	CG370721	CG370721
425	19	2.1	933	5	BU145513	BU145513
426	19	2.1	940	7	CF664996	CF664996
427	19	2.1	943	9	CC653316	CC653316
428	19	2.1	944	9	CNS03H95	CNS03H95
429	19	2.1	950	5	BE900888	BE900888
430	19	2.1	951	2	BE386774	BE386774
431	19	2.1	953	2	BQ925622	BQ925622
432	19	2.1	956	2	BE675407	BE675407
433	19	2.1	975	2	BQ715147	BQ715147
434	19	2.1	986	5	BX384447	BX384447
435	19	2.1	1023	5	AL551217	AL551217
436	19	2.1	1037	1	AL551217	AL551217
437	19	2.1	1071	4	BM557325	BM557325
438	19	2.1	1078	1	AL533735	AL533735
439	19	2.1	1087	5	BX386150	BX386150
440	19	2.1	1088	9	CNS02MGM	CNS02MGM
441	19	2.1	1109	5	BQ421980	BQ421980
442	19	2.1	1112	8	BZ563120	BZ563120
443	19	2.1	1127	5	BQ278930	BQ278930
444	19	2.1	1136	7	CK027826	CK027826
445	19	2.1	1188	3	CR721391	CR721391
446	19	2.1	1195	5	BUS39777	BUS39777
447	19	2.1	1195	5	AG053290	AG053290
448	19	2.1	1217	8	BZ569571	BZ569571
449	19	2.1	1218	4	BI160309	BI160309
450	19	2.1	1257	7	CK028239	CK028239
451	19	2.1	1366	6	BZ566520	BZ566520
452	19	2.1	1411	3	CR7065329	CR7065329
453	19	2.1	1411	3	CR7065329	CR7065329
454	19	2.1	1411	3	CR7065329	CR7065329
455	19	2.1	1411	3	CR7065329	CR7065329
456	19	2.1	1411	3	CR7065329	CR7065329
457	19	2.1	1411	3	CR7065329	CR7065329
458	19	2.1	1411	3	CR7065329	CR7065329
459	19	2.1	1411	3	CR7065329	CR7065329
460	19	2.1	1411	3	CR7065329	CR7065329
461	19	2.1	1411	3	CR7065329	CR7065329
462	19	2.1	1411	3	CR7065329	CR7065329

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463	18	2.0	79	9	CG712928	CG712928
464	18	2.0	88	9	CG799660	CG799660
465	18	2.0	90	9	CG708258	CG708258
466	18	2.0	92	9	CG800743	CG800743
467	18	2.0	92	9	CG800743	CG800743
468	18	2.0	96	1	MA398502	MA398502
469	18	2.0	106	9	GG4270141	GG4270141
470	18	2.0	109	9	CG799342	CG799342
471	18	2.0	117	9	CG733263	CG733263
472	18	2.0	118	6	CD942346	CD942346
473	18	2.0	118	6	CD955092	CD955092
474	18	2.0	118	6	CG728764	CG728764
475	18	2.0	121	9	CG800161	CG800161
476	18	2.0	123	8	CG023002	CG023002
477	18	2.0	129	9	CG712317	CG712317
478	18	2.0	131	9	CG800665	CG800665
479	18	2.0	132	9	CG712922	CG712922
480	18	2.0	132	9	CG716809	CG716809
481	18	2.0	132	9	CG724950	CG724950
482	18	2.0	132	9	CG728665	CG728665
483	18	2.0	132	9	CG799158	CG799158
484	18	2.0	132	9	CG806025	CG806025
485	18	2.0	132	9	CG806335	CG806335
486	18	2.0	133	9	CG716660	CG716660
487	18	2.0	134	8	AZ577389	AZ577389
488	18	2.0	139	8	CG022559	CG022559
489	18	2.0	139	8	CG713343	CG713343
490	18	2.0	146	1	AL047726	AL047726
491	18	2.0	148	9	CG037808	CG037808
492	18	2.0	148	9	CG733081	CG733081
493	18	2.0	149	9	CG716436	CG716436
494	18	2.0	149	9	CG725404	CG725404
495	18	2.0	150	8	AZ577701	AZ577701
496	18	2.0	151	9	CG716897	CG716897
497	18	2.0	152	9	CG725510	CG725510
498	18	2.0	153	1	AT154457	AT154457
499	18	2.0	155	8	CC021678	CC021678
500	18	2.0	155	7	CG801858	CG801858
501	18	2.0	156	7	CV306343	CV306343
502	18	2.0	156	7	CV306344	CV306344
503	18	2.0	156	9	CG728541	CG728541
504	18	2.0	157	7	CV306373	CV306373
505	18	2.0	157	7	CV306374	CV306374
506	18	2.0	159	9	BX205534	BX205534
507	18	2.0	160	9	CG799299	CG799299
508	18	2.0	164	9	CG799351	CG799351
509	18	2.0	166	6	CD733673	CD733673
510	18	2.0	167	8	CG120536	CG120536
511	18	2.0	167	8	CG712894	CG712894
512	18	2.0	169	4	BG089501	BG089501
513	18	2.0	169	4	CG729632	CG729632
514	18	2.0	170	8	CC023063	CC023063
515	18	2.0	171	8	CC029228	CC029228
516	18	2.0	171	9	CG799273	CG799273
517	18	2.0	172	9	CG713168	CG713168
518	18	2.0	173	9	CG731635	CG731635
519	18	2.0	176	8	CC028999	CC028999
520	18	2.0	177	8	CC020557	CC020557
521	18	2.0	182	8	CG799296	CG799296
522	18	2.0	186	8	CC020481	CC020481
523	18	2.0	186	9	CG716939	CG716939
524	18	2.0	188	8	CC037281	CC037281
525	18	2.0	190	8	CC029499	CC029499
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529	18	2.0	198	9	CG713142	CG713142
530	18	2.0	198	9	CG716217	CG716217
531	18	2.0	198	9	CG716712	CG716712
532	18	2.0	198	9	CG724935	CG724935
533	18	2.0	198	9	CG728421	CG728421
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CG712928	111802960
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C 539	18	2.0	208	1	A1216466	qho7h07.x	C 612	18	2.0	318	9	CL171903
C 540	18	2.0	208	9	CG716805	CG716805	C 613	18	2.0	319	9	BY347016
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544	18	2.0	217	8	CC021711	111802F0	C 617	18	2.0	323	1	AA325478
545	18	2.0	217	9	CG728595	1119T01H0	C 618	18	2.0	323	5	BY345319
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548	18	2.0	221	9	CG728735	1119102G0	C 621	18	2.0	327	5	BY327530
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552	18	2.0	222	9	CG804436	111805F0	C 625	18	2.0	332	5	BY343935
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554	18	2.0	223	8	CC028961	3591.1.10	C 627	18	2.0	333	5	BY346798
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571	18	2.0	249	4	BJ064724	BJ064724	C 644	18	2.0	364	7	CK994744
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575	18	2.0	257	4	BM540220	BM540220 hd19e03.g	C 648	18	2.0	373	4	BM486849
576	18	2.0	257	9	CG728330	CG728330	C 649	18	2.0	374	2	BE281887
577	18	2.0	257	9	CG799597	CG799597	C 650	18	2.0	376	6	BY674979
C 578	18	2.0	258	2	AM796327	AM796327 PM2-UM002	C 651	18	2.0	377	2	AM478437
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581	18	2.0	262	9	CG729650	CG729650	C 654	18	2.0	378	2	BP116388
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586	18	2.0	274	1	A1914462	A1914462 w486e09.x	C 659	18	2.0	395	4	BT113352
587	18	2.0	276	1	CG728579	CG728579	C 660	18	2.0	397	1	AA822764
C 588	18	2.0	277	2	BE086039	BE086039 PM2-BT067	C 661	18	2.0	397	4	BM536502
589	18	2.0	279	8	CC027084	3591.1.56	C 662	18	2.0	398	1	AU020459
590	18	2.0	279	9	CL600520	CL600520 OB_Ba006	C 663	18	2.0	398	2	BB739326
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C 592	18	2.0	283	2	AM610920	un62e11.x	C 665	18	2.0	399	2	BB739465
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C 602	18	2.0	297	7	CN373148	170005321	C 675	18	2.0	407	2	AM678919
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604	18	2.0	298	9	CG727653	CG727653	C 677	18	2.0	408	2	BB739051
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C 607	18	2.0	300	1	AA353896	EST62084	C 680	18	2.0	411	9	CG406789
C 608	18	2.0	301	4	BG056807	naf88d12.	C 681	18	2.0	412	5	BQ291765

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C 684	18	2.0	414	7	W71222	C 757	18	2.0	480	2	BF483049
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C 686	18	2.0	416	2	BE634013	C 759	18	2.0	482	2	BF656225
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C 688	18	2.0	417	2	BB867725	C 761	18	2.0	488	2	BE018390
C 689	18	2.0	417	9	CG665766	C 762	18	2.0	489	4	BG069417
C 690	18	2.0	418	1	A1306647	C 763	18	2.0	489	5	BMS19056
C 691	18	2.0	419	4	B1306647	C 764	18	2.0	490	9	CG644319
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C 694	18	2.0	420	5	BY455428	C 767	18	2.0	493	8	CC037853
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C 698	18	2.0	423	8	CC317303	C 771	18	2.0	497	2	BB703584
C 699	18	2.0	424	5	BY452483	C 772	18	2.0	498	6	CD884415
C 700	18	2.0	424	5	BY453155	C 773	18	2.0	498	7	CO608169
C 701	18	2.0	424	5	BY455417	C 774	18	2.0	500	9	CL389511
C 702	18	2.0	425	8	AZ336226	C 775	18	2.0	501	1	AA764559
C 703	18	2.0	429	7	CK994685	C 776	18	2.0	501	2	BB700621
C 704	18	2.0	432	4	BMS38399	C 777	18	2.0	502	1	AA798644
C 705	18	2.0	432	5	BY453513	C 778	18	2.0	503	2	BF059094
C 706	18	2.0	433	8	BM019942	C 779	18	2.0	504	1	A1825817
C 707	18	2.0	434	1	A1786425	C 780	18	2.0	504	2	BE495206
C 708	18	2.0	435	6	CD625238	C 781	18	2.0	506	2	BE141827
C 709	18	2.0	436	6	AJ618873	C 782	18	2.0	507	5	BX283844
C 710	18	2.0	437	1	AA244956	C 783	18	2.0	508	4	BJ545550
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C 712	18	2.0	437	5	BY452708	C 785	18	2.0	509	7	AV507941
C 713	18	2.0	438	1	A1866387	C 786	18	2.0	510	1	AV911558
C 714	18	2.0	439	1	AA312899	C 787	18	2.0	510	4	BM366990
C 715	18	2.0	440	8	AQ844593	C 788	18	2.0	512	1	A1929965
C 716	18	2.0	441	2	AA297264	C 789	18	2.0	512	6	CA250095
C 717	18	2.0	442	1	AV911632	C 790	18	2.0	512	2	CG733221
C 718	18	2.0	442	1	AV922863	C 791	18	2.0	513	2	BB768478
C 719	18	2.0	444	9	CL618608	C 792	18	2.0	513	6	CD287197
C 720	18	2.0	444	1	AA255215	C 793	18	2.0	515	1	A1870328
C 721	18	2.0	446	2	BF923718	C 794	18	2.0	515	7	CO606302
C 722	18	2.0	446	6	CA665679	C 795	18	2.0	516	5	CO608192
C 723	18	2.0	447	1	AL830276	C 796	18	2.0	517	5	BQ935673
C 724	18	2.0	447	5	BY461700	C 797	18	2.0	518	7	CO607265
C 725	18	2.0	447	6	BY552354	C 798	18	2.0	518	9	CG729571
C 726	18	2.0	450	2	BF304902	C 799	18	2.0	521	1	CD822234
C 727	18	2.0	450	2	BB861943	C 800	18	2.0	523	6	CD469905
C 728	18	2.0	450	5	BY465589	C 801	18	2.0	523	8	BH220165
C 729	18	2.0	451	2	BE499160	C 802	18	2.0	524	2	CG576389
C 730	18	2.0	451	7	R22000	C 803	18	2.0	526	2	BB656608
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C 733	18	2.0	454	2	AM989325	C 806	18	2.0	527	4	BU544434
C 734	18	2.0	454	6	BY598720	C 807	18	2.0	527	6	CA592300
C 735	18	2.0	455	2	BB747344	C 808	18	2.0	527	8	BH643063
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C 737	18	2.0	455	8	AQ849731	C 810	18	2.0	528	6	CA144206
C 738	18	2.0	456	2	BE676463	C 811	18	2.0	529	1	A1235000
C 739	18	2.0	456	4	BU210495	C 812	18	2.0	529	2	BF782362
C 740	18	2.0	460	1	AV927584	C 813	18	2.0	530	6	CA068313
C 741	18	2.0	460	7	CN399772	C 814	18	2.0	531	9	CG665190
C 742	18	2.0	462	4	BU518848	C 815	18	2.0	532	8	B2982140
C 743	18	2.0	462	6	CG713443	C 816	18	2.0	534	7	BU204086
C 744	18	2.0	468	1	CD730451	C 817	18	2.0	534	5	CK368584
C 745	18	2.0	469	2	BB796623	C 818	18	2.0	535	4	B2697505
C 746	18	2.0	469	7	CO608783	C 819	18	2.0	537	8	BH224999
C 747	18	2.0	470	2	AM198536	C 820	18	2.0	538	4	B2260932
C 748	18	2.0	470	7	CN218892	C 821	18	2.0	538	7	CO710311
C 749	18	2.0	471	2	BE692879	C 822	18	2.0	539	2	AM610923
C 750	18	2.0	473	6	BY589761	C 823	18	2.0	541	4	BM791927
C 751	18	2.0	475	4	BI346249	C 824	18	2.0	541	9	CG565430
C 752	18	2.0	477	5	W07718	C 825	18	2.0	542	6	CD727848
C 753	18	2.0	477	5	BP745837	C 826	18	2.0	543	7	CO609929
C 754	18	2.0	479	1	AI379719	C 827	18	2.0	545	4	BM596180

C 828	18	2.0	548	4	BG236294	na24f08.	C 901	18	2.0	601	6	CD306522
C 829	18	2.0	550	1	AI885504	wm24h02.x	902	18	2.0	602	6	CD817546
C 830	18	2.0	551	1	AI762288	wh66d05.x	903	18	2.0	602	6	CD820663
C 831	18	2.0	551	1	AA546528	vk65e09.18	C 904	18	2.0	603	8	BH832020
C 832	18	2.0	551	7	CO594172	DG2-91f19	C 905	18	2.0	604	6	BH718536
C 833	18	2.0	552	1	AI605786	mu24a07.y	C 906	18	2.0	605	2	BF228005
C 834	18	2.0	553	6	CA741698	AI605786	C 907	18	2.0	605	7	CO604962
C 835	18	2.0	555	6	CR303436	wia1c.pk0	C 908	18	2.0	607	2	BE493790
C 836	18	2.0	555	4	BZ56742	Medicago	C 909	18	2.0	607	2	BE664533
C 837	18	2.0	556	4	BP767143	BP767143	C 910	18	2.0	608	7	CO712807
C 838	18	2.0	556	5	BQ239244	TAE05035D	C 911	18	2.0	608	8	AI052547
C 839	18	2.0	556	5	BU96044	HM12D19-	C 912	18	2.0	608	8	BH915497
C 840	18	2.0	556	6	CA593280	wpa1c.pk0	C 913	18	2.0	609	9	FR0029055
C 841	18	2.0	557	7	CO719056	DG14-76f1	C 914	18	2.0	611	2	BB623694
C 842	18	2.0	558	1	AY909731	AY909731	C 915	18	2.0	612	4	BM660455
C 843	18	2.0	559	4	BI100783	602886081	C 916	18	2.0	612	8	AO116232
C 844	18	2.0	559	5	BP306588	BP306588	C 917	18	2.0	614	4	BI245744
C 845	18	2.0	560	4	BJ260984	BJ260984	C 918	18	2.0	615	4	BU256520
C 846	18	2.0	560	5	BO655359	NXRV093.D	C 919	18	2.0	615	7	CN399778
C 847	18	2.0	560	6	CA215572	SCRLAD13	C 920	18	2.0	615	8	BE940341
C 848	18	2.0	561	2	BP195052	BP195052	C 921	18	2.0	616	4	BI067502
C 849	18	2.0	561	5	BP768884	BP768884	C 922	18	2.0	616	4	BM734823
C 850	18	2.0	562	6	CA086011	SCMCM208	C 923	18	2.0	617	7	CR959453
C 851	18	2.0	562	7	BI011266	WHE2648.E	C 924	18	2.0	618	9	CE409178
C 852	18	2.0	563	4	AI799505	QV2-EN009	C 925	18	2.0	619	2	BF048855
C 853	18	2.0	564	1	CR456896	t1gr-g88-	C 926	18	2.0	620	2	BE364671
C 854	18	2.0	566	2	BE075017	PM3-BT058	C 927	18	2.0	623	4	BM226244
C 855	18	2.0	567	2	BZ951001	CH240_430	C 928	18	2.0	623	4	BU619028
C 856	18	2.0	567	8	CG266643	CG266643	C 929	18	2.0	624	6	CD675259
C 857	18	2.0	568	9	CO606268	DG8-4e2.D	C 930	18	2.0	624	6	CO610908
C 858	18	2.0	569	2	AM955331	EST67401	C 931	18	2.0	626	7	CP125918
C 859	18	2.0	572	2	AA863889	vx15611.r	C 932	18	2.0	628	1	AI7889261
C 860	18	2.0	573	1	CO604848	DG8-2E20	C 933	18	2.0	628	1	BU546833
C 861	18	2.0	574	8	AZ149003	SP_0048.A	C 934	18	2.0	628	6	CA187967
C 862	18	2.0	575	8	AI802012	AI802012	C 935	18	2.0	629	1	AV944406
C 863	18	2.0	576	1	BM18499	P11_14.C1	C 936	18	2.0	629	7	CO610014
C 864	18	2.0	577	4	BP291361	BP291361	C 937	18	2.0	632	4	BM425797
C 865	18	2.0	577	5	AU018875	AU018875	C 938	18	2.0	632	4	CH255543
C 866	18	2.0	578	7	CO534389	CO534389	C 939	18	2.0	632	6	CA255543
C 867	18	2.0	578	1	BM702300	BM702300	C 940	18	2.0	636	6	CA078491
C 868	18	2.0	581	4	BH219763	BH219763	C 941	18	2.0	636	6	BM660454
C 869	18	2.0	581	8	BE405439	WHE1216.D	C 942	18	2.0	637	6	CD468639
C 870	18	2.0	583	2	BF035663	60145349	C 943	18	2.0	637	6	CD818213
C 871	18	2.0	583	2	CE161053	t1gr-g88-	C 944	18	2.0	642	6	CD819830
C 872	18	2.0	583	9	BM426831	PG12n.pk0	C 945	18	2.0	642	6	BJ481569
C 873	18	2.0	585	4	CO609060	DG8-7911	C 946	18	2.0	644	8	BE968205
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C 875	18	2.0	585	7	CK995633	050E6R1.	C 948	18	2.0	646	1	AJ788752
C 876	18	2.0	586	4	BM539700	hb12h06.y	C 949	18	2.0	646	1	BB652074
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C 881	18	2.0	587	6	CR771287	DKF2D469M	C 954	18	2.0	650	4	BJ247197
C 882	18	2.0	588	4	BI695945	BI695945	C 955	18	2.0	650	4	BJ698517
C 883	18	2.0	590	1	AA544952	vk38e08.r	C 956	18	2.0	650	4	CD454430
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C 885	18	2.0	591	2	CK991859	004G10A1.	C 958	18	2.0	651	6	BY737916
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C 887	18	2.0	592	2	AJ560115	AJ560115	C 960	18	2.0	652	9	AG050060
C 888	18	2.0	593	1	AL661308	AL661308	C 961	18	2.0	653	9	CO534798
C 889	18	2.0	594	1	CB157849	K-EST0216	C 962	18	2.0	653	8	AZ935348
C 890	18	2.0	594	4	BM598418	BM598418	C 963	18	2.0	654	5	BY308757
C 891	18	2.0	594	6	CD817293	BN20_04IG	C 964	18	2.0	654	5	CD822730
C 892	18	2.0	594	6	CO534799	3530_1_23	C 965	18	2.0	655	6	BM737916
C 893	18	2.0	595	6	CD824540	BN25_0530	C 966	18	2.0	656	6	CD426447
C 894	18	2.0	595	6	CE095785	t1gr-g88-	C 967	18	2.0	657	8	BH390838
C 895	18	2.0	597	9	CG177790	PUI0M687D	C 968	18	2.0	660	1	AJ794462
C 896	18	2.0	597	9	AW764187	ut72c11.x	C 969	18	2.0	660	2	BE385619
C 897	18	2.0	598	2	BJ545295	BU545295	C 970	18	2.0	662	1	AI991964
C 898	18	2.0	598	4	CD822173	BN25_044E	C 971	18	2.0	662	1	CD353332
C 899	18	2.0	601	1	AJ804038	AJ804038	C 972	18	2.0	662	6	CG179399
C 900	18	2.0	601	1	AJ804038	AJ804038	C 973	18	2.0	662	9	CG179399

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C 974 18 2.0 663 2 BE253429 601111691
C 975 18 2.0 663 6 CD222742 CCC1_23-A
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C 977 18 2.0 668 2 AM700937 un68a09.x
C 978 18 2.0 671 8 AZ934855 BJ_Ba000
C 979 18 2.0 672 5 BU683533 UI-CP-EC1
C 980 18 2.0 672 7 CP127051 UI-HF-E70
C 981 18 2.0 672 7 CN743121 SAL_US031
C 982 18 2.0 673 6 CA053928 s8a1xga50
C 983 18 2.0 675 2 CF627730 zmrw05.0
C 984 18 2.0 676 2 AM974521 EST386625
C 985 18 2.0 676 4 BG477951 602522935
C 986 18 2.0 676 5 BM973307 UI-CP-EC1
C 987 18 2.0 676 8 AZ933847 BJ_Ba000
C 988 18 2.0 677 9 AG150161 Pan t901
C 989 18 2.0 678 2 AM641538 cm08e06.w
C 990 18 2.0 679 5 BU661207 c169b12.z
C 991 18 2.0 680 7 CO473387 G00048_TB
C 992 18 2.0 680 9 CC686909 OG0AG821V
C 993 18 2.0 681 2 BE728278 BU1662143
C 994 18 2.0 681 6 CA211643 SCRLAD110
C 995 18 2.0 683 4 BU622127 BU622127
C 996 18 2.0 683 5 BU630191 UI-H-FE1-
C 997 18 2.0 684 1 AV257436 AV257436
C 998 18 2.0 684 5 BM971607 UI-CP-EC1
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## ALIGNMENTS

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RESULT 1 1053 bp mRNA linear HTC 21-JUL-2004
CR604307 full-length cDNA clone CS0DL006YLO9 of B cells (Ramos cell line)
LOCUS CR604307 Cot 25-normalized of Homo sapiens (human).
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ACCESSION CR604307.1 GI:50485114  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1053)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@life.technet.com URL:  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1053)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail: seque@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES  
Location/Qualifiers  
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/mol\_type="mRNA"  
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/clone="CS0DL006YLO9"  
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/plasmid="pCMVSPORT\_6"

ORIGIN

Query Match 94.4%; Score 858; DB 3; Length 1053;

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Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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99 ATGGCGCATCCGGGTCGACCCCGGCGCGTGGAGAGAGATGCTGGACATC 158  
61 TACGGGATGCTGCTTCAACCGATATGTTGAGGTGTGGCGGCACTGACAGTGC 120  
159 TACGGGATGCTGCTTCAACCGATATGTTGAGGTGTGGCGGCACTGACAGTGC 218  
121 GAGCTGAGGCTTCTGCTTCTGCTGATGAGGTCTCTGGCGCGCGGAGGCTTACC 180  
219 GAGCTGAGGCTTCTGCTTCTGCTGATGAGGTCTCTGGCGCGCGGAGGCTTACC 278  
181 CGGGCCGCGCGGCTTCTGCTTCTGCTGAGTGGAGCGCGCGGCGGCGGCGAG 240  
279 CGGGCCGCGCGGCTTCTGCTTCTGCTGAGTGGAGCGCGCGGCGGCGGCGAG 338  
241 AGCAACCTGCGGCTGCTGGGCAACTCTGCGCGTGTGACCGCGCACTGCTGCG 300  
339 AGCAACCTGCGGCTGCTGGGCAACTCTGCGCGTGTGACCGCGCACTGCTGCG 398  
301 CACCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
399 CACCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 458  
361 AGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
459 AGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518  
421 AATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
519 AATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578  
481 CGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
579 CGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 638  
541 CAGAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
639 CAGAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698  
601 CGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
699 CGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 758  
661 CGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
759 CGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 818  
721 TCAAGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
819 TCAAGGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878  
781 GCCTTCTGGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
879 GCCTTCTGGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938  
841 ACTGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
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999 GAGGCTGAC 1007
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RESULT 2 1860 bp mRNA linear HTC 21-JUL-2004  
CR593642 full-length cDNA clone CS0DK010YK16 of HeLa cells Cot 25-normalized  
LOCUS CR593642  
DEFINITION of Homo sapiens (human).
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ACCESSION CR593642  
VERSION CR593642.1 GI:50474449  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@life.technet.com URL :  
http://fulllength.invitrogen.com/InvitrogenCorporation1600  
Faraday Avenue  
2 (bases 1 to 1860)  
REFERENCE  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
LOCATION/Qualifiers  
1..1860  
/organism="Homo sapiens"  
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/clone="CSODK010YK16"  
/issue\_type="Hela cells Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 94.4%; Score 858; DB 3; Length 1860;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGGGCTATCCGGGTCGACCCCGGCGGCTGCTGGAGAGAGATGAGCTTGAATC 60  
DB 71 ATGGGCTATCCGGGTCGACCCCGGCGGCTGCTGGAGAGAGATGAGCTTGAATC 130  
QY 61 TACGGGATGCTGCTGCTTACCGATATGTCGAGTGTGGGGGCAATGACCGAGTTC 120  
DB 131 TACGGGATGCTGCTGCTTACCGATATGTCGAGTGTGGGGGCAATGACCGAGTTC 190  
QY 121 GAGCTGAGACTCTGCGCTTCTGCTGAGTGAAGCTCTGCGCGCCGCGAGGCTTAA 180  
DB 191 GAGCTGAGACTCTGCGCTTCTGCTGAGTGAAGCTCTGCGCGCCGCGAGGCTTAA 250  
QY 181 CGGGCCCGGAGCGGCTTGAAGCTCTGCTGAGTGAAGCTCTGCGCGCGAGTTCG 240  
DB 251 CGGGCCCGGAGCGGCTTGAAGCTCTGCTGAGTGAAGCTCTGCGCGCGAGTTCG 310  
QY 241 AGCAACTGCGGCTGCTGCGGCACTCTGCGGCTGCTGCGCGCGAGGCTTGA 300  
DB 311 AGCAACTGCGGCTGCTGCGGCACTCTGCGGCTGCTGCGCGCGAGGCTTGA 370  
QY 301 CACCTGCGCGGAGCGGCGCGGCGGCACTCTGCGGCGGAGGCTTGA 360  
DB 371 CACCTGCGCGGAGCGGCGCGGCGGCACTCTGCGGCGGAGGCTTGA 430  
QY 361 AGCTTCTTCAAG 420  
DB 431 AGCTTCTTCAAG 490  
QY 421 AATTCTCAGCAG 480  
DB 491 AATTCTCAGCAG 550  
QY 481 CGGGGCGGCGGAGTGTGTGTCAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 540

DB 551 CGGGGCGGCGGAGTGTGTGTCAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 610  
QY 541 CAGCAGTGAAG 600  
DB 611 CAGCAGTGAAG 670  
QY 601 CGGGTTCAG 660  
DB 671 CGGGTTCAG 730  
QY 661 CGGGCCCGGAGCGGCTGCGCGGAGTGAAGCTGTTGGGCAAGCCAGAGTTCGCG 720  
DB 731 CGGGCCCGGAGCGGCTGCGCGGAGTGAAGCTGTTGGGCAAGCCAGAGTTCGCG 790  
QY 721 TCAAGGAGCTGGGCTGTGTGTTGATGATCAAGTCTCAGAGCTCCATCTGAGC 780  
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QY 781 GCTTCTGGGCGAGTCACTGAGTGGCGGCTGCTGAGAGGCTTGGGCGGCTGTTCTG 840  
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QY 841 ACTGAGGCTTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900  
DB 911 ACTGAGGCTTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 970  
QY 901 GAGGCTGAC 909  
DB 971 GAGGCTGAC 979  
RESULT 3  
CR619301  
LOCUS CR619301 1866 bp mRNA linear HTC 21-JUL-2004  
DEFINITION Full-length cDNA clone CSODC015Y24 of Neuroblastoma Cot  
25-normalized of Homo sapiens (human).  
ACCESSION CR619301  
VERSION CR619301.1 GI:50500108  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@life.technet.com URL :  
http://fulllength.invitrogen.com/InvitrogenCorporation1600  
Faraday Avenue  
2 (bases 1 to 1860)  
REFERENCE  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
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Query Match 94.4%; Score 858; DB 3; Length 1866;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches	908; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
Qy	1	ATGGGCGCTATCCGGGGTCCACCCCGGCCCCGCTGCTGGAGAGAGATGAGTGCCTTGGACATAC	60		
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Qy	61	TACGGGATGCTGTGCTTCACCGTATGTTTCAGAGTGTGTGGCGGGCAACTGACCCAGTGC	120		
Db	136	TACGGGATGCTGTGCTTCACCGTATGTTTCAGAGTGTGTGGCGGGCAACTGACCCAGTGC	195		
Qy	121	GAGCTGGAAGCTCTTGGGCTTTTCTGCTGGAATGAGGCTCCTGGCGCGGACGGAGCTTACGC	180		
Db	136	GAGCTGGAAGCTCTTGGGCTTTTCTGCTGGAATGAGGCTCCTGGCGCGGACGGAGCTTACGC	255		
Qy	181	CGGGCCCGCAGCGGAGCTAGAGCTCTGCTGAGCTGAGACGCGCGGCGGAGTGCAGCAG	240		
Db	256	CGGGCCCGCAGCGGAGCTAGAGCTCTGCTGAGCTGAGACGCGCGGCGGAGTGCAGCAG	315		
Qy	241	AGCAACTGTGGGCTGTGGGGCACTCTGCGCGTGTCTGGCCCGCAGCACTGTGTGCG	300		
Db	316	AGCAACTGTGGGCTGTGGGGCACTCTGCGCGTGTCTGGCCCGCAGCACTGTGTGCG	375		
Qy	301	CACCTGGGCGGCAAGGGGCGCGGCGCAGTGTCTCAGAAAGCTATAGCTATAGGCACTCC	360		
Db	376	CACCTGGGCGGCAAGGGGCGCGGCGCAGTGTCTCAGAAAGCTATAGCTATAGGCACTCC	435		
Qy	361	AGCTCTTCAAAAGAGACAGAGGGTAGCTGCGCTGCCTCGCTCGCAGTCAAGCATTTCTGCA	420		
Db	436	AGCTCTTCAAAAGAGACAGAGGGTAGCTGCGCTGCCTCGCTCGCAGTCAAGCATTTCTGCA	495		
Qy	421	AATTTTCAGCAGGGTCACTGTGGGAGACAGGCTTCCCCCAACCAAGCGGACGGCGGAGT	480		
Db	496	AATTTTCAGCAGGGTCACTGTGGGAGACAGGCTTCCCCCAACCAAGCGGACGGCGGAGT	555		
Qy	481	CGGGCCCGGCGCAGTGTGTGTGTCACAGACGCGCGGAGAGGGGGCCGACCGGCAACCCAG	540		
Db	556	CGGGCCCGGCGCAGTGTGTGTGTCACAGACGCGCGGAGAGGGGGCCGACCGGCAACCCAG	615		
Qy	541	CAGCAGTGAAGACCCGCGCAGACTTCTCTGTGAAGCAAGTGA	CCTGTGACATCCGAGTCC	600	
Db	616	CAGCAGTGAAGACCCGCGCAGACTTCTCTGTGAAGCAAGTGA	CCTGTGACATCCGAGTCC	675	
Qy	601	CGGGTTCGAGCAGATATCTGCGAGATGGGCCAGGCTTGGAGCAAGGGGCTGTGCAATCCCGG	660		
Db	676	CGGGTTCGAGCAGATATCTGCGAGATGGGCCAGGCTTGGAGCAAGGGGCTGTGCAATCCCGG	735		
Qy	661	CGGCCCCAGGCGCTGCGCGCGCAGCTGAGCGTGTGTGGGACGATGTCAGTGTGCGC	720		
Db	736	CGGCCCCAGGCGCTGCGCGCGCAGCTGAGCGTGTGTGGGACGATGTCAGTGTGCGC	795		
Qy	721	TCAAGGAGCTGGGGCTGTGTGGTTTGTACATCAAGTTCTCAGAGCTCTCTATCTGAGC	780		
Db	796	TCAAGGAGCTGGGGCTGTGTGGTTTGTACATCAAGTTCTCAGAGCTCTCTATCTGAGC	855		
Qy	781	GCCTTCGCGGCGACTTACCTGAGTGGCGCCCTGTCTGACAGGCTTGGGGGGGTGTTCTCG	840		
Db	856	GCCTTCGCGGCGACTTACCTGAGTGGCGCCCTGTCTGACAGGCTTGGGGGGGTGTTCTCG	915		
Qy	841	ACTGAGGCGCTTGCAGAGGCTGTGGGCGGAGGCTGTTCCGCTGCTGTCAGTGTGAT	900		
Db	916	ACTGAGGCGCTTGCAGAGGCTGTGGGCGGAGGCTGTTCCGCTGCTGTCAGTGTGAT	975		
Qy	901	GAGGCTGAC	909		
Db	976	GAGGCTGAC	984		

RESULT 4

CR625070

LOCUS

DEFINITION

ACCESSION

1894 bp

mRNA

linear

HTC 21-JUL-2004

Full-length cDNA clone CS0DC001Y18 of Neuroblastoma Cot

25-normalized of Homo sapiens (human).

CR625070

RESULT 4  
CR625070  
LOCUS  
DEFINITION  
ACCESSION

CR625070  
full-length cDNA clone CS0DC001Y18 of Neuroblastoma Cot  
25-normalized of Homo sapiens (human).

1894 bp mRNA linear HTC 21-JUL-2004

CR625070

VERSION	CR625070.1	GI:50505877		
KEYWORDS	HTC; cNSLT_cDNA.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1894)			
REFERENCE	Genoscope.			
AUTHORS	Direct Submission			
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ;			
JOURNAL	BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)			
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(4T) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.			
FEATURES	Location/Qualifiers			
source	1..1894 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DC001Y18" /tissue_type="Neuroblastoma Cot 25-normalized" /plasmid="pCMVSPORT_6"			
ORIGIN				
Query Match	94.4%; Score 858; DB 3; Length 1894;			
Best Local Similarity	99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;			
Matches	908; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
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Db	89	ATGGCGTATCCGGGTGCA	CCCCGGCCCCGCTGCTGGAAGAGATGAGTGCCTGAGATAC	148
Qy	61	TACGGGATGCTGCTGCTTCA	CCGTTATGTTTCAAGTGTGTGGCGGCAACTGACCCAGTGC	120
Db	149	TACGGGATGCTGCTGCTTCA	CCGTTATGTTTCAAGTGTGTGGCGGCAACTGACCCAGTGC	208
Qy	121	GAGCTGAGAGCTCTGGGCTTTCTG	CGATGAGTGGGCTCCGGGGCCGCGGAGAGCTTACGC	180
Db	209	GAGCTGAGAGCTCTGGGCTTTCTG	CGATGAGTGGGCTCCGGGGCCGCGGAGAGCTTACGC	268
Qy	181	CGGGCCCGCAGCGGCTTGAAGCTCT	GTGAGTGAAGCGCCGCGGCGAGTGCAGCAG	240
Db	269	CGGGCCCGCAGCGGCTTGAAGCTCT	GTGAGTGAAGCGCCGCGGCGAGTGCAGCAG	328
Qy	241	AGCAACTGCGGCTGCTGAGGCA	CTCTGCGCGTGTGCGCCGCGCAGACTGCTGCG	300
Db	329	AGCAACTGCGGCTGCTGAGGCA	CTCTGCGCGTGTGCGCCGCGCAGACTGCTGCG	388
Qy	301	CACCTGCGCGCAAGCGGCGCGG	CGCAGTGTCTCAGAAAGCTATAGCTATGGCACTCC	360
Db	389	CACCTGCGCGCAAGCGGCGCGG	CGCAGTGTCTCAGAAAGCTATAGCTATGGCACTCC	448
Qy	361	AGCTCTTCAAAAGAGACAGAGG	TAGTGTGCGCGCTGCGCGGCGAGTCAAGCATTTCTGCA	420
Db	449	AGCTCTTCAAAAGAGACAGAGG	TAGTGTGCGCGCTGCGCGGCGAGTCAAGCATTTCTGCA	508
Qy	421	AATTTTCAGCAGGGTCACTG	GGAGACAGGCTTCCCCCAACCAAGCGGACGGCGGAGT	480
Db	509	AATTTTCAGCAGGGTCACTG	GGAGACAGGCTTCCCCCAACCAAGCGGACGGCGGAGT	568
Qy	481	CGGGCCCGGCGCAGTGTGTG	TGTCAGACGCGCGGAGAGGGGGCCGACCGGCAACCCAG	540
Db	569	CGGGCCCGGCGCAGTGTGTG	TGTCAGACGCGCGGAGAGGGGGCCGACCGGCAACCCAG	628

QY 541 CAGCAGTCAAGAGCCGCGGAGACCTTCTCTGAAGCAAGTACCTGTGACATCGGCTC 600  
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 QY 601 CGGGTTTCAGAGCAAGTACTGCGAGCATGCGCCAGCTTGGAGCAGGCGCTGGCATCCCGG 660  
 DB 689 CGGGTTTCAGAGCAAGTACTGCGAGCATGCGCCAGCTTGGAGCAGGCGCTGGCATCCCGG 748  
 QY 661 CGGGCCCGAGCGCTGCGGCGGAGCTGGAAGCTGTTTGGGCAAGCCACCGCATGCTGCGC 720  
 DB 749 CGGGCCCGAGCGCTGCGGCGGAGCTGGAAGCTGTTTGGGCAAGCCACCGCATGCTGCGC 808  
 QY 721 TCAAGGAGCCTGGGCTGTGTGTTTGTGATCAATGATTCAGAGCTCTCATCTGAGC 780  
 DB 809 TCAAGGAGCCTGGGCTGTGTGTTTGTGATCAATGATTCAGAGCTCTCATCTGAGC 868  
 QY 781 GCGTTTCTGGGCGGAGTACCTGAGTGGCGCCCTGCTGACAGGCGCTGGGCGGCTGCTG 840  
 DB 869 GCGTTTCTGGGCGGAGTACCTGAGTGGCGCCCTGCTGACAGGCGCTGGGCGGCTGCTG 928  
 QY 841 ACTGAGGCGCTGCGAGAGGCTGTGGCGCGGAGGCTGTGCTGCTGCTGCTGCTGCTG 900  
 DB 929 ACTGAGGCGCTGCGAGAGGCTGTGGCGCGGAGGCTGTGCTGCTGCTGCTGCTGCTG 988  
 QY 901 GAGGCTGAC 909  
 DB 989 GAGGCTGAC 997

RESULT 5  
 LOCUS BM920838 1090 bp mRNA linear EST 12-MAR-2002  
 DEFINITION AGENCOURT\_6706034 NIH\_MGC\_115 Homo sapiens CDNA clone IMAGE:5752092  
 5', mRNA sequence.  
 ACCESSION BM920838  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 1090)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLMT at:  
 http://image.llnl.gov  
 Plate: L14M12785 row: 1 column: 13  
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 /clone\_lib="NIH\_MGC\_115"  
 /note="Organ: Pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27, and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.

ORIGIN  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."

Query Match 66.8%; Score 607; DB 5; Length 1090;  
 Best Local Similarity 99.8%; Pred. No. 2.2e-297;  
 Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCGGGTCGACCCCGGCGGCTGCGGAGAGAGATGAGCTTGGACTAC 60  
 DB 102 ATGGCGCTATCGGGTCGACCCCGGCGGCTGCGGAGAGATGAGCTTGGACTAC 161  
 QY 61 TACGGAGATGCTGCTTCAACCGTATGTTGAGTGTGGCGGCAACTGACCGAGTGC 120  
 DB 162 TACGGAGATGCTGCTTCAACCGTATGTTGAGTGTGGCGGCAACTGACCGAGTGC 221  
 QY 121 GAGCTGAGAGCTCTGCGCTTTTCTGCTGATGAGGCTCTGCGCGCGCGGAGCTTAAAGC 180  
 DB 222 GAGCTGAGAGCTCTGCGCTTTTCTGCTGATGAGGCTCTGCGCGCGCGGAGCTTAAAGC 281  
 QY 181 CGGGCCCGAGCGGCTGAGAGCTCTGCTGAGGCTGAGGCGCGGCGGAGCTGCGGCGG 240  
 DB 282 CGGGCCCGAGCGGCTGAGAGCTCTGCTGAGGCTGAGGCGCGGCGGAGCTGCGGCGG 341  
 QY 241 AGCAACTGCGGCTGCTGCGGCACTCTGCGGCTGAGGCTGCGGCGGCACTGCTGCGG 300  
 DB 342 AGCAACTGCGGCTGCTGCGGCACTCTGCGGCTGAGGCTGCGGCGGCACTGCTGCGG 401  
 QY 301 CACTGGGCGCGAGCGGCGGCGGCGGCACTGCTGCGGCACTGCTGCGGCACTGCTGCGG 360  
 DB 402 CACTGGGCGCGAGCGGCGGCGGCGGCACTGCTGCGGCACTGCTGCGGCACTGCTGCGG 461  
 QY 361 AGCTTTTAAAGAGAGAGAGGCTGAGGCTGCGGCTGCGGCGGCACTGCTGCGGCACTG 420  
 DB 462 AGCTTTTAAAGAGAGAGGCTGAGGCTGCGGCTGCGGCGGCACTGCTGCGGCACTG 521  
 QY 421 AATTCTCAGCAGAGGCTGAGGAGAGAGGCTGCGGCTGCGGCGGCACTGCTGCGGCACT 480  
 DB 522 AATTCTCAGCAGAGGCTGAGGAGAGAGGCTGCGGCTGCGGCGGCACTGCTGCGGCACT 581  
 QY 481 CGGGCCCGGCGGAGGCTGAGGAGAGAGGCTGCGGCTGCGGCGGCACTGCTGCGGCACT 540  
 DB 582 CGGGCCCGGCGGAGGCTGAGGAGAGAGGCTGCGGCTGCGGCGGCACTGCTGCGGCACT 641  
 QY 541 CAGCAGTCAAGAGCCGCGGAGACCTTCTCTGAAGCAAGTACCTGTGACATCGGCTC 600  
 DB 642 CAGCAGTCAAGAGCCGCGGAGACCTTCTCTGAAGCAAGTACCTGTGACATCGGCTC 701  
 QY 601 CGGGTTTCAGAGCAAGTACTGCGAGCATGCGCCAGCTTGGAGCAGGCGCTGGCATCC 658  
 DB 702 CGGGTTTCAGAGCAAGTACTGCGAGCATGCGCCAGCTTGGAGCAGGCGCTGGCATCC 759

RESULT 6  
 LOCUS BG685173 800 bp mRNA linear EST 01-MAY-2001  
 DEFINITION 602637058P1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:474639 5',  
 mRNA sequence.  
 ACCESSION BG685173  
 VERSION BG685173.1 GI:13916570  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 800)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.jnl.gov>  
Plate: LNCM1622 row: d column: 16  
High quality sequence stop: 794.  
Location/Qualifiers

FEATURES  
source

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/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming;
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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## ORIGIN

Query Match 64.5%; Score 586; DB 4; Length 800;  
Best Local Similarity 100.0%; Pred. No. 1.1e-286;  
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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119 CGAGGCAACCTGCGGCTGCTGGGCAACTCTCTGGCGCTGCGCCGCGACGACTTCT 178
297 GCCGCACTGGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAAAGCTATAGTATGAGAC 356
179 GCCGCACTGGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAAAGCTATAGTATGAGAC 238
357 CTCGAGCTCTTCAAGAGAGACAGAGAGTGTCTGCGCGCGCTGCGGAGTCAAGAGTTTC 416
239 CTCGAGCTCTTCAAGAGAGACAGAGAGTGTCTGCGCGCGCTGCGGAGTCAAGAGTTTC 298
417 TGCAAATTTCTCAGCAGGAGTCAAGAGAGTGTCTGCGCGCGCTGCGGAGTCAAGAGTTTC 476
299 TGCAAATTTCTCAGCAGGAGTCAAGAGAGTGTCTGCGCGCGCTGCGGAGTCAAGAGTTTC 358
477 GAGTCGGGCGGCGGCAAGCGGCGCGGCGAGTGTCTGCGCGCGCTGCGGAGTCAAGAGTTTC 536
359 GAGTCGGGCGGCGGCAAGCGGCGCGGCGAGTGTCTGCGCGCGCTGCGGAGTCAAGAGTTTC 418
537 CCAGCAGCAGTCAAGAGCGGCGGCAAGCTTCTCTGAAAGCAAGTGAATCTGAGATCCG 596
419 CCAGCAGCAGTCAAGAGCGGCGGCAAGCTTCTCTGAAAGCAAGTGAATCTGAGATCCG 478
597 GCTCCGGGTTGAGAGAGTACTGAGAGATGAGGCGACGCTTGGAGAGCGGCGTGGCATC 656
479 GCTCCGGGTTGAGAGAGTACTGAGAGATGAGGCGACGCTTGGAGAGCGGCGTGGCATC 538
657 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 716
539 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 598
717 GCGCTCAAGGAGACCTGGGCTGTGGTTTGTGAATCAAGTTCTCAGAGCTCTCTAATCT 776
599 GCGCTCAAGGAGACCTGGGCTGTGGTTTGTGAATCAAGTTCTCAGAGCTCTCTAATCT 658
777 GGAAGCCTTCTGGGCGGAGTACTGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 822
659 GGAAGCCTTCTGGGCGGAGTACTGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 704
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RESULT 7

B1907024 634 bp mRNA linear EST 16-OCT-2001  
LOCUS 603064980F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5214211 5',  
DEFINITION mRNA sequence.  
ACCESSION B1907024  
VERSION B1907024.1 GI:16169804  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 634)  
NIH-MGC <http://nigc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.jnl.gov>  
Plate: LNCM11537 row: p column: 20  
High quality sequence stop: 632.  
Location/Qualifiers

FEATURES  
source

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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donor. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
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## ORIGIN

Query Match 64.0%; Score 582; DB 4; Length 634;  
Best Local Similarity 100.0%; Pred. No. 1.2e-284;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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328 GTGTCTCCAGAACCTATAGTATGACACTTCAGCTCTTCAAGAGAGAGAGGTTAGC 387
32 GTGTCTCCAGAACCTATAGTATGACACTTCAGCTCTTCAAGAGAGAGAGGTTAGC 91
388 TGCCTGCGCGTGGGAGTCAAGAGTGTCTGCAAAATTTCTAGCAGGGTCACTGGAGACA 447
92 TGCCTGCGCGTGGGAGTCAAGAGTGTCTGCAAAATTTCTAGCAGGGTCACTGGAGACA 151
448 GGTCTCCCCCAACCAAGCGGCGGAGGAGTGTGGGGGCGGCGGCGGCGGCGGCGGCGG 507
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508 CCGGCGGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 567
212 CCGGCGGAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 271
568 TCTGAAGGCAAGTGAACCTGTGACATCGGCTCCGGGTTGAGAGAGTACTGGAGCAT 627
272 TCTGAAGGCAAGTGAACCTGTGACATCGGCTCCGGGTTGAGAGAGTACTGGAGCAT 331
628 GGGCGAGCCTTGGAGAGAGGAGTGGCATCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 687
332 GGGCGAGCCTTGGAGAGAGGAGTGGCATCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 391
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QY 688 GACGTGTTGGGACAGCCACCGCAGTGTGCGCTCAAGGAGCCTGGGCTCTGTGGTTGT 747  
DB 392 GACGTGTTGGGACAGCCACCGCAGTGTGCGCTCAAGGAGCCTGGGCTCTGTGGTTGT 451  
QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGAGTACTTGAAGTGC 807  
DB 452 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGAGTACTTGAAGTGC 511  
QY 808 GCGGCGCTGACAGCCCTGCGGGGCGTGTCTGACGAGGCGCTGCGAGAGGCTGTGGC 867  
DB 512 GCGGCGCTGACAGCCCTGCGGGGCGTGTCTGACGAGGCGCTGCGAGAGGCTGTGGC 571  
QY 868 GCGGAGGCTGTGCGCTGCTGTGCTGATGTGATGAGGCTGAC 909  
DB 572 GCGGAGGCTGTGCGCTGCTGTGCTGATGTGATGAGGCTGAC 613

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DEFINITION mRNA sequence.

ACCESSION BI910528  
VERSION BI910528.1 GI:16173927  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 905)  
NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHM11545 row: n column: 03  
High quality sequence stop: 863.

FEATURES  
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/clone\_1fb="NIH\_MGC\_118"  
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC library."

## ORIGIN

Query Match 64.0%; Score 582; DB 4; Length 905;  
Best Local Similarity 100.0%; Pred. No. 1.2e-284;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 GGTGTCGCAAGCGCATAGCATAGGCACTCCAGCTCTTCAAGGAGCAGAGGGTACG 387  
DB 38 GTGTCTCCAGAACGCTATAGCTATGGCACCTCCAGCTTCAAGGAGCAGAGGGTACG 97

QY 388 TGCCGTGCGCCGTGCGCAGTCAAGCATTTCTGCAAAATTTCTCAGCAGGCTCACTGGAGACA 447  
DB 98 TGCCGTGCGCCGTGCGCAGTCAAGCAGTTCTGCAAAATTTCTCAGCAGGCTCACTGGAGACA 157  
QY 448 GGCTCCCCCACAACACGGGACAGGGGAGTCCGGGGCCGGCCCAAGTGTGTCCAGA 507  
DB 158 GGCTCCCCCACAACACGGGACAGGGGAGTCCGGGGCCGGCCCAAGTGTGTCCAGA 217  
QY 508 GCGGCGCGGAGAGGGGGCCCGACCGGACCCGACAGAGTGAAGCCCGGACGACTTCC 567  
DB 218 GCGGCGCGGAGAGGGGGCCCGACCGGACCCGACAGAGTGAAGCCCGGACGACTTCC 277  
QY 568 TCTGAAGCAAAAGTACCTGTGACATCCGCGCTCGGGTTTGGACAGAGTACTGCGAGCAT 627  
DB 278 TCTGAAGCAAAAGTACCTGTGACATCCGCGCTCGGGTTTGGACAGAGTACTGCGAGCAT 337  
QY 628 GGGCCAGCTTTGAGACAGGCGTGGCATTCGGGCGGGCCCGACGGCTGGCGGCGAGCTG 687  
DB 338 GGGCCAGCTTTGAGACAGGCGTGGCATTCGGGCGGGCCCGACGGCTGGCGGCGAGCTG 397  
QY 688 GACGTGTTGGGACAGCCACCGCAGTGTGCGCTCAAGGAGCCTGGGCTCTGTGGTTGT 747  
DB 398 GACGTGTTGGGACAGCCACCGCAGTGTGCGCTCAAGGAGCCTGGGCTCTGTGGTTGT 457  
QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGAGTACTTGAAGTGC 807  
DB 458 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGAGTACTTGAAGTGC 517  
QY 808 GCGGCTGTGACAGGCGCTTGGGGGCGTGTCTGATGAGGCGCTTGGAGAGGCTGTGGC 867  
DB 518 GCGGCTGTGACAGGCGCTTGGGGGCGTGTCTGATGAGGCGCTTGGAGAGGCTGTGGC 577  
QY 868 GCGGAGGCTGTGCGCTGCTGTGCTGATGTGATGAGGCTGAC 909  
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RESULT 9  
BG251151 927 bp mRNA linear EST 13-FEB-2001  
LOCUS 602364954P1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4473349 5',  
DEFINITION mRNA sequence.

ACCESSION BG251151  
VERSION BG251151.1 GI:12760967  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 927)  
NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHM10295 row: k column: 14  
High quality sequence stop: 715.

## FEATURES

source location/Qualifiers  
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## ORIGIN

/note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

Query Match 64.0%; Score 582; DB 4; Length 927;  
Best Local Similarity 100.0%; Pred. No. 1.2e-284;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 GTGTCTCCAGAAAGCGTATAGCTATAGCACTTCCTTCAAGAGAGAGAGGTTAGC 387  
DB 60 GTGTCTCCAGAAAGCGTATAGCTATAGCACTTCCTTCAAGAGAGAGAGGTTAGC 119  
QY 388 TGGCGTCCCGTCCGAGAGTCAAGCAAGTTCTGCAATTCTCAGCAGAGTCAAGAGACA 447  
DB 120 TGGCGTCCCGTCCGAGAGTCAAGCAAGTTCTGCAATTCTCAGCAGAGTCAAGAGACA 179  
QY 448 GGCCTCCCCCAACCAAGCGGAGGCGGAGTCCGGGCGGCGCAAGTGTGTCCAGA 507  
DB 180 GGCCTCCCCCAACCAAGCGGAGGCGGAGTCCGGGCGGCGCAAGTGTGTCCAGA 239  
QY 508 CGGCGGCGGAGAGGCGGCGGAGCGGCGGAGCGGAGAGTCAAGAGTCCGCGCAAGCTTCC 567  
DB 240 CGGCGGCGGAGAGGCGGCGGAGCGGCGGAGCGGAGAGTCAAGAGTCCGCGCAAGCTTCC 299  
QY 568 TCTGAAGGCAAAAGTACCTGTGACATCCGAGCTCCGGGTTCCAGCAGAGTACCTGAGCAT 627  
DB 300 TCTGAAGGCAAAAGTACCTGTGACATCCGAGCTCCGGGTTCCAGCAGAGTACCTGAGCAT 359  
QY 628 GGGCGGAGGCGGAGGCGGAGTCCGGGCGGCGGCGGAGTGTGGCGGCGGAGCTG 687  
DB 360 GGGCGGAGGCGGAGGCGGAGTCCGGGCGGCGGCGGAGTGTGGCGGCGGAGCTG 419  
QY 688 GACCTGTTGGGCGAGGCGGAGGCGGAGTGTGGCGGCGGAGTGTGGGTTGT 747  
DB 420 GACCTGTTGGGCGAGGCGGAGGCGGAGTGTGGCGGCGGAGTGTGGGTTGT 479  
QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGCGGAGTACCTGAGTGGC 807  
DB 480 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGCGGAGTACCTGAGTGGC 539  
QY 808 GCCCTGCTGAGAGGCGGCGGAGGCGGAGTGTGGGCGGAGTGTGGGCGGAGTGTGGGCG 867  
DB 540 GCCCTGCTGAGAGGCGGCGGAGGCGGAGTGTGGGCGGAGTGTGGGCGGAGTGTGGGCG 599  
QY 868 CGGAGAGCTGTGCGCTGCTGCTGAGTGTGAGTGTGAGGCTGAC 909  
DB 600 CGGAGAGCTGTGCGCTGCTGCTGAGTGTGAGTGTGAGGCTGAC 641

RESULT 10  
BI910416 947 bp mRNA linear EST 16-OCT-2001  
LOCUS 603068087F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5217213 5',  
DEFINITION mRNA sequence.  
ACCESSION BI910416  
VERSION BI910416.1 GI:16173804  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
TITLE NIH-MGC http://mgc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incey Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
http://image.llnl.gov  
Plate: LIML1545 row: m column: 22  
High quality sequence stop: 853.  
Location/Qualifiers

## FEATURES

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## ORIGIN

Query Match 64.0%; Score 582; DB 4; Length 947;  
Best Local Similarity 100.0%; Pred. No. 1.2e-284;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 GTGTCTCCAGAAAGCGTATAGCTATAGCACTTCCTTCAAGAGAGAGGTTAGC 387  
DB 72 GTGTCTCCAGAAAGCGTATAGCTATAGCACTTCCTTCAAGAGAGAGGTTAGC 131  
QY 388 TGGCGTCCCGTCCGAGAGTCAAGCAAGTTCTGCAATTCTCAGCAGAGTCAAGAGACA 447  
DB 132 TGGCGTCCCGTCCGAGAGTCAAGCAAGTTCTGCAATTCTCAGCAGAGTCAAGAGACA 191  
QY 448 GGCCTCCCCCAACCAAGCGGAGGCGGAGTCCGGGCGGCGGAGTGTGGCGGAGCTG 507  
DB 192 GGCCTCCCCCAACCAAGCGGAGGCGGAGTCCGGGCGGCGGAGTGTGGCGGAGCTG 251  
QY 508 CGGCGGAGGCGGAGGCGGAGTCCGGGCGGCGGAGTGTGGCGGAGCTG 567  
DB 252 CGGCGGAGGCGGAGGCGGAGTCCGGGCGGCGGAGTGTGGCGGAGCTG 311  
QY 568 TCTGAAGGCAAAAGTACCTGTGACATCCGAGCTCCGGGTTCCAGAGAGTACTGGAGCAT 627  
DB 312 TCTGAAGGCAAAAGTACCTGTGACATCCGAGCTCCGGGTTCCAGAGAGTACTGGAGCAT 371  
QY 628 GGGCGAGCTTGTGAGAGGCGGAGTCCGGGCGGCGGAGGCGGAGCTGCGGAGCTG 687  
DB 372 GGGCGAGCTTGTGAGAGGCGGAGTCCGGGCGGCGGAGGCGGAGCTGCGGAGCTG 431  
QY 688 GACCTGTTGGGCGAGGCGGAGGCGGAGTGTGGGCGGAGTGTGGGCGGAGTGTGGGCG 747  
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QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGAGGCTTCTGGGCGGAGTACTAGTGGC 807  
DB 492 GACATCAAGTTCTCAGAGCTCTCTATCTGAGAGGCTTCTGGGCGGAGTACTAGTGGC 551  
QY 808 GCCCTGCTGAGAGGCGGCGGAGGCGGAGTGTGGGCGGAGGCGGAGGCTGTGGGCG 867  
DB 552 GCCCTGCTGAGAGGCGGCGGAGGCGGAGTGTGGGCGGAGGCGGAGGCTGTGGGCG 611  
QY 868 CGGAGAGCTGTGCGCTGCTGCTGAGTGTGAGTGTGAGGCTGAC 909  
DB 612 CGGAGAGCTGTGCGCTGCTGCTGAGTGTGAGTGTGAGGCTGAC 653

RESULT 11  
BM908148



LOCUS BM908148 1062 bp mRNA linear EST 12-MAR-2002  
 DEFINITION AGENCOURT 6707554 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5745179  
 5', mRNA sequence.  
 ACCESSION BM908148  
 VERSION BM908148.1 GI:19358527  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 1062)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 EMAIL: cgep@b-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM12767 row: 1 column: 12  
 High quality sequence stop: 651.  
 Location/Qualifiers

## FEATURES

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 Site\_2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC Library."

## ORIGIN

Query Match 64.0%; Score 582; DB 5; Length 1062;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-284;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

328 GGTCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGACAGAGGGTAC 387  
 73 GTGTCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGACAGAGGGTAC 132  
 388 TCCGCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGAGAGTGGAGACA 447  
 133 TCCGCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGAGAGTGGAGACA 192  
 448 GGCTCCCCCAACCAAGGCGAGCGGAGTTCGGGCGGCGCCAGTGTGTGTCACA 507  
 193 GGCTCCCCCAACCAAGGCGAGCGGAGTTCGGGCGGCGCCAGTGTGTGTCACA 252  
 508 CGGCGCGGAGAGAGGCGCCAGCGGAGCGGAGCTTCAGAGAGAGCGCCAGAGCTTCC 567  
 253 CGGCGCGGAGAGAGGCGCCAGCGGAGCGGAGCTTCAGAGAGAGCGCCAGAGCTTCC 312  
 568 TCTGAAGGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 627  
 313 TCTGAAGGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 372  
 628 GGGCGAGCTTTGAG 687  
 373 GGGCGAGCTTTGAG 432

QY 688 GACGTGTTGGGACAGCCAGCGAGCTGCGCTCAAGGAGACTGCGCTGTGTGTTGT 747  
 DB 433 GACGTGTTGGGACAGCCAGCGAGCTGCGCTCAAGGAGACTGCGCTGTGTGTTGT 492  
 QY 748 GACATCAAGTTCTCAGAGCTCTCTATTTGAGAGCGCTTCTGCGGCGACTTACTGAGTGC 807  
 DB 493 GACATCAAGTTCTCAGAGCTCTCTATTTGAGAGCGCTTCTGCGGCGACTTACTGAGTGC 552  
 QY 808 GCCCTGTCAGAGCGCCCTGCGGCGGCTGTTCTGAGCTGAGGCGCTGCGAGAGCTGTGAGC 867  
 DB 553 GCCCTGTCAGAGCGCCCTGCGGCGGCTGTTCTGAGCTGAGGCGCTGCGAGAGCTGTGAGC 612  
 QY 868 CGGAGGCTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909  
 DB 613 CGGAGGCTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 654

RESULT 12  
 BS907425 1131 bp mRNA linear EST 20-OCT-2000  
 LOCUS BM907425  
 DEFINITION 601500161P1 NIH\_MGC\_70 Homo sapiens cDNA clone IMAGE:3901934 5',  
 mRNA sequence.  
 ACCESSION BS907425  
 VERSION BS907425.1 GI:10400971  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 1131)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 EMAIL: cgep@b-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM9703 row: j column: 15  
 High quality sequence stop: 686.  
 Location/Qualifiers

## FEATURES

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 Average insert size 1.1 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Query Match 64.0%; Score 582; DB 2; Length 1131;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-284;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 30 GTGTCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGAGAGGGTAC 89  
 QY 388 TCCGCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGAGAGGGTAC 447  
 DB 90 TCCGCTCCGAGAGCTATAGTATGAGCACTTCAGCTTTCAAGAGAGAGGGTAC 149  
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FEATURES  
source

Location/Qualifiers  
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## ORIGIN

Query Match 64.0%; Score 582; DB 3; Length 1586;  
Best Local Similarity 100.0%; Pred. No. 1.2e-284;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 111 GTGCTCCAGAACGCTATAGCTATGCACTTCAGCTTCAAGAGAGAGAGAGGCTAGC 170
QY 388 TGCCGTCGCGCTGCGAGTCAAGCAGTTCTGCAATTCTCAGCAGGCTCAGTGGAGACA 447
DB 171 TGCCGTCGCGCTGCGAGTCAAGCAGTTCTGCAATTCTCAGCAGGCTCAGTGGAGACA 230
QY 448 GCGTCCCGCCCAACCAAGCGGAGCGCGAGTCCGGGCGCGCCCAAGTGTGTCCAGA 507
DB 231 GCGTCCCGCCCAACCAAGCGGAGCGCGAGTCCGGGCGCGCCCAAGTGTGTCCAGA 290
QY 508 CGGCGCGGAGAGGGGGCCCGCAGCCGCAAGCAGTCAAGAGCCCGCAGACTTCC 567
DB 291 CGGCGCGGAGAGGGGGCCCGCAGCCGCAAGCAGTCAAGAGCCCGCAGACTTCC 350
QY 568 TCTGAAGCAAAAGTACCTGTGACATCCGGCTCCGGGTTCCAGAGAGTACTGAGAGAT 627
DB 351 TCTGAAGCAAAAGTACCTGTGACATCCGGCTCCGGGTTCCAGAGAGTACTGAGAGAT 410
QY 628 GCGGCAAGCTTGTGAGCAGAGCGGTGCATCCGGCGCGCCCGCAGCTGGCGCGAGCTG 687
DB 411 GCGGCAAGCTTGTGAGCAGAGCGGTGCATCCGGCGCGCCCGCAGCTGGCGCGAGCTG 470
QY 688 GACGCTTTGGGCAAGCCAGCGCAGTGGCTCAAGGAGACTTGGGCTGTGTGTGTGT 747
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QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGCAGCTTCTGAGGAGGAGTACTGAGTGC 807
DB 531 GACATCAAGTTCTCAGAGCTCTCTATCTGAGCAGCTTCTGAGGAGGAGTACTGAGTGC 590
QY 808 GCCCTGCTGCAAGCGCTTGGGGGCGGTGTCTGACTGAGGCCCTTGGAGAGGCTGTGGC 867
DB 591 GCCCTGCTGCAAGCGCTTGGGGGCGGTGTCTGACTGAGGCCCTTGGAGAGGCTGTGGC 650
QY 868 CGGAGAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
DB 651 CGGAGAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
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## RESULT 15

BM925969

LOCUS BM925969 1089 bp mRNA linear EST 12-MAR-2002  
DEFINITION AGENCOURT\_6649774 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5764272  
5', mRNA sequence.

ACCESSION BM925969  
VERSION BM925969.1 GI:19376336  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

FEATURES  
source

Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LNL12817 row: h column: 01  
High quality sequence start: 14  
High quality sequence stop: 586.

## Location/Qualifiers

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upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC library."

## ORIGIN

Query Match 61.4%; Score 558; DB 5; Length 1089;  
Best Local Similarity 99.7%; Pred. No. 2e-272;

Matches 658; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 71 ATGGGCTATTCGGGTGACCCCGGCTGCTGGAGAGAGTGTGCTGAGTAC 130
QY 61 TACGGATGCTGTGCTTCAACGATATGTTCAAGGTGTGGCGGCACTGACGAGTGC 120
DB 131 TACGGATGCTGTGCTTCAACGATATGTTCAAGGTGTGGCGGCACTGACGAGTGC 190
QY 121 GAGCTGAGCTCTTGAGCTTTCTGCTGATAGAGCTCTTGCGCGCGCGGAGCTTACCC 180
DB 191 GAGCTGAGCTCTTGAGCTTTCTGCTGATAGAGCTCTTGCGCGCGCGGAGCTTACCC 250
QY 181 CCGGCGCGGAGCGCTGAGACTCTGCTGAGAGTGTGAGCGCGCGGAGAGCGGCGAG 240
DB 251 CCGGCGCGGAGCGCTGAGACTCTGCTGAGAGTGTGAGCGCGCGGAGAGCGGCGAG 310
QY 241 AGCAACCTGCGGCTGCTGGGCAACTCTGCGCGGTGCGCGCGCGAGACTGCTGCGG 300
DB 311 AGCAACCTGCGGCTGCTGGGCAACTCTGCGCGGTGCGCGCGCGAGACTGCTGCGG 370
QY 301 CACTGCGCGCAGAGCGCGCGCGCAGTGTCTCCAGAACTATAGTATGCACTTCC 360
DB 371 CACTGCGCGCAGAGCGCGCGCGCAGTGTCTCCAGAACTATAGTATGCACTTCC 430
QY 361 AGCTTTTAAAGAGAGAGAGGTAGTGTGCTGCGCTGCGCTGCGCACTCAAGAGTTCTGCA 420
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QY 421 AATTCTGAGCAGGCTCACTGAGGAGAGCAGGCTCCCCCAACCAAGCGGAGCGGAGT 480
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Scoring table: OLIGO NUC  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	281	30.9	1067	4	US-09-620-312D-853
2	20	2.2	2673	4	US-09-252-991A-2993
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4	20	2.2	2814	4	US-09-252-991A-2875
5	19	2.1	601	4	US-09-949-016-21931
6	19	2.1	601	4	US-09-949-016-21932
7	19	2.1	601	4	US-09-949-016-21933
8	19	2.1	601	4	US-09-949-016-21934
9	19	2.1	601	4	US-09-949-016-21935
10	19	2.1	601	4	US-09-949-016-84252
11	19	2.1	601	4	US-09-949-016-84253
12	19	2.1	601	4	US-09-949-016-84254
13	19	2.1	601	4	US-09-949-016-84255
14	19	2.1	601	4	US-09-949-016-84256
15	19	2.1	878	4	US-09-270-767-27566
16	19	2.1	988	4	US-09-270-767-11903
17	19	2.1	1742	4	US-09-799-451-383
18	19	2.1	2019	4	US-09-252-991A-5836
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21	19	2.1	2748	4	US-09-252-991A-5773
22	19	2.1	14555	4	US-09-902-540-1096
23	19	2.1	32584	4	US-09-949-016-16766
24	19	2.1	60095	4	US-09-949-016-12419
25	19	2.1	60095	4	US-09-949-016-14457
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27	19	2.1	481115	4	US-09-949-016-11940

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31	18	2.0	601	4	US-09-949-016-69186	Sequence 69186, A
32	18	2.0	969	4	US-09-902-540-8543	Sequence 8543, Ap
33	18	2.0	1011	4	US-09-252-991A-13074	Sequence 13074, A
34	18	2.0	1056	3	US-09-363-189B-3	Sequence 3, Appl1
35	18	2.0	1242	4	US-09-902-540-9670	Sequence 9670, Ap
36	18	2.0	1268	4	US-09-902-540-8471	Sequence 8471, Ap
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57	17	1.9	36	4	US-09-098-877B-53	Sequence 53, Appl
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59	17	1.9	250	4	US-09-313-294A-1481	Sequence 1481, A
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61	17	1.9	354	4	US-09-252-991A-12550	Sequence 12550, A
62	17	1.9	405	4	US-09-252-991A-7771	Sequence 7771, Ap
63	17	1.9	432	4	US-09-252-991A-13256	Sequence 13256, A
64	17	1.9	432	4	US-09-749-340-1	Sequence 1, Appl1
65	17	1.9	503	4	US-09-902-540-2739	Sequence 2739, Ap
66	17	1.9	515	3	US-08-943-731-182	Sequence 182, App
67	17	1.9	528	4	US-09-252-991A-6991	Sequence 6991, Ap
68	17	1.9	537	4	US-09-902-540-4825	Sequence 4825, Ap
69	17	1.9	549	4	US-09-902-540-7450	Sequence 7450, Ap
70	17	1.9	601	4	US-09-949-016-37380	Sequence 37380, A
71	17	1.9	601	4	US-09-949-016-65350	Sequence 65350, A
72	17	1.9	601	4	US-09-949-016-65348	Sequence 65348, A
73	17	1.9	601	4	US-09-949-016-176851	Sequence 176851, Sequence 187832, Sequence 8, Appl1
74	17	1.9	601	4	US-09-949-016-187832	Sequence 8798, Ap
75	17	1.9	630	4	US-09-733-167A-8	Sequence 5788, Ap
76	17	1.9	672	4	US-09-902-540-8798	Sequence 21070, A
77	17	1.9	811	4	US-09-270-767-5788	Sequence 4202, Ap
78	17	1.9	811	4	US-09-270-767-21070	Sequence 8841, Ap
79	17	1.9	843	4	US-09-902-540-4202	Sequence 8953, Ap
80	17	1.9	969	4	US-09-252-991A-8841	Sequence 1, Appl1
81	17	1.9	1008	4	US-09-252-991A-8953	Sequence 3, Appl1
82	17	1.9	1011	4	US-09-582-324-1	Sequence 3, Appl1
83	17	1.9	1045	3	US-08-859-167-3	Sequence 3, Appl1
84	17	1.9	1045	3	US-09-109-297-3	Sequence 3, Appl1
85	17	1.9	1045	3	US-09-276-993-3	Sequence 3, Appl1
86	17	1.9	1045	3	US-09-723-450-3	Sequence 3, Appl1
87	17	1.9	1050	3	US-09-655-270A-16	Sequence 16, Appl
88	17	1.9	1050	3	US-09-651-94A-20	Sequence 20, Appl
89	17	1.9	1050	3	US-09-955-597-20	Sequence 27, Appl
90	17	1.9	1056	3	US-09-364-230-27	Sequence 27, Appl
91	17	1.9	1107	4	US-09-489-038A-6582	Sequence 6582, Ap
92	17	1.9	1114	4	US-09-602-777A-135	Sequence 135, App
93	17	1.9	1142	4	US-09-733-167A-2	Sequence 2, Appl1
94	17	1.9	1142	4	US-09-733-167A-4	Sequence 4, Appl1
95	17	1.9	1200	3	US-08-859-167-5	Sequence 5, Appl1
96	17	1.9	1200	3	US-08-109-297-5	Sequence 5, Appl1
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98	17	1.9	1200	3	US-09-723-450-5	Sequence 5, Appl1
99	17	1.9	1257	2	US-08-491-988-8	Sequence 8, Appl1
100	17	1.9	1273	1	US-08-507-431-1	Sequence 1, Appl1

C 101	17	1.9	1273	2	US-08-902-655A-1	Sequence 1, Appli	174	17	1.9	14467	4	US-09-902-540-1058	Sequence 1058, Ap
C 102	17	1.9	1273	3	US-09-116-622-1	Sequence 1, Appli	175	17	1.9	15331	4	US-09-949-016-11355	Sequence 11355, A
C 103	17	1.9	1273	3	US-09-219-277-1	Sequence 1, Appli	176	17	1.9	15377	4	US-09-902-540-1116	Sequence 1116, Ap
C 104	17	1.9	1273	3	US-08-599-661-1	Sequence 1, Appli	177	17	1.9	15689	4	US-09-902-540-1129	Sequence 1129, Ap
C 105	17	1.9	1296	2	US-08-491-988-6	Sequence 6, Appli	178	17	1.9	17606	3	US-08-943-721-4	Sequence 4, Appli
C 106	17	1.9	1320	4	US-09-949-016-2223	Sequence 2223, Ap	179	17	1.9	17622	4	US-09-902-540-1125	Sequence 1125, Ap
C 107	17	1.9	1323	4	US-09-902-540-2671	Sequence 2671, Ap	180	17	1.9	18508	4	US-09-949-016-13843	Sequence 13843, A
C 108	17	1.9	1353	4	US-09-252-991A-17715	Sequence 7715, Ap	181	17	1.9	19726	4	US-09-902-540-1164	Sequence 1164, Ap
C 109	17	1.9	1356	2	US-08-491-988-4	Sequence 4, Appli	182	17	1.9	21330	4	US-09-902-540-1209	Sequence 1209, Ap
C 110	17	1.9	1485	4	US-09-902-540-8926	Sequence 8926, Ap	183	17	1.9	23902	4	US-09-949-016-14220	Sequence 14220, A
C 111	17	1.9	1485	4	US-09-902-540-2554	Sequence 2554, Ap	184	17	1.9	26599	4	US-09-902-540-1237	Sequence 1237, Ap
C 112	17	1.9	1629	4	US-09-602-777A-133	Sequence 133, App	185	17	1.9	26709	4	US-09-949-016-17520	Sequence 17520, A
C 113	17	1.9	1686	4	US-09-724-797-9	Sequence 9, Appli	186	17	1.9	28213	4	US-09-949-016-12738	Sequence 12738, A
C 114	17	1.9	1730	4	US-09-489-847-48	Sequence 48, Appli	187	17	1.9	28216	4	US-09-949-016-13652	Sequence 13652, A
C 115	17	1.9	1902	4	US-09-902-540-8758	Sequence 8758, Ap	188	17	1.9	28588	4	US-09-902-540-1231	Sequence 1231, Ap
C 116	17	1.9	1927	3	US-08-606-505B-64	Sequence 64, Appli	189	17	1.9	28619	4	US-09-949-016-15806	Sequence 15806, A
C 117	17	1.9	1927	3	US-09-616-990-64	Sequence 64, Appli	190	17	1.9	44608	4	US-09-949-016-15604	Sequence 15604, A
C 118	17	1.9	2005	4	US-08-208-108-1	Sequence 1, Appli	191	17	1.9	58014	4	US-09-949-016-17448	Sequence 17448, A
C 119	17	1.9	2136	4	US-09-252-991A-13089	Sequence 13089, A	192	17	1.9	59252	4	US-09-949-016-12150	Sequence 12150, A
C 120	17	1.9	2187	4	US-09-252-991A-7042	Sequence 7042, Ap	193	17	1.9	59252	4	US-09-949-016-15374	Sequence 15374, A
C 121	17	1.9	2367	3	US-09-056-556-201	Sequence 201, App	194	17	1.9	63282	4	US-09-949-016-16789	Sequence 16789, A
C 122	17	1.9	2367	3	US-09-072-967-201	Sequence 196, App	195	17	1.9	67014	4	US-09-949-016-17110	Sequence 17110, A
C 123	17	1.9	2406	4	US-09-252-991A-12703	Sequence 12703, A	196	17	1.9	104077	4	US-09-949-016-13593	Sequence 13593, A
C 124	17	1.9	2454	4	US-09-902-540-5316	Sequence 5316, Ap	197	17	1.9	112114	4	US-09-949-016-17292	Sequence 17292, A
C 125	17	1.9	2454	4	US-08-073-384C-2	Sequence 2, Appli	198	17	1.9	118923	4	US-09-949-016-13227	Sequence 13227, A
C 126	17	1.9	2496	1	US-08-254-359A-2	Sequence 2, Appli	199	17	1.9	118923	4	US-09-949-016-11894	Sequence 11894, A
C 127	17	1.9	2496	1	US-08-483-043-2	Sequence 2, Appli	200	17	1.9	154915	4	US-09-949-016-15584	Sequence 15584, A
C 128	17	1.9	2496	1	US-08-481-238-2	Sequence 2, Appli	201	17	1.9	313366	4	US-09-949-016-16001	Sequence 16001, A
C 129	17	1.9	2496	2	US-08-471-066B-2	Sequence 2, Appli	202	17	1.9	321022	4	US-09-949-016-11852	Sequence 11852, A
C 130	17	1.9	2496	2	US-08-484-955-2	Sequence 2, Appli	203	17	1.9	321022	4	US-09-949-016-14166	Sequence 14166, A
C 131	17	1.9	2496	2	US-08-757-653-2	Sequence 2, Appli	204	17	1.9	536165	4	US-09-214-808-1	Sequence 1, Appli
C 132	17	1.9	2496	2	US-08-599-491-2	Sequence 2, Appli	205	17	1.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 133	17	1.9	2496	2	US-08-756-385-2	Sequence 2, Appli	206	17	1.9	4403765	3	US-09-103-840A-1	Sequence 1, Appli
C 134	17	1.9	2496	2	US-08-823-515-2	Sequence 2, Appli	207	17	1.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 135	17	1.9	2496	3	US-08-682-853A-2	Sequence 2, Appli	208	17	1.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 136	17	1.9	2496	3	US-08-759-038-2	Sequence 2, Appli	209	17	1.8	23	4	US-10-003-998A-3	Sequence 3, Appli
C 137	17	1.9	2496	3	US-08-758-314-2	Sequence 2, Appli	210	17	1.8	25	4	US-09-336-126G-124207	Sequence 124207, A
C 138	17	1.9	2496	3	US-08-758-314-2	Sequence 2, Appli	211	17	1.8	65	6	5314995-2	Sequence 6, Appli
C 139	17	1.9	2496	3	US-09-350-309-2	Sequence 2, Appli	212	17	1.8	65	6	5314995-2	Sequence 6, Appli
C 140	17	1.9	2496	3	US-08-520-946-2	Sequence 2, Appli	213	17	1.8	66	4	US-10-002-389-6	Sequence 6, Appli
C 141	17	1.9	2496	4	US-09-684-938-2	Sequence 2, Appli	214	17	1.8	92	4	US-09-513-999C-32641	Sequence 32641, A
C 142	17	1.9	2496	4	US-09-308-825A-2	Sequence 2, Appli	215	17	1.8	189	4	US-09-248-765A-8460	Sequence 8460, Ap
C 143	17	1.9	2496	4	US-09-758-282B-2	Sequence 2, Appli	216	17	1.8	203	4	US-09-270-767-79003	Sequence 79003, A
C 144	17	1.9	2496	4	US-09-653-378A-2	Sequence 2, Appli	217	17	1.8	236	4	US-09-513-999C-23964	Sequence 23964, A
C 145	17	1.9	2496	4	US-09-940-244-2	Sequence 2, Appli	218	17	1.8	241	4	US-09-016-434-83	Sequence 83, Appli
C 146	17	1.9	2496	4	US-09-333-145-2	Sequence 2, Appli	219	17	1.8	253	4	US-09-513-999C-36518	Sequence 36518, A
C 147	17	1.9	2496	4	US-09-577-304A-2	Sequence 2, Appli	220	17	1.8	297	4	US-09-252-991A-15051	Sequence 15051, A
C 148	17	1.9	2511	4	US-09-252-991A-9132	Sequence 9132, Ap	221	17	1.8	297	4	US-09-252-991A-14609	Sequence 14609, A
C 149	17	1.9	2527	4	US-09-555-790A-1	Sequence 1, Appli	222	17	1.8	305	2	US-08-808-982-4	Sequence 4, Appli
C 150	17	1.9	2527	4	US-09-202-047A-1	Sequence 1, Appli	223	17	1.8	305	3	US-09-306-902A-4	Sequence 4, Appli
C 151	17	1.9	2575	4	US-09-620-312D-371	Sequence 371, App	224	17	1.8	314	3	US-09-277-016-7-72	Sequence 7, Appli
C 152	17	1.9	2588	2	US-08-796-414B-6	Sequence 6, Appli	225	17	1.8	314	4	US-09-883-548-7	Sequence 7, Appli
C 153	17	1.9	2616	4	US-09-252-991A-12851	Sequence 12851, A	226	17	1.8	314	4	US-09-883-548-7	Sequence 7, Appli
C 154	17	1.9	2875	4	US-09-774-528-198	Sequence 198, App	227	17	1.8	314	4	US-09-757-949-7	Sequence 7, Appli
C 155	17	1.9	2976	4	US-09-902-540-4698	Sequence 4698, Ap	228	17	1.8	320	4	US-09-270-767-77286	Sequence 77286, A
C 156	17	1.9	3154	4	US-09-949-016-2101	Sequence 2101, Ap	229	17	1.8	321	4	US-09-252-991A-14933	Sequence 14933, A
C 157	17	1.9	3615	4	US-09-016-434-1254	Sequence 1254, Ap	230	17	1.8	360	4	US-09-270-767-11670	Sequence 11670, A
C 158	17	1.9	3828	4	US-09-902-540-3453	Sequence 3453, Ap	231	17	1.8	360	4	US-09-513-999C-13098	Sequence 13098, A
C 159	17	1.9	3930	3	US-09-162-373-2	Sequence 2, Appli	232	17	1.8	374	4	US-09-270-767-7520	Sequence 7520, Ap
C 160	17	1.9	3930	3	US-09-467-946-2	Sequence 2, Appli	233	17	1.8	374	4	US-09-270-767-24802	Sequence 24802, A
C 161	17	1.9	3975	4	US-09-949-016-4064	Sequence 4064, Ap	234	17	1.8	388	4	US-09-621-976-3006	Sequence 3006, Ap
C 162	17	1.9	6731	4	US-09-949-016-5047	Sequence 5047, Ap	235	17	1.8	405	4	US-09-902-540-1218	Sequence 1218, Ap
C 163	17	1.9	7679	4	US-09-949-016-13965	Sequence 13965, A	236	17	1.8	405	4	US-09-270-767-75926	Sequence 75926, Ap
C 164	17	1.9	9956	4	US-09-902-540-929	Sequence 929, App	237	17	1.8	405	4	US-09-270-767-75926	Sequence 75926, Ap
C 165	17	1.9	9992	4	US-09-902-540-952	Sequence 952, App	238	17	1.8	424	4	US-09-513-999C-2621	Sequence 2621, Ap
C 166	17	1.9	10096	4	US-09-902-540-935	Sequence 935, App	239	17	1.8	444	4	US-09-489-039A-6615	Sequence 6615, Ap
C 167	17	1.9	10541	4	US-09-949-016-15958	Sequence 15958, A	240	17	1.8	445	4	US-09-270-767-69423	Sequence 69423, A
C 168	17	1.9	11706	4	US-09-902-540-1038	Sequence 1038, Ap	241	17	1.8	450	4	US-09-513-999C-2171	Sequence 2171, Ap
C 169	17	1.9	12249	4	US-09-949-016-16839	Sequence 16839, A	242	17	1.8	462	4	US-09-270-767-57466	Sequence 57466, Ap
C 170	17	1.9	12249	4	US-09-949-016-16840	Sequence 16840, A	243	17	1.8	462	4	US-09-270-767-20748	Sequence 20748, Ap
C 171	17	1.9	12508	3	US-09-655-270A-1	Sequence 1, Appli	244	17	1.8	467	4	US-09-621-976-531	Sequence 531, App
C 172	17	1.9	12523	3	US-09-651-941-1	Sequence 1, Appli	245	17	1.8	471	4	US-09-252-991A-15879	Sequence 15879, A
C 173	17	1.9	12523	3	US-09-955-597-1	Sequence 1, Appli	246	17	1.8	486	4	US-09-489-039A-5766	Sequence 5766, Ap

247	16	1.8	486	4	US-09-513-999C-9795	Sequence 9795, Ap	C 320	16	1.8	615	4	US-09-252-991A-16534	Sequence 16534, A
248	16	1.8	492	4	US-09-252-991A-14901	Sequence 14901, A	321	16	1.8	615	4	US-09-904-196B-8	Sequence 8, Appl1
249	16	1.8	506	3	US-09-105-542A-5	Sequence 5, Appl1	322	16	1.8	615	4	US-09-760-008A-8	Sequence 8, Appl1
250	16	1.8	507	4	US-09-252-991A-4603	Sequence 4603, Ap	323	16	1.8	615	4	US-10-197-294-8	Sequence 8, Appl1
C 251	16	1.8	507	4	US-09-902-540-9265	Sequence 9265, Ap	324	16	1.8	624	4	US-09-252-991A-4404	Sequence 4404, Ap
C 252	16	1.8	513	3	US-09-199-637A-155	Sequence 155, App	325	16	1.8	627	3	US-09-064-414-5	Sequence 5, Appl1
C 253	16	1.8	531	4	US-09-902-540-8969	Sequence 8969, Ap	326	16	1.8	636	4	US-09-252-991A-5379	Sequence 5379, Ap
C 254	16	1.8	537	4	US-09-252-991A-161070	Sequence 161070, A	C 327	16	1.8	639	4	US-09-252-991A-13260	Sequence 13260, Ap
C 255	16	1.8	546	4	US-09-252-991A-11071	Sequence 11071, A	C 328	16	1.8	639	4	US-09-902-540-9299	Sequence 9299, Ap
C 256	16	1.8	573	4	US-09-252-991A-5367	Sequence 5367, Ap	C 329	16	1.8	669	2	US-08-896-410-3	Sequence 3, Appl1
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C 258	16	1.8	579	4	US-09-252-991A-6132	Sequence 6132, Ap	331	16	1.8	702	2	US-08-800-751-4	Sequence 4, Appl1
C 259	16	1.8	585	4	US-09-252-991A-4628	Sequence 4628, Ap	332	16	1.8	702	2	US-08-990-818-4	Sequence 10, Appl1
C 260	16	1.8	591	4	US-09-252-991A-6636	Sequence 6636, Ap	C 333	16	1.8	712	4	US-09-252-991A-6046	Sequence 6046, Ap
C 261	16	1.8	593	4	US-09-669-751-48	Sequence 48, Appl1	C 334	16	1.8	712	4	US-09-270-767-13449	Sequence 13449, Ap
C 262	16	1.8	597	4	US-09-669-751-67	Sequence 67, Appl1	C 335	16	1.8	720	4	US-09-489-039A-6326	Sequence 6326, Ap
C 263	16	1.8	601	4	US-09-949-016-19938	Sequence 19938, A	336	16	1.8	723	4	US-09-791-540-5	Sequence 5, Appl1
C 264	16	1.8	601	4	US-09-949-016-22806	Sequence 22806, A	337	16	1.8	731	2	US-08-392-338A-10	Sequence 10, Appl1
C 265	16	1.8	601	4	US-09-949-016-26895	Sequence 26895, A	338	16	1.8	731	3	US-09-166-750-10	Sequence 10, Appl1
C 266	16	1.8	601	4	US-09-949-016-28199	Sequence 28199, A	339	16	1.8	731	3	US-09-166-093-10	Sequence 10, Appl1
C 267	16	1.8	601	4	US-09-949-016-28433	Sequence 28433, A	340	16	1.8	731	3	US-09-172-019-10	Sequence 10, Appl1
C 268	16	1.8	601	4	US-09-949-016-30077	Sequence 30077, A	341	16	1.8	731	3	US-09-166-094-10	Sequence 10, Appl1
C 269	16	1.8	601	4	US-09-949-016-33283	Sequence 33283, A	342	16	1.8	731	4	US-09-443-213-10	Sequence 10, Appl1
C 270	16	1.8	601	4	US-09-949-016-33284	Sequence 33284, A	343	16	1.8	735	3	US-09-079-970A-1	Sequence 1, Appl1
C 271	16	1.8	601	4	US-09-949-016-42975	Sequence 42975, A	C 344	16	1.8	762	3	US-09-199-637A-153	Sequence 153, App
C 272	16	1.8	601	4	US-09-949-016-46200	Sequence 46200, A	C 345	16	1.8	771	3	US-08-253-155A-17	Sequence 17, Appl1
C 273	16	1.8	601	4	US-09-949-016-57560	Sequence 57560, A	346	16	1.8	771	3	US-09-079-970A-4	Sequence 4, Appl1
C 274	16	1.8	601	4	US-09-949-016-57561	Sequence 57561, A	347	16	1.8	783	4	US-09-252-991A-927	Sequence 927, App
C 275	16	1.8	601	4	US-09-949-016-59659	Sequence 59659, A	348	16	1.8	792	4	US-09-902-540-8438	Sequence 8438, Ap
C 276	16	1.8	601	4	US-09-949-016-59660	Sequence 59660, A	349	16	1.8	797	1	US-08-323-445A-3	Sequence 3, Appl1
C 277	16	1.8	601	4	US-09-949-016-66010	Sequence 66010, A	350	16	1.8	797	5	US-08-515-902A-3	Sequence 3, Appl1
C 278	16	1.8	601	4	US-09-949-016-66019	Sequence 66019, A	351	16	1.8	797	5	PCT-US95-12840-3	Sequence 3, Appl1
C 279	16	1.8	601	4	US-09-949-016-66020	Sequence 66020, A	352	16	1.8	801	4	US-09-902-540-7321	Sequence 7321, Ap
C 280	16	1.8	601	4	US-09-949-016-72408	Sequence 72408, A	353	16	1.8	803	1	US-08-323-445A-7	Sequence 7, Appl1
C 281	16	1.8	601	4	US-09-949-016-80891	Sequence 80891, A	354	16	1.8	803	1	US-08-515-902A-7	Sequence 7, Appl1
C 282	16	1.8	601	4	US-09-949-016-86867	Sequence 86867, A	355	16	1.8	803	5	PCT-US95-12840-7	Sequence 7, Appl1
C 283	16	1.8	601	4	US-09-949-016-95030	Sequence 95030, A	356	16	1.8	810	4	US-09-252-991A-154782	Sequence 3647, Ap
C 284	16	1.8	601	4	US-09-949-016-95142	Sequence 95142, A	357	16	1.8	816	4	US-09-252-991A-11434	Sequence 11434, A
C 285	16	1.8	601	4	US-09-949-016-134281	Sequence 95142, A	358	16	1.8	828	4	US-09-252-991A-1643	Sequence 1643, Ap
C 286	16	1.8	601	4	US-09-949-016-136139	Sequence 136139, A	C 359	16	1.8	831	1	US-07-882-329-1	Sequence 1, Appl1
C 287	16	1.8	601	4	US-09-949-016-136140	Sequence 136140, A	360	16	1.8	831	4	US-08-183-213-1	Sequence 1, Appl1
C 288	16	1.8	601	4	US-09-949-016-137594	Sequence 137594, A	361	16	1.8	840	4	US-09-252-991A-15782	Sequence 4529, Ap
C 289	16	1.8	601	4	US-09-949-016-137955	Sequence 137955, A	362	16	1.8	852	4	US-09-893-737-151	Sequence 13957, A
C 290	16	1.8	601	4	US-09-949-016-137955	Sequence 137955, A	363	16	1.8	852	4	US-09-893-737-297	Sequence 151, App
C 291	16	1.8	601	4	US-09-949-016-137956	Sequence 137956, A	364	16	1.8	852	4	US-09-893-737-297	Sequence 297, App
C 292	16	1.8	601	4	US-09-949-016-137957	Sequence 137957, A	C 365	16	1.8	855	4	US-09-252-991A-11001	Sequence 11001, A
C 293	16	1.8	601	4	US-09-949-016-141163	Sequence 141163, A	366	16	1.8	879	4	US-09-252-991A-3602	Sequence 3602, Ap
C 294	16	1.8	601	4	US-09-949-016-141164	Sequence 141164, A	C 367	16	1.8	891	4	US-09-252-991A-15439	Sequence 15782, A
C 295	16	1.8	601	4	US-09-949-016-151100	Sequence 151100, A	C 368	16	1.8	897	4	US-09-252-991A-13439	Sequence 13439, A
C 296	16	1.8	601	4	US-09-949-016-158367	Sequence 158367, A	369	16	1.8	897	4	US-09-252-991A-4427	Sequence 4427, Ap
C 297	16	1.8	601	4	US-09-949-016-158368	Sequence 158368, A	370	16	1.8	897	4	US-09-902-540-7446	Sequence 7446, Ap
C 298	16	1.8	601	4	US-09-949-016-158369	Sequence 158369, A	371	16	1.8	909	1	US-08-133-804-1	Sequence 1, Appl1
C 299	16	1.8	601	4	US-09-949-016-165025	Sequence 165025, A	372	16	1.8	909	1	US-08-461-184-7	Sequence 7, Appl1
C 300	16	1.8	601	4	US-09-949-016-172825	Sequence 172825, A	373	16	1.8	909	1	US-08-461-678-7	Sequence 7, Appl1
C 301	16	1.8	601	4	US-09-949-016-172826	Sequence 172826, A	374	16	1.8	909	1	US-08-461-683-1	Sequence 7, Appl1
C 302	16	1.8	601	4	US-09-949-016-181757	Sequence 181757, A	375	16	1.8	909	2	US-08-461-683-1	Sequence 1, Appl1
C 303	16	1.8	601	4	US-09-949-016-181757	Sequence 181757, A	376	16	1.8	909	2	US-08-461-386-1	Sequence 1, Appl1
C 304	16	1.8	601	4	US-09-949-016-181995	Sequence 181895, A	377	16	1.8	909	2	US-09-252-991A-11185	Sequence 11185, A
C 305	16	1.8	601	4	US-09-949-016-183042	Sequence 183042, A	378	16	1.8	918	4	US-09-902-540-7975	Sequence 7975, Ap
C 306	16	1.8	601	4	US-09-949-016-183043	Sequence 183043, A	379	16	1.8	924	4	US-09-252-991A-1483	Sequence 1483, Ap
C 307	16	1.8	601	4	US-09-949-016-185638	Sequence 185638, A	C 380	16	1.8	948	4	US-09-489-039A-3064	Sequence 3064, Ap
C 308	16	1.8	601	4	US-09-949-016-186975	Sequence 186975, A	C 381	16	1.8	951	4	US-09-902-540-5206	Sequence 5206, Ap
C 309	16	1.8	601	4	US-09-949-016-186975	Sequence 186975, A	C 382	16	1.8	960	4	US-09-902-540-7932	Sequence 7932, Ap
C 310	16	1.8	601	4	US-09-949-016-194578	Sequence 194578, A	383	16	1.8	966	4	US-09-252-991A-6602	Sequence 6602, Ap
C 311	16	1.8	601	4	US-09-949-016-194579	Sequence 194579, A	C 384	16	1.8	984	4	US-09-252-991A-1038	Sequence 1038, Ap
C 312	16	1.8	601	4	US-09-949-016-203219	Sequence 203219, A	385	16	1.8	1011	4	US-09-902-540-3195	Sequence 3195, Ap
C 313	16	1.8	601	4	US-09-949-016-203220	Sequence 203220, A	386	16	1.8	1079	4	US-09-135-121B-6	Sequence 6, Appl1
C 314	16	1.8	601	4	US-09-949-016-203279	Sequence 203279, A	387	16	1.8	1080	2	US-08-918-727-2	Sequence 2, Appl1
C 315	16	1.8	601	4	US-09-949-016-203580	Sequence 203580, A	388	16	1.8	1080	3	US-09-205-680A-2	Sequence 2, Appl1
C 316	16	1.8	601	4	US-09-949-016-206933	Sequence 206933, A	389	16	1.8	1080	3	US-09-252-991A-4554	Sequence 4554, Ap
C 317	16	1.8	606	3	US-09-064-414-1	Sequence 1, Appl1	390	16	1.8	1081	2	US-09-016-366A-22	Sequence 22, Appl1
C 318	16	1.8	606	3	US-09-064-414-3	Sequence 3, Appl1	391	16	1.8	1081	2	US-08-978-404B-17	Sequence 17, Appl1
C 319	16	1.8	609	4	US-09-621-976-1139	Sequence 1139, Ap	392	16	1.8	1081	4	US-09-917-254-50	Sequence 50, Appl1

393	16	1.8	1083	4	US-09-489-039A-5884	Sequence 5884, Ap
394	16	1.8	1093	4	US-09-010-147B-1	Sequence 1, Appli
395	16	1.8	1093	4	US-09-489-039A-3658	Sequence 3658, Ap
396	16	1.8	1098	4	US-09-252-991A-5384	Sequence 5384, Ap
C 397	16	1.8	1120	1	US-07-882-329-3	Sequence 3, Appli
C 398	16	1.8	1120	1	US-08-183-213-3	Sequence 3, Appli
C 399	16	1.8	1125	4	US-09-489-039A-5507	Sequence 5507, Ap
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401	16	1.8	1128	2	US-08-978-404B-15	Sequence 15, Appl
402	16	1.8	1137	2	US-09-016-366A-18	Sequence 18, Appl
403	16	1.8	1137	2	US-08-978-404B-13	Sequence 13, Appl
404	16	1.8	1154	2	US-09-016-366A-16	Sequence 16, Appl
405	16	1.8	1154	2	US-08-978-404B-11	Sequence 11, Appl
C 406	16	1.8	1159	4	US-09-665-189A-57	Sequence 57, Appl
407	16	1.8	1167	4	US-09-489-039A-5896	Sequence 5896, Ap
408	16	1.8	1170	4	US-09-489-039A-3821	Sequence 3821, Ap
C 409	16	1.8	1173	4	US-09-252-991A-5197	Sequence 5197, Ap
410	16	1.8	1173	4	US-09-902-540-7010	Sequence 7010, Ap
411	16	1.8	1176	4	US-09-252-991A-11843	Sequence 11843, A
412	16	1.8	1203	4	US-09-252-991A-6250	Sequence 6250, Ap
413	16	1.8	1205	4	US-09-620-312D-949	Sequence 949, App
414	16	1.8	1206	4	US-09-949-016-5866	Sequence 5866, Ap
415	16	1.8	1227	4	US-09-252-991A-5278	Sequence 5278, Ap
416	16	1.8	1250	4	US-09-270-767-13107	Sequence 13107, A
C 417	16	1.8	1254	4	US-09-252-991A-11478	Sequence 11478, A
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C 420	16	1.8	1275	4	US-09-252-991A-13638	Sequence 13638, A
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C 422	16	1.8	1281	4	US-09-902-540-377	Sequence 377, App
423	16	1.8	1299	4	US-09-902-540-3581	Sequence 3581, Ap
424	16	1.8	1302	4	US-09-902-540-2306	Sequence 2306, Ap
425	16	1.8	1305	2	US-08-896-410-37	Sequence 37, Appl
426	16	1.8	1313	4	US-09-949-016-5475	Sequence 5475, Ap
C 427	16	1.8	1314	4	US-09-902-540-5877	Sequence 5877, Ap
428	16	1.8	1315	4	US-09-902-540-156	Sequence 156, App
C 429	16	1.8	1329	1	US-07-882-329-4	Sequence 4, Appli
C 430	16	1.8	1329	1	US-08-183-213-4	Sequence 4, Appli
431	16	1.8	1334	4	US-09-949-016-602	Sequence 602, App
C 432	16	1.8	1362	4	US-09-023-655-485	Sequence 485, App
C 433	16	1.8	1364	4	US-09-949-016-233	Sequence 233, App
C 434	16	1.8	1364	4	US-09-949-016-3758	Sequence 3758, Ap
435	16	1.8	1396	4	US-09-902-540-2206	Sequence 2206, Ap
436	16	1.8	1404	2	US-08-487-113D-119	Sequence 119, App
437	16	1.8	1404	2	US-08-720-420A-119	Sequence 119, App
438	16	1.8	1419	4	US-09-489-039A-5224	Sequence 5224, Ap
439	16	1.8	1440	4	US-09-902-540-8052	Sequence 8052, Ap
C 440	16	1.8	1452	4	US-09-252-991A-15812	Sequence 15812, A
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C 442	16	1.8	1458	3	US-09-489-039A-6655	Sequence 6655, Ap
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444	16	1.8	1460	3	US-09-166-750-18	Sequence 18, Appl
445	16	1.8	1460	3	US-09-166-093-18	Sequence 18, Appl
446	16	1.8	1460	3	US-09-172-019-18	Sequence 18, Appl
447	16	1.8	1460	3	US-09-166-094-18	Sequence 18, Appl
448	16	1.8	1460	4	US-09-443-213-18	Sequence 18, Appl
449	16	1.8	1473	4	US-09-252-991A-4196	Sequence 4196, Ap
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C 451	16	1.8	1488	1	US-08-393-246-9	Sequence 9, Appli
C 452	16	1.8	1488	1	US-08-525-058A-9	Sequence 9, Appli
C 453	16	1.8	1488	2	US-08-696-731-9	Sequence 9, Appli
C 454	16	1.8	1488	3	US-09-042-531-9	Sequence 9, Appli
455	16	1.8	1514	3	US-09-162-524-4	Sequence 4, Appli
C 456	16	1.8	1515	4	US-09-252-991A-12935	Sequence 12935, A
C 457	16	1.8	1517	4	US-09-902-540-214	Sequence 214, App
C 458	16	1.8	1524	4	US-09-252-991A-11455	Sequence 11455, A
C 459	16	1.8	1533	4	US-09-252-991A-800	Sequence 800, App
460	16	1.8	1539	3	US-09-364-230-289	Sequence 29, Appl
C 461	16	1.8	1554	4	US-09-902-540-2897	Sequence 2897, Ap
462	16	1.8	1565	3	US-09-320-878-24	Sequence 24, Appl
463	16	1.8	1565	4	US-09-141-908-22	Sequence 22, Appl
464	16	1.8	1565	4	US-09-657-440-24	Sequence 24, Appl
465	16	1.8	1572	4	US-09-252-991A-15025	Sequence 15025, A
466	16	1.8	1581	4	US-09-902-540-3972	Sequence 3972, Ap
C 467	16	1.8	1583	3	US-09-370-838-224	Sequence 224, App
C 468	16	1.8	1583	3	US-09-854-133-224	Sequence 224, App
469	16	1.8	1587	4	US-09-489-039A-6670	Sequence 6670, Ap
C 470	16	1.8	1590	4	US-09-252-991A-2259	Sequence 2259, Ap
471	16	1.8	1617	4	US-09-620-312D-265	Sequence 265, App
C 472	16	1.8	1623	4	US-09-252-991A-15700	Sequence 15700, A
C 473	16	1.8	1632	4	US-09-252-991A-3859	Sequence 3859, Ap
474	16	1.8	1637	4	US-09-949-016-2339	Sequence 2339, Ap
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476	16	1.8	1642	4	US-09-023-655-1485	Sequence 1485, Ap
477	16	1.8	1642	4	US-08-844-681A-1	Sequence 1, Appli
478	16	1.8	1644	4	US-09-252-991A-6420	Sequence 6420, Ap
C 479	16	1.8	1701	3	US-09-357-072-1	Sequence 1, Appli
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481	16	1.8	1701	4	US-09-516-747-1	Sequence 1, Appli
482	16	1.8	1701	4	US-09-933-814-1	Sequence 1, Appli
483	16	1.8	1701	5	PCT-US95-16542-1	Sequence 1, Appli
484	16	1.8	1701	5	PCT-US96-10521-1	Sequence 1, Appli
485	16	1.8	1762	4	US-09-265-383-2	Sequence 2, Appli
C 486	16	1.8	1788	4	US-09-252-991A-863	Sequence 863, App
C 487	16	1.8	1791	4	US-09-902-540-2785	Sequence 2785, Ap
488	16	1.8	1796	3	US-09-255-392-1	Sequence 1, Appli
489	16	1.8	1797	4	US-09-270-767-13142	Sequence 13142, A
C 490	16	1.8	1824	4	US-09-799-451-301	Sequence 301, App
C 491	16	1.8	1860	4	US-09-902-540-6841	Sequence 6841, A
C 492	16	1.8	1866	3	US-09-224-048A-1	Sequence 1, Appli
493	16	1.8	1869	2	US-08-356-786-15	Sequence 15, Appli
494	16	1.8	1900	4	US-09-949-016-1941	Sequence 1941, Ap
C 495	16	1.8	1919	4	US-09-949-016-801	Sequence 801, App
C 496	16	1.8	1919	4	US-09-949-016-634	Sequence 634, Ap
C 497	16	1.8	1947	4	US-09-252-991A-14778	Sequence 14728, A
498	16	1.8	1958	4	US-09-620-312D-354	Sequence 354, App
499	16	1.8	1992	4	US-09-252-991A-15580	Sequence 15580, A
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502	16	1.8	2005	3	US-08-465-375-1	Sequence 1, Appli
503	16	1.8	2005	3	US-09-788-070-1	Sequence 1, Appli
504	16	1.8	2005	3	US-10-142-373-1	Sequence 1, Appli
505	16	1.8	2005	4	US-09-155-252A-1	Sequence 1, Appli
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507	16	1.8	2037	3	US-09-252-991A-4499	Sequence 4499, Ap
508	16	1.8	2048	3	US-09-199-637A-136	Sequence 136, App
509	16	1.8	2097	3	US-09-002-567B-2	Sequence 2, Appli
510	16	1.8	2097	3	US-09-571-347-2	Sequence 2, Appli
511	16	1.8	2097	4	US-09-252-991A-885	Sequence 885, App
512	16	1.8	2097	4	US-09-949-016-5524	Sequence 5524, Ap
513	16	1.8	2097	4	US-09-902-540-7039	Sequence 7039, Ap
514	16	1.8	2100	4	US-09-949-016-530	Sequence 530, App
515	16	1.8	2103	4	US-09-252-991A-11773	Sequence 11773, A
516	16	1.8	2208	4	US-09-252-991A-13675	Sequence 13675, A
C 517	16	1.8	2208	4	US-09-252-991A-15669	Sequence 15669, A
C 518	16	1.8	2209	4	US-09-489-847-16	Sequence 16, Appl
C 519	16	1.8	2211	2	US-09-324-258-4	Sequence 4, Appli
520	16	1.8	2218	3	US-08-845-988-5	Sequence 5, Appli
521	16	1.8	2218	3	US-09-206-537-5	Sequence 5, Appli
522	16	1.8	2218	3	US-09-430-854-5	Sequence 5, Appli
523	16	1.8	2218	4	US-09-814-915A-4	Sequence 4, Appli
C 524	16	1.8	2233	4	US-09-949-016-126	Sequence 526, App
C 525	16	1.8	2235	4	US-09-949-016-766	Sequence 4766, Ap
C 526	16	1.8	2237	5	PCT-US93-08282-1	Sequence 1, Appli
C 527	16	1.8	2254	4	US-09-620-312D-73	Sequence 73, Appl
528	16	1.8	2259	2	US-08-845-998-3	Sequence 3, Appli
529	16	1.8	2259	3	US-09-206-537-3	Sequence 3, Appli
530	16	1.8	2259	3	US-09-430-854-3	Sequence 3, Appli
531	16	1.8	2274	4	US-09-252-991A-15970	Sequence 15970, A
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533	16	1.8	2302	1	US-07-999-280A-1	Sequence 1, Appli
534	16	1.8	2302	1	US-08-426-036-1	Sequence 1, Appli
535	16	1.8	2302	1	US-08-426-279-1	Sequence 1, Appli
536	16	1.8	2302	1	US-08-401-013-1	Sequence 1, Appli
537	16	1.8	2302	1	US-08-426-570-1	Sequence 1, Appli
538	16	1.8	2302	3	US-08-425-876-1	Sequence 1, Appli



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540	16	1.8	2302	3	US-08-401-632-1	Sequence 1, Appl1	C 613	16	1.8	6063	4	US-09-902-540-807	Sequence 807, App
541	16	1.8	2327	3	US-08-868-435-1	Sequence 1, Appl1	C 614	16	1.8	6119	4	US-09-949-016-16794	Sequence 16794, A
542	16	1.8	2327	3	US-08-744-231-1	Sequence 1, Appl1	C 615	16	1.8	6567	4	US-09-902-540-769	Sequence 769, App
543	16	1.8	2327	4	US-09-635-504-1	Sequence 1, Appl1	C 616	16	1.8	6791	4	US-09-771-035A-1	Sequence 1, Appl1
544	16	1.8	2361	4	US-09-352-991A-13870	Sequence 13870, A	C 617	16	1.8	7460	4	US-09-949-016-12375	Sequence 12375, A
545	16	1.8	2376	4	US-09-352-991A-6630	Sequence 6630, Ap	C 618	16	1.8	7462	4	US-09-949-016-13384	Sequence 14384, A
546	16	1.8	2469	4	US-09-489-039A-6749	Sequence 6749, Ap	C 619	16	1.8	7546	4	US-09-902-540-801	Sequence 801, App
547	16	1.8	2493	4	US-09-620-912A-4346	Sequence 4346, Ap	C 620	16	1.8	7700	4	US-09-949-016-15619	Sequence 15619, A
548	16	1.8	2539	4	US-09-620-912B-454	Sequence 454, App	C 621	16	1.8	7988	3	US-08-984-709A-49	Sequence 49, Appl
549	16	1.8	2575	3	US-09-077-354B-1	Sequence 1, Appl1	C 622	16	1.8	7958	4	US-09-949-016-15531	Sequence 16531, A
550	16	1.8	2592	4	US-09-352-991A-5260	Sequence 5260, Ap	C 623	16	1.8	8025	4	US-09-949-016-14081	Sequence 14081, A
551	16	1.8	2638	4	US-09-976-594-474	Sequence 474, App	C 624	16	1.8	8144	4	US-09-902-540-820	Sequence 820, App
552	16	1.8	2631	4	US-09-949-016-3148	Sequence 3148, Ap	C 625	16	1.8	8279	4	US-09-949-016-13478	Sequence 13478, A
553	16	1.8	2652	4	US-09-489-039A-5584	Sequence 5584, Ap	C 626	16	1.8	8371	4	US-09-065-027-1	Sequence 1, Appl1
554	16	1.8	2681	4	US-09-749-340-8	Sequence 8, Appl1	C 627	16	1.8	8831	4	US-09-949-016-17608	Sequence 17608, A
555	16	1.8	2687	4	US-09-949-016-4588	Sequence 4588, Ap	C 628	16	1.8	8817	4	US-09-902-540-887	Sequence 887, App
556	16	1.8	2698	4	US-09-749-340-5	Sequence 5, Appl1	C 629	16	1.8	8976	3	US-09-495-797-44	Sequence 44, Appl
557	16	1.8	2714	4	US-09-949-016-1021	Sequence 1021, Ap	C 630	16	1.8	9146	4	US-09-902-540-930	Sequence 930, App
558	16	1.8	2715	4	US-09-352-991A-12548	Sequence 12548, A	C 631	16	1.8	9382	4	US-09-949-016-15306	Sequence 15306, A
559	16	1.8	2793	1	US-08-309-747-1	Sequence 1, Appl1	C 632	16	1.8	9960	3	US-08-822-586-46	Sequence 46, Appl
560	16	1.8	2793	1	US-08-458-298-1	Sequence 1, Appl1	C 633	16	1.8	10380	3	US-09-077-354B-3	Sequence 3, Appl1
561	16	1.8	2805	3	US-09-651-636-4	Sequence 4, Appl1	C 634	16	1.8	10391	4	US-09-902-540-998	Sequence 998, App
562	16	1.8	2805	3	US-09-650-855-4	Sequence 4, Appl1	C 635	16	1.8	10396	4	US-09-949-016-15573	Sequence 15573, A
563	16	1.8	2841	4	US-09-902-540-9681	Sequence 9681, Ap	C 636	16	1.8	11652	4	US-09-902-540-11360	Sequence 11560, A
564	16	1.8	2862	4	US-09-352-991A-13468	Sequence 13468, A	C 637	16	1.8	11854	4	US-09-902-540-1037	Sequence 1037, Ap
565	16	1.8	2862	4	US-09-949-016-5406	Sequence 5406, Ap	C 638	16	1.8	12824	4	US-09-902-540-993	Sequence 993, App
566	16	1.8	2871	4	US-09-949-016-3998	Sequence 3998, Ap	C 639	16	1.8	12715	4	US-09-949-016-11718	Sequence 17148, A
567	16	1.8	2947	1	US-08-457-176-1	Sequence 1, Appl1	C 640	16	1.8	12725	4	US-09-902-540-1132	Sequence 1132, Ap
568	16	1.8	2947	1	US-08-457-175-1	Sequence 1, Appl1	C 641	16	1.8	13426	4	US-09-949-016-13683	Sequence 13683, A
569	16	1.8	2976	4	US-09-220-132-8	Sequence 8, Appl1	C 642	16	1.8	13613	3	US-09-105-537-3	Sequence 3, Appl1
570	16	1.8	2976	4	US-09-902-540-554	Sequence 554, App	C 643	16	1.8	13637	4	US-09-902-540-1097	Sequence 1097, Ap
571	16	1.8	3027	4	US-09-352-991A-12848	Sequence 12848, A	C 644	16	1.8	13844	4	US-09-949-016-13054	Sequence 13054, A
572	16	1.8	3070	4	US-09-799-451-652	Sequence 652, App	C 645	16	1.8	15445	4	US-09-949-016-17271	Sequence 17271, A
573	16	1.8	3105	4	US-09-352-991A-4398	Sequence 4398, Ap	C 646	16	1.8	17247	4	US-09-902-540-1185	Sequence 1185, Ap
574	16	1.8	3145	4	US-09-708-200-14	Sequence 14, Appl	C 647	16	1.8	17662	4	US-09-902-540-1146	Sequence 1146, Ap
575	16	1.8	3145	4	US-09-788-657-9	Sequence 9, Appl1	C 648	16	1.8	18324	4	US-09-902-540-1196	Sequence 1196, Ap
576	16	1.8	3145	4	US-09-712-691-12	Sequence 12, Appl	C 649	16	1.8	19062	4	US-09-949-016-1487	Sequence 14877, A
577	16	1.8	3145	4	US-09-707-468C-12	Sequence 12, Appl	C 650	16	1.8	19112	4	US-09-902-540-1181	Sequence 1181, Ap
578	16	1.8	3153	4	US-09-922-501-13	Sequence 13, Appl1	C 651	16	1.8	19598	4	US-09-902-540-1143	Sequence 1143, Ap
579	16	1.8	3488	4	US-09-105-470B-8	Sequence 7, Appl1	C 652	16	1.8	20211	4	US-09-949-016-12344	Sequence 12344, A
580	16	1.8	3512	4	US-09-749-340-7	Sequence 7, Appl1	C 653	16	1.8	22212	4	US-09-949-016-17217	Sequence 17217, A
581	16	1.8	3512	4	US-09-902-540-674	Sequence 674, App	C 654	16	1.8	22927	4	US-09-949-016-11849	Sequence 11849, A
582	16	1.8	3641	4	US-09-949-016-3877	Sequence 3877, Ap	C 655	16	1.8	22927	4	US-09-949-016-13071	Sequence 13071, A
583	16	1.8	3650	4	US-09-620-312B-30	Sequence 30, Appl	C 656	16	1.8	22958	4	US-09-949-016-12894	Sequence 12894, A
584	16	1.8	3657	4	US-09-976-451-10	Sequence 10, Appl	C 657	16	1.8	23260	4	US-09-949-016-13300	Sequence 14300, A
585	16	1.8	3675	4	US-09-352-991A-16309	Sequence 16309, A	C 658	16	1.8	23560	4	US-09-949-016-13416	Sequence 13416, A
586	16	1.8	3699	4	US-09-902-540-3731	Sequence 3731, Ap	C 659	16	1.8	25044	4	US-09-949-016-13464	Sequence 13464, A
587	16	1.8	3924	4	US-09-902-540-572	Sequence 572, App	C 660	16	1.8	25933	4	US-09-949-016-15740	Sequence 15740, A
588	16	1.8	3924	4	US-09-023-655-1168	Sequence 1168, Ap	C 661	16	1.8	26289	4	US-09-902-540-1210	Sequence 1210, Ap
589	16	1.8	3924	4	US-09-762-195-2	Sequence 2, Appl1	C 662	16	1.8	26389	4	US-09-902-540-1210	Sequence 12578, A
590	16	1.8	4018	4	US-09-902-540-616	Sequence 616, App	C 663	16	1.8	27008	4	US-09-949-016-12397	Sequence 12397, A
591	16	1.8	4042	4	US-09-902-540-609	Sequence 609, App	C 664	16	1.8	27909	4	US-09-949-016-11082	Sequence 17082, A
592	16	1.8	4175	4	US-09-749-340-3	Sequence 3, Appl1	C 665	16	1.8	29067	4	US-09-949-016-12535	Sequence 12535, A
593	16	1.8	4195	4	US-09-902-540-695	Sequence 695, App	C 666	16	1.8	29933	4	US-09-949-016-1476	Sequence 17476, A
594	16	1.8	4279	4	US-09-672-725C-1	Sequence 1, Appl1	C 667	16	1.8	29885	4	US-09-785-381-6	Sequence 6, Appl1
595	16	1.8	4279	4	US-09-672-725C-22	Sequence 22, Appl	C 668	16	1.8	29885	4	US-09-949-016-13682	Sequence 13682, A
596	16	1.8	4279	4	US-09-672-725C-24	Sequence 24, Appl	C 669	16	1.8	30336	4	US-09-949-016-12268	Sequence 12268, A
597	16	1.8	4279	4	US-09-672-725C-26	Sequence 26, Appl	C 670	16	1.8	30337	4	US-09-949-016-15508	Sequence 16508, A
598	16	1.8	4317	4	US-09-672-725C-3	Sequence 3, Appl1	C 671	16	1.8	31035	4	US-09-949-016-12272	Sequence 12272, A
599	16	1.8	4317	4	US-10-044-671-1	Sequence 1, Appl1	C 672	16	1.8	31305	4	US-09-949-016-12766	Sequence 17266, A
600	16	1.8	4663	4	US-09-949-016-2387	Sequence 2387, Ap	C 673	16	1.8	31444	4	US-09-949-016-12578	Sequence 12578, A
601	16	1.8	4991	4	US-09-902-540-719	Sequence 719, App	C 674	16	1.8	31444	4	US-09-949-016-15400	Sequence 16400, A
602	16	1.8	5184	4	US-09-845-583A-9	Sequence 9, Appl1	C 675	16	1.8	34312	4	US-09-949-016-13352	Sequence 12352, A
603	16	1.8	5184	4	US-09-561-709B-4	Sequence 4, Appl1	C 676	16	1.8	35812	2	US-08-752-760A-1	Sequence 1, Appl1
604	16	1.8	5570	4	US-09-902-540-623	Sequence 623, App	C 677	16	1.8	36387	4	US-09-949-016-12370	Sequence 12370, A
605	16	1.8	5570	4	US-09-262-537-57	Sequence 57, Appl	C 678	16	1.8	37068	4	US-09-949-016-12543	Sequence 12543, A
606	16	1.8	5931	3	US-09-556-706B-1	Sequence 1, Appl1	C 679	16	1.8	37068	4	US-09-949-016-12376	Sequence 17376, A
607	16	1.8	5931	3	US-09-724-418A-1	Sequence 1, Appl1	C 680	16	1.8	38653	4	US-09-922-445-1	Sequence 1, Appl1
608	16	1.8	5931	3	US-09-949-016-11975	Sequence 11975, A	C 681	16	1.8	39113	4	US-08-311-731A-125	Sequence 125, App
609	16	1.8	5931	4			C 682	16	1.8	40429	4		
610	16	1.8	5931	4			C 683	16	1.8				
611	16	1.8	5931	4			C 684	16	1.8				

685	16	1.8	41927	4	US-09-902-540-1268	Sequence 1268, Ap	758	16	1.8	156895	4	US-09-949-016-16958	Sequence 16958, Ap
C 686	16	1.8	44377	2	US-08-804-227C-7	Sequence 7, Appl.1	759	16	1.8	156895	4	US-09-949-016-16959	Sequence 16959, A
C 687	16	1.8	44377	2	US-08-804-198-1	Sequence 1, Appl.1	760	16	1.8	161652	4	US-09-947-855A-40	Sequence 40, Appl.1
C 688	16	1.8	47727	4	US-09-949-016-12904	Sequence 12904, A	761	16	1.8	177669	4	US-09-949-016-13713	Sequence 13713, A
C 689	16	1.8	50937	3	US-09-428-517-1	Sequence 1, Appl.1	762	16	1.8	177669	4	US-09-949-016-13713	Sequence 13713, A
C 690	16	1.8	51849	4	US-09-949-016-15433	Sequence 15433, A	763	16	1.8	178883	4	US-09-949-016-12733	Sequence 12733, A
C 691	16	1.8	52139	4	US-09-949-016-12763	Sequence 12763, A	764	16	1.8	183202	4	US-09-949-016-13039	Sequence 13039, A
C 692	16	1.8	52203	4	US-09-949-016-16330	Sequence 16330, A	765	16	1.8	183202	4	US-09-949-016-13614	Sequence 12614, A
C 693	16	1.8	61399	4	US-09-949-016-14386	Sequence 14386, A	766	16	1.8	187848	4	US-09-949-016-12111	Sequence 12111, A
C 694	16	1.8	61461	4	US-09-949-016-16419	Sequence 16419, A	767	16	1.8	187916	4	US-09-949-016-12580	Sequence 12980, A
C 695	16	1.8	61933	4	US-09-949-016-15338	Sequence 15338, A	C 767	16	1.8	236964	4	US-09-949-016-15763	Sequence 15753, A
C 696	16	1.8	61932	4	US-09-949-016-11732	Sequence 11732, A	768	16	1.8	239527	4	US-09-949-016-15980	Sequence 15980, A
C 697	16	1.8	62386	4	US-09-949-016-12823	Sequence 12823, A	769	16	1.8	247781	4	US-09-949-016-14123	Sequence 14193, A
C 698	16	1.8	62728	4	US-09-949-016-12539	Sequence 12539, A	C 770	16	1.8	390890	4	US-09-949-016-14720	Sequence 14720, A
C 699	16	1.8	65424	4	US-09-949-016-12426	Sequence 12426, A	771	16	1.8	784019	4	US-09-949-016-14033	Sequence 14033, A
C 700	16	1.8	67745	4	US-09-949-016-17251	Sequence 17251, A	772	16	1.8	828152	4	US-09-949-016-12777	Sequence 12777, A
C 701	16	1.8	69924	4	US-09-949-016-15367	Sequence 15367, A	773	16	1.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl.1
C 702	16	1.8	70828	4	US-09-949-016-12122	Sequence 12122, A	C 774	16	1.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl.1
C 703	16	1.8	72782	4	US-09-949-016-16161	Sequence 16161, A	775	16	1.8	1664976	4	US-09-632-570-1	Sequence 1, Appl.1
C 704	16	1.8	76610	4	US-09-949-016-15521	Sequence 15521, A	C 776	16	1.8	1664976	4	US-09-632-570-1	Sequence 1, Appl.1
C 705	16	1.8	77626	4	US-09-949-016-12608	Sequence 12608, A	C 777	15	1.7	21	4	US-09-778-510-14	Sequence 14, Appl.1
C 706	16	1.8	81433	4	US-09-949-016-11941	Sequence 11941, A	C 778	15	1.7	25	4	US-09-396-196G-36122	Sequence 36122, A
C 707	16	1.8	84237	4	US-09-949-016-17374	Sequence 17374, A	C 779	15	1.7	25	4	US-09-396-196G-36577	Sequence 36577, A
C 708	16	1.8	84875	4	US-09-949-016-17334	Sequence 17334, A	780	15	1.7	25	4	US-09-396-196G-76630	Sequence 76630, A
C 709	16	1.8	84875	4	US-09-949-016-17335	Sequence 17335, A	C 781	15	1.7	76	4	US-09-270-767-8890	Sequence 4890, Ap
C 710	16	1.8	84875	4	US-09-949-016-17337	Sequence 17336, A	C 782	15	1.7	76	4	US-09-270-767-8890	Sequence 20172, A
C 711	16	1.8	84875	4	US-09-949-016-17337	Sequence 17337, A	C 783	15	1.7	81	2	US-07-814-220-34	Sequence 34, Appl.1
C 712	16	1.8	85152	4	US-09-949-016-12655	Sequence 12655, A	C 784	15	1.7	81	2	US-07-814-220-34	Sequence 34, Appl.1
C 713	16	1.8	85152	4	US-09-949-016-12665	Sequence 12665, A	C 785	15	1.7	82	2	US-07-814-220-31	Sequence 31, Appl.1
C 714	16	1.8	85152	4	US-09-949-016-12667	Sequence 12667, A	C 786	15	1.7	82	2	US-07-814-220-31	Sequence 31, Appl.1
C 715	16	1.8	85152	4	US-09-949-016-12668	Sequence 12668, A	787	15	1.7	82	2	US-07-814-220-35	Sequence 35, Appl.1
C 716	16	1.8	86127	4	US-09-949-016-12609	Sequence 12209, A	788	15	1.7	89	2	US-07-814-221-35	Sequence 35, Appl.1
C 717	16	1.8	86128	4	US-09-949-016-12608	Sequence 12209, A	789	15	1.7	90	2	US-07-814-220-32	Sequence 32, Appl.1
C 718	16	1.8	87563	3	US-09-453-702B-57	Sequence 57, Appl.1	790	15	1.7	90	2	US-07-814-221-32	Sequence 32, Appl.1
C 719	16	1.8	89210	4	US-09-949-016-16988	Sequence 16988, A	791	15	1.7	138	4	US-09-902-540-1103	Sequence 5103, Ap
C 720	16	1.8	92227	4	US-09-949-016-11929	Sequence 11929, A	792	15	1.7	150	4	US-09-455-052-39	Sequence 39, Appl.1
C 721	16	1.8	92232	4	US-09-949-016-15421	Sequence 15421, A	793	15	1.7	156	3	US-09-277-078-45	Sequence 45, Appl.1
C 722	16	1.8	93364	4	US-09-949-016-14890	Sequence 14890, A	794	15	1.7	156	4	US-09-621-976-8095	Sequence 9095, Ap
C 723	16	1.8	98838	4	US-09-949-016-16630	Sequence 16630, A	795	15	1.7	164	4	US-09-313-294A-6924	Sequence 6924, Ap
C 724	16	1.8	104428	4	US-09-949-016-12737	Sequence 12737, A	796	15	1.7	166	4	US-09-513-999C-29205	Sequence 29205, A
C 725	16	1.8	104429	4	US-09-949-016-13814	Sequence 13814, A	C 797	15	1.7	173	4	US-09-513-999C-14602	Sequence 14602, A
C 726	16	1.8	113966	4	US-09-949-016-12277	Sequence 12277, A	798	15	1.7	177	1	US-08-470-179-84	Sequence 84, Appl.1
C 727	16	1.8	113967	4	US-09-949-016-17051	Sequence 17051, A	799	15	1.7	181	4	US-09-270-767-6608	Sequence 6608, Ap
C 728	16	1.8	113967	4	US-09-949-016-15525	Sequence 15525, A	800	15	1.7	181	4	US-09-270-767-19890	Sequence 19890, A
C 729	16	1.8	118143	4	US-09-949-016-17196	Sequence 17196, A	801	15	1.7	183	4	US-09-583-110-713	Sequence 713, Appl.1
C 730	16	1.8	119032	4	US-09-949-016-12160	Sequence 12160, A	C 802	15	1.7	184	4	US-09-513-999C-28288	Sequence 28288, A
C 731	16	1.8	119032	4	US-09-949-016-12160	Sequence 12160, A	803	15	1.7	186	4	US-09-583-110-2405	Sequence 2405, Ap
C 732	16	1.8	125188	4	US-09-949-016-11980	Sequence 11980, A	804	15	1.7	186	4	US-09-248-796A-11182	Sequence 11182, A
C 733	16	1.8	125672	4	US-09-949-016-16956	Sequence 16956, A	805	15	1.7	186	4	US-09-107-433-1988	Sequence 1988, Ap
C 734	16	1.8	128470	4	US-09-949-016-13765	Sequence 13765, A	806	15	1.7	189	4	US-09-583-110-1598	Sequence 1598, Ap
C 735	16	1.8	139936	4	US-09-949-016-11782	Sequence 11782, A	807	15	1.7	192	4	US-09-107-433-1394	Sequence 1394, Ap
C 736	16	1.8	139952	4	US-09-949-016-13380	Sequence 13380, A	C 808	15	1.7	192	4	US-09-583-110-1578	Sequence 1578, Ap
C 737	16	1.8	141115	4	US-09-949-016-17930	Sequence 17490, A	809	15	1.7	192	4	US-09-583-110-1585	Sequence 1585, Ap
C 738	16	1.8	143644	4	US-09-949-016-15338	Sequence 15238, A	C 810	15	1.7	192	4	US-09-583-110-2607	Sequence 2607, Ap
C 739	16	1.8	146307	4	US-09-949-016-14881	Sequence 14881, A	C 811	15	1.7	195	4	US-09-583-110-2404	Sequence 2404, Ap
C 740	16	1.8	146307	4	US-09-949-016-14882	Sequence 14882, A	C 812	15	1.7	195	4	US-09-107-433-1550	Sequence 1550, Ap
C 741	16	1.8	146307	4	US-09-949-016-14883	Sequence 14883, A	C 813	15	1.7	195	4	US-09-107-433-1121	Sequence 12121, Ap
C 742	16	1.8	146307	4	US-09-949-016-14884	Sequence 14884, A	C 814	15	1.7	196	4	US-09-513-999C-26305	Sequence 26305, Ap
C 743	16	1.8	146307	4	US-09-949-016-14885	Sequence 14885, A	C 815	15	1.7	197	4	US-09-513-999C-26305	Sequence 26305, Ap
C 744	16	1.8	146307	4	US-09-949-016-14886	Sequence 14886, A	816	15	1.7	198	4	US-09-107-433-13593	Sequence 13593, Ap
C 745	16	1.8	146307	4	US-09-949-016-14887	Sequence 14887, A	C 817	15	1.7	204	4	US-09-107-433-34	Sequence 34, Appl.1
C 746	16	1.8	146307	4	US-09-949-016-14888	Sequence 14888, A	C 818	15	1.7	207	4	US-09-513-999C-33173	Sequence 33173, A
C 747	16	1.8	148405	4	US-09-949-016-11747	Sequence 11747, A	C 819	15	1.7	210	4	US-09-107-433-998	Sequence 998, App
C 748	16	1.8	148405	4	US-09-949-016-12835	Sequence 12835, A	C 820	15	1.7	213	4	US-09-107-433-32291	Sequence 32291, Ap
C 749	16	1.8	148405	4	US-09-949-016-12836	Sequence 12836, A	C 821	15	1.7	216	4	US-09-992-540-2083	Sequence 2083, Ap
C 750	16	1.8	148405	4	US-09-949-016-12837	Sequence 12837, A	C 822	15	1.7	222	4	US-09-107-433-1595	Sequence 1595, Ap
C 751	16	1.8	152393	4	US-09-949-016-12837	Sequence 12837, A	C 823	15	1.7	225	4	US-09-107-433-3129	Sequence 3129, Ap
C 752	16	1.8	152393	4	US-09-949-016-14514	Sequence 14514, A	C 824	15	1.7	228	4	US-09-583-110-1039	Sequence 1039, Ap
C 753	16	1.8	154746	4	US-09-827-688-8	Sequence 14515, A	C 825	15	1.7	228	4	US-09-107-433-2366	Sequence 2366, Ap
C 754	16	1.8	154746	4	US-09-827-688-8	Sequence 8, Appl.1	C 826	15	1.7	231	4	US-09-583-110-1408	Sequence 1408, Ap
C 755	16	1.8	156894	4	US-09-949-016-12765	Sequence 12765, A	C 827	15	1.7	234	4	US-09-248-796A-8806	Sequence 8806, Ap
C 756	16	1.8	156894	4	US-09-949-016-12766	Sequence 12766, A	C 828	15	1.7	237	4	US-09-583-110-1040	Sequence 1040, Ap
C 757	16	1.8	156895	4	US-09-949-016-16957	Sequence 16957, A	C 829	15	1.7	240	4	US-09-459-039A-6782	Sequence 6782, Ap
							830	15	1.7	240	4	US-09-583-110-1921	Sequence 1921, Ap

C 831	15	1.7	240	4	US-09-583-110-2175	Sequence 2175, Ap	C 904	15	1.7	404	5	PCT-US94-04208-3	Sequence 3, Appli
C 832	15	1.7	241	4	US-09-621-976-13984	Sequence 13984, A	C 905	15	1.7	405	4	US-09-252-991A-9388	Sequence 9388, Ap
C 833	15	1.7	246	4	US-09-107-433-1091	Sequence 1091, Ap	C 906	15	1.7	411	4	US-09-252-991A-5236	Sequence 5236, Ap
C 834	15	1.7	255	4	US-09-107-433-1591	Sequence 1591, Ap	C 907	15	1.7	411	4	US-09-252-991A-8167	Sequence 8167, Ap
C 835	15	1.7	258	4	US-09-313-294A-3678	Sequence 3678, Ap	C 908	15	1.7	411	4	US-09-252-991A-14549	Sequence 14549, A
C 836	15	1.7	258	4	US-09-583-110-2022	Sequence 2022, Ap	C 909	15	1.7	414	4	US-09-252-991A-11145	Sequence 11145, A
C 837	15	1.7	258	4	US-09-489-039A-2233	Sequence 2233, Ap	C 910	15	1.7	420	4	US-09-252-991A-1637	Sequence 1637, Ap
C 838	15	1.7	264	4	US-09-107-433-1090	Sequence 1090, Ap	C 911	15	1.7	420	4	US-09-252-991A-2420	Sequence 2420, Ap
C 839	15	1.7	270	4	US-09-107-433-1060	Sequence 1060, Ap	C 912	15	1.7	420	4	US-09-252-991A-1967	Sequence 1967, Ap
C 840	15	1.7	277	4	US-09-313-294A-1922	Sequence 1922, Ap	C 913	15	1.7	420	4	US-09-252-991A-13552	Sequence 13552, A
C 841	15	1.7	277	4	US-09-313-294A-3430	Sequence 3430, Ap	C 914	15	1.7	422	4	US-09-621-976-1564	Sequence 1564, A
C 842	15	1.7	278	4	US-09-313-294A-1198	Sequence 1198, Ap	C 915	15	1.7	423	4	US-09-270-767-6099	Sequence 6099, Ap
C 843	15	1.7	278	4	US-09-702-705-1121	Sequence 1121, Ap	C 916	15	1.7	423	4	US-09-270-767-21381	Sequence 21381, A
C 844	15	1.7	278	4	US-09-702-705-1640	Sequence 1640, Ap	C 917	15	1.7	423	4	US-09-902-540-7940	Sequence 7940, Ap
C 845	15	1.7	278	4	US-09-736-457-1121	Sequence 1121, Ap	C 918	15	1.7	432	4	US-09-583-110-2608	Sequence 2608, Ap
C 846	15	1.7	278	4	US-09-736-457-1540	Sequence 1640, Ap	C 919	15	1.7	432	4	US-09-107-433-2680	Sequence 2580, Ap
C 847	15	1.7	278	4	US-09-614-124B-1121	Sequence 1121, Ap	C 920	15	1.7	438	4	US-09-252-991A-5442	Sequence 3442, Ap
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C 850	15	1.7	278	4	US-09-671-325-1640	Sequence 1640, Ap	C 923	15	1.7	453	4	US-09-252-991A-1149	Sequence 1149, Ap
C 851	15	1.7	278	4	US-09-658-824-1121	Sequence 1121, Ap	C 924	15	1.7	461	2	US-08-825-556A-1	Sequence 1, Appli
C 852	15	1.7	278	4	US-09-658-824-1640	Sequence 1640, Ap	C 925	15	1.7	461	4	US-09-238-184-1	Sequence 8695, Ap
C 853	15	1.7	279	4	US-09-658-824-1640	Sequence 335, Ap	C 926	15	1.7	461	4	US-09-513-999C-8695	Sequence 546, Ap
C 854	15	1.7	282	2	US-08-716-942-21	Sequence 21, Appl	C 927	15	1.7	462	4	US-09-252-991A-546	Sequence 634, Ap
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C 856	15	1.7	290	4	US-09-602-777A-317	Sequence 317, App	C 929	15	1.7	466	4	US-09-270-767-6896	Sequence 6896, Ap
C 857	15	1.7	291	4	US-09-902-540-3335	Sequence 3235, Ap	C 930	15	1.7	466	4	US-09-270-767-22178	Sequence 1139, Ap
C 858	15	1.7	293	4	US-09-513-999C-11354	Sequence 11354, A	C 931	15	1.7	467	4	US-09-621-976-1199	Sequence 1199, Ap
C 859	15	1.7	297	4	US-09-513-999C-13485	Sequence 13485, A	C 932	15	1.7	469	4	US-09-513-999C-12161	Sequence 12161, A
C 860	15	1.7	300	4	US-09-640-211A-1640	Sequence 1640, Ap	C 933	15	1.7	470	3	US-09-615-192A-189	Sequence 189, Ap
C 861	15	1.7	302	4	US-09-513-999C-35158	Sequence 35158, A	C 934	15	1.7	471	4	US-09-252-991A-4041	Sequence 4041, Ap
C 862	15	1.7	309	4	US-09-513-999C-13960	Sequence 13960, A	C 935	15	1.7	478	3	US-09-221-017B-149	Sequence 149, Ap
C 863	15	1.7	311	3	US-09-657-453A-15	Sequence 15, Appl	C 936	15	1.7	486	4	US-09-252-991A-13452	Sequence 13452, A
C 864	15	1.7	313	2	US-09-513-999C-34917	Sequence 34917, A	C 937	15	1.7	486	4	US-09-252-991A-15808	Sequence 15808, A
C 865	15	1.7	318	2	US-08-318-157B-3	Sequence 3, Appli	C 938	15	1.7	491	4	US-09-573-080A-866	Sequence 366, Ap
C 866	15	1.7	318	2	US-09-253-794-3	Sequence 3, Appli	C 939	15	1.7	493	2	US-08-630-822A-89	Sequence 89, Appl
C 867	15	1.7	321	3	US-09-406-535-3	Sequence 3, Appli	C 940	15	1.7	493	2	US-09-005-069-89	Sequence 89, Appl
C 868	15	1.7	321	4	US-09-107-433-2236	Sequence 2236, Ap	C 941	15	1.7	493	3	US-09-171-156A-38	Sequence 38, Appl
C 869	15	1.7	331	4	US-09-270-767-7837	Sequence 7837, Ap	C 942	15	1.7	493	4	US-09-004-730A-38	Sequence 38, Appl
C 870	15	1.7	331	4	US-09-270-767-23119	Sequence 23119, A	C 943	15	1.7	493	4	US-08-981-799A-38	Sequence 38, Appl
C 871	15	1.7	333	4	US-09-852-991A-8960	Sequence 8960, A	C 944	15	1.7	495	4	US-09-252-991A-374	Sequence 274, Ap
C 872	15	1.7	336	2	US-07-814-220-3	Sequence 3, Appli	C 945	15	1.7	495	4	US-09-902-540-4325	Sequence 4325, Ap
C 873	15	1.7	336	2	US-07-814-220-4	Sequence 4, Appli	C 946	15	1.7	498	4	US-08-854-133-345	Sequence 345, Ap
C 874	15	1.7	336	2	US-07-812-421-3	Sequence 3, Appli	C 947	15	1.7	501	4	US-09-252-991A-14775	Sequence 14775, A
C 875	15	1.7	336	2	US-07-812-421-4	Sequence 4, Appli	C 948	15	1.7	501	4	US-09-513-999C-3220	Sequence 3220, A
C 876	15	1.7	336	2	US-07-812-421-100	Sequence 100, Appl	C 949	15	1.7	507	4	US-09-248-796A-1773	Sequence 1773, Ap
C 877	15	1.7	340	3	US-08-836-075A-77	Sequence 77, Appl	C 950	15	1.7	510	4	US-09-252-991A-11546	Sequence 11546, A
C 878	15	1.7	340	4	US-09-878-281A-145	Sequence 145, App	C 951	15	1.7	512	4	US-09-949-016-3161	Sequence 3161, Ap
C 879	15	1.7	342	4	US-09-583-110-1573	Sequence 1573, Ap	C 952	15	1.7	513	4	US-09-252-991A-5213	Sequence 5213, Ap
C 880	15	1.7	356	4	US-09-513-999C-21472	Sequence 21472, A	C 953	15	1.7	519	4	US-09-902-540-7661	Sequence 7661, Ap
C 881	15	1.7	363	4	US-09-252-991A-8832	Sequence 8832, Ap	C 954	15	1.7	522	4	US-09-248-796A-11108	Sequence 11108, A
C 882	15	1.7	363	4	US-09-621-976-2573	Sequence 2573, Ap	C 955	15	1.7	528	3	US-08-478-486F-10	Sequence 10, Appl
C 883	15	1.7	368	4	US-09-513-999C-30974	Sequence 30974, A	C 956	15	1.7	528	4	US-09-613-304A-4	Sequence 4, Appli
C 884	15	1.7	373	4	US-09-471-276-734	Sequence 734, App	C 957	15	1.7	530	4	US-09-513-999C-14129	Sequence 14129, A
C 885	15	1.7	374	5	US-09-513-999C-1590	Sequence 1590, Ap	C 958	15	1.7	537	4	US-09-252-991A-9518	Sequence 9518, Ap
C 886	15	1.7	378	5	PCT-US94-04208-5	Sequence 5, Appli	C 959	15	1.7	537	4	US-09-252-991A-14815	Sequence 14815, A
C 887	15	1.7	381	4	US-09-252-991A-5155	Sequence 5155, Ap	C 960	15	1.7	537	4	US-09-270-767-6157	Sequence 6157, Ap
C 888	15	1.7	381	4	US-09-583-110-1574	Sequence 1574, Ap	C 961	15	1.7	537	4	US-09-270-767-21439	Sequence 21439, A
C 889	15	1.7	381	4	US-09-270-767-2850	Sequence 2850, Ap	C 962	15	1.7	549	4	US-09-489-039A-1789	Sequence 1789, Ap
C 890	15	1.7	381	4	US-09-270-767-18132	Sequence 18132, A	C 963	15	1.7	554	3	US-09-276-531-64	Sequence 64, Appl
C 891	15	1.7	381	4	US-09-107-433-2086	Sequence 2086, Ap	C 964	15	1.7	561	1	US-08-832-883-4	Sequence 4, Appli
C 892	15	1.7	382	4	US-09-573-080A-4	Sequence 4, Appli	C 965	15	1.7	561	2	US-08-832-883-4	Sequence 4, Appli
C 893	15	1.7	384	4	US-09-902-540-7240	Sequence 7240, Ap	C 966	15	1.7	564	4	US-09-252-991A-1538	Sequence 1538, Ap
C 894	15	1.7	387	3	US-08-765-907A-4	Sequence 4, Appli	C 967	15	1.7	564	4	US-09-252-991A-1488	Sequence 1488, Ap
C 895	15	1.7	387	4	US-09-073-009-133	Sequence 133, App	C 968	15	1.7	574	4	US-09-513-999C-11385	Sequence 11385, A
C 896	15	1.7	387	4	US-09-073-010-133	Sequence 133, App	C 969	15	1.7	582	4	US-09-010-147B-13	Sequence 13, Appl
C 897	15	1.7	387	4	US-09-987-614A-4	Sequence 4, Appli	C 970	15	1.7	588	2	US-08-924-659A-3	Sequence 3, Appl
C 898	15	1.7	389	4	US-09-621-976-14888	Sequence 14888, A	C 971	15	1.7	588	4	US-09-252-991A-3396	Sequence 4396, Ap
C 899	15	1.7	390	4	US-09-107-433-755	Sequence 755, App	C 972	15	1.7	591	4	US-09-252-991A-10849	Sequence 10849, A
C 900	15	1.7	402	4	US-09-252-991A-9640	Sequence 9640, Ap	C 973	15	1.7	591	3	US-08-833-488B-6	Sequence 6, Appli
C 901	15	1.7	402	4	US-09-252-991A-14652	Sequence 14652, Ap	C 974	15	1.7	591	3	US-08-833-488B-7	Sequence 7, Appli
C 902	15	1.7	402	4	US-09-328-352-1008	Sequence 1008, Ap	C 975	15	1.7	591	3	US-08-833-488B-11	Sequence 11, Appl
C 903	15	1.7	402	4	US-09-328-352-4069	Sequence 4069, Ap	C 976	15	1.7	591	3	US-08-833-488B-12	Sequence 12, Appl

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c 977 15 1.7 591 3 US-08-833-488B-27
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c 979 15 1.7 591 3 US-09-252-991A-4592
c 980 15 1.7 591 4 US-09-252-991A-6492
c 981 15 1.7 596 4 US-09-949-016-4581
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c 999 15 1.7 601 4 US-09-949-016-33021
c1000 15 1.7 601 4 US-09-949-016-33706
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## ALIGNMENTS

## RESULT 1

US-09-620-312D-853  
Sequence 853, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yundong

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: PL\_FL\_genes Version 1.0

SEQ ID NO 853

LENGTH: 1067

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (151)..(984)

US-09-620-312D-853

Sequence 27, Appl  
Sequence 29, Appl  
Sequence 4592, Ap  
Sequence 4592, Ap  
Sequence 4581, Ap  
Sequence 17, Appl  
Sequence 19058, A  
Sequence 19059, A  
Sequence 19122, A  
Sequence 19632, A  
Sequence 19633, A  
Sequence 19634, A  
Sequence 22840, A  
Sequence 22841, A  
Sequence 22888, A  
Sequence 22889, A  
Sequence 23002, A  
Sequence 23252, A  
Sequence 23528, A  
Sequence 30538, A  
Sequence 33020, A  
Sequence 33021, A  
Sequence 33706, A

Matches 431; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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QY 61 TACGGAGTCTGTGCTTACCGTATGTTGAGTGTGGCGGGCACTGACGATGC 120  
Db 211 TACGGAGTCTGTGCTTACCGTATGTTGAGTGTGGCGGGCACTGACGATGC 270  
QY 121 GAGCTGAGCTCTGCGCTTCTGTGATGATGAGCTCTGCGCGCGGAGGCTTACG 180  
Db 211 GAGCTGAGCTCTGCGCTTCTGTGATGATGAGCTCTGCGCGCGGAGGCTTACG 330  
QY 271 GAGCTGAGCTCTGCGCTTCTGTGATGATGAGCTCTGCGCGCGGAGGCTTACG 330  
Db 181 CGGGCCGACGCGGCTTACGCTCTGCTGAGCTGAGCTGAGCGCGCGGCACTGCGCAG 240  
QY 331 CGGGCCGACGCGGCTTACGCTCTGCTGAGCTGAGCTGAGCGCGCGGCACTGCGCAG 390  
Db 241 AGCAACTGCGGCTGCTGCTGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
QY 391 AGCAACTGCGGCTGCTGCTGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450  
Db 301 CACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
QY 451 CACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 510  
Db 361 AGCTCTTCAAG 420  
QY 511 AGCTCTTCAAG 570  
QY 421 AATTCTCAGCAGG 434  
Db 571 AATTCTCAGCAGG 584

## RESULT 2

US-09-252-991A-2993/c  
Sequence 2993, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 2993

LENGTH: 2673

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-2993

Query Match 2.2%; Score 20; DB 4; Length 2673;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 308 CGCGCAGCGCGCGCGCGCA 327  
Db 1472 CGCGCAGCGCGCGCGCGCA 1453

## RESULT 3

US-09-252-991A-2686  
Sequence 2686, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 2686
/ LENGTH: 2715
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2686

Query Match      2.2%; Score 20; DB 4; Length 2715;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      308 CGCGCAAGCGCGCGCGCA 327
DB      1313 CGCGCAAGCGCGCGCGCA 1332

RESULT 4
US-09-252-991A-2875
/ Sequence 2875, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 2875
/ LENGTH: 2814
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2875

Query Match      2.2%; Score 20; DB 4; Length 2814;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      308 CGCGCAAGCGCGCGCGCA 327
DB      1371 CGCGCAAGCGCGCGCGCA 1390

RESULT 5
US-09-949-016-21931/C
/ Sequence 21931, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ TYPE: DNA
/ ORGANISM: Human

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21931
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-21932/C
/ Sequence 21932, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21932
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-21933/C
/ Sequence 21933, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21933
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human

US-09-949-016-21934/C
/ Sequence 21934, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21934
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
```

US-09-949-016-21933

Query Match 2.1%; Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGCAGACA 380  
DB 93 GCTCTTCAAGAGCAGACA 75

RESULT 8

US-09-949-016-21934/C  
; Sequence 21934, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21934  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-21934

Query Match 2.1%; Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGCAGACA 380  
DB 77 GCTCTTCAAGAGCAGACA 59

RESULT 9

US-09-949-016-21935/C  
; Sequence 21935, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21935  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-21935

Query Match 2.1%; Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGCAGACA 380  
DB 30 GCTCTTCAAGAGCAGACA 12

RESULT 10

US-09-949-016-84252/C  
; Sequence 84252, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84252  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-84252

Query Match 2.1%; Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGCAGACA 380  
DB 584 GCTCTTCAAGAGCAGACA 566

RESULT 11

US-09-949-016-84253/C  
; Sequence 84253, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84253  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-84253

Query Match 2.1%; Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGCAGACA 380  
DB 233 GCTCTTCAAGAGCAGACA 215

```
RESULT 12
US-09-949-016-84254/C
; Sequence 84254, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84254
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84254
```

```
Query Match          2.1% Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      362 GCTCTTCAAGAGACAGA 380
DB      93 GCTCTTCAAGAGACAGA 75
```

```
RESULT 13
US-09-949-016-84255/C
; Sequence 84255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84255
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84255
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```
Query Match          2.1% Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      362 GCTCTTCAAGAGACAGA 380
DB      77 GCTCTTCAAGAGACAGA 59
```

```
RESULT 14
US-09-949-016-84256/C
; Sequence 84256, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84256
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84256
```

```
Query Match          2.1% Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      362 GCTCTTCAAGAGACAGA 380
DB      30 GCTCTTCAAGAGACAGA 12
```

```
RESULT 15
US-09-270-767-27566
; Sequence 27566, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27566
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-27566
```

```
Query Match          2.1% Score 19; DB 4; Length 878;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      123 GCTGAGCTCTGCGCTTT 141
DB      388 GCTGAGCTCTGCGCTTT 406
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Search completed: February 12, 2005, 15:26:52
Job time : 181 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 11:02:57 ; Search time 148 Seconds  
(without alignments)  
10049.835 Million cell updates/sec

Title: US-10-030-271-1  
Perfect score: 909  
Sequence: 1 atggcgcataccggatcgac.....tcagtgatgagcgcgcac 909

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, NA:  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCDS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	541	55.5	1067	4 US-09-620-312D-853	Sequence 853, App
2	193.8	21.3	1142	4 US-09-733-167A-2	Sequence 2, Appl
3	192.2	21.1	1045	3 US-08-859-167-3	Sequence 3, Appl
4	192.2	21.1	1045	3 US-09-109-273-3	Sequence 3, Appl
5	192.2	21.1	1045	3 US-09-276-993-3	Sequence 3, Appl
6	192.2	21.1	1045	4 US-09-723-450-3	Sequence 3, Appl
7	190.6	21.0	1142	4 US-09-733-167A-4	Sequence 4, Appl
8	190.6	21.0	1200	3 US-08-859-167-5	Sequence 5, Appl
9	190.6	21.0	1200	3 US-09-109-273-5	Sequence 5, Appl
10	190.6	21.0	1200	3 US-09-276-993-5	Sequence 5, Appl
11	190.6	21.0	1200	4 US-09-733-450-5	Sequence 5, Appl
12	146.2	16.1	630	4 US-09-733-167A-8	Sequence 8, Appl
13	88.4	9.7	342	4 US-09-733-167A-7	Sequence 7, Appl
14	50.8	5.6	1151	1 US-07-704-288C-2	Sequence 2, Appl
15	50.8	5.6	1151	1 US-08-093-372-1	Sequence 1, Appl
16	50.8	5.6	1151	1 US-08-379-259-2	Sequence 2, Appl
17	49.8	5.5	999	4 US-09-902-540-3684	Sequence 3684, Ap
18	49.8	5.5	16824	4 US-09-902-540-1178	Sequence 1178, Ap
19	49	5.4	929	4 US-09-902-540-3093	Sequence 3093, Ap
20	49	5.4	15789	4 US-09-902-540-1139	Sequence 1139, Ap
21	48.2	5.3	861	4 US-09-902-540-7313	Sequence 7313, Ap
22	48.2	5.3	5764	4 US-09-902-540-693	Sequence 693, App
23	47	5.2	603	4 US-09-902-540-9070	Sequence 9070, Ap
24	47	5.2	7719	4 US-09-902-540-969	Sequence 969, App
25	46.8	5.1	774	4 US-09-266-965-43	Sequence 43, Appl
26	46.8	5.1	1515	4 US-09-902-540-8120	Sequence 8120, Ap
27	46.8	5.1	7846	4 US-09-902-540-830	Sequence 830, App

C	28	46.8	5.1	53500	4 US-09-266-965-76	Sequence 76, Appl
	29	46.6	5.1	1509	4 US-09-724-797-89	Sequence 89, Appl
	30	46.4	5.1	9937	4 US-09-902-540-946	Sequence 946, Appl
	31	46.2	5.1	663	4 US-09-902-540-7269	Sequence 7269, Ap
C	32	46.2	5.1	4324	4 US-09-902-540-684	Sequence 684, App
	33	45.8	5.0	699	4 US-09-902-540-9109	Sequence 9109, App
C	34	45.8	5.0	831	4 US-09-252-991A-1479	Sequence 1479, Ap
	35	45.8	5.0	1962	4 US-09-252-991A-1693	Sequence 1693, Ap
C	36	45.8	5.0	11963	4 US-09-902-540-1072	Sequence 1072, Appl
	37	45.8	5.0	43280	2 US-08-804-227C-1	Sequence 1, Appl
C	38	45.6	5.0	601	4 US-09-949-016-19456	Sequence 19456, A
	39	45.6	5.0	601	4 US-09-949-016-19457	Sequence 19457, A
C	40	45.6	5.0	601	4 US-09-949-016-49701	Sequence 49701, A
C	41	45.6	5.0	601	4 US-09-949-016-49702	Sequence 49702, A
C	42	45.6	5.0	126200	4 US-09-949-016-11824	Sequence 11824, A
C	43	45.6	5.0	126200	4 US-09-949-016-13193	Sequence 13193, A
C	44	45.2	5.0	2635	3 US-09-126-280-3	Sequence 3, Appl
	45	45.2	5.0	2670	3 US-09-126-280-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-09-620-312D-853  
; Sequence 853, Application US/09620312D  
; Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Ruihong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yundong  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinphast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
FILE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pc FL\_genes Version 1.0  
SEQ ID NO 853  
LENGTH: 1067  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (151)..(984)  
US-09-620-312D-853

Query Match 59.5%; Score 541; DB 4; Length 1067;  
Best Local Similarity 95.8%; Pred. No. 8.7e-113;  
Matches 572; Conservative 0; Mismatches 10; Indels 15; Gaps 1;

QY 1 ATGGGCTATCCGGATCGACCCCGCGCTCGGAGAGATGCTGACATAC 60  
DB 151 ATGGGCTATCCGGATCGACCCCGCGCTCGGAGAGATGATGCTGACATAC 210

QY 61 TACGGAGTCTGTCCCTTCAACCGTATGTTTCAGAGTGTGGGCGGCACTGACCCAGTGC 120  
Db 211 TACGGAGTCTGTCCCTTCAACCGTATGTTTCAGAGTGTGGGCGGCACTGACCCAGTGC 270  
QY 121 GAGCTGAGACTCTGTGCTTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 180  
Db 271 GAGCTGAGACTCTGTGCTTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 330  
QY 181 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 240  
Db 331 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 390  
QY 241 AGCAACCTGTGGGCTGTGGGAGCACTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 300  
Db 391 AGCAACCTGTGGGCTGTGGGAGCACTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 450  
QY 301 CACCTGTGGGCGGAGCGGCTTGAAGCTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 360  
Db 451 CACCTGTGGGCGGAGCGGCTTGAAGCTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 510  
QY 361 AGCTTTCAAG 420  
Db 511 AGCTTTCAAG 570  
QY 421 AATTTTCAG 480  
Db 571 AATTTTCAG 615  
QY 481 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 540  
Db 616 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGAGGCTCCGTGGGCGGCGGAGGCTTATGC 675  
QY 541 CAGAGTCAAG 597  
Db 676 CAGAGTCAAG 732

## RESULT 2

US-09-733-167A-2

Sequence 2, Application US/09733167A  
Patent No. 6696547  
GENERAL INFORMATION:  
APPLICANT: Peter, Marcus  
APPLICANT: Kramer, Peter  
TITLE OF INVENTION: Protein for Regulation of Apoptosis  
FILE REFERENCE: 4121-120  
CURRENT FILING DATE: 2000-12-08  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: PCT/DE99/01712  
PRIOR FILING DATE: 1998-06-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent version 3.1  
SEQ ID NO 2  
LENGTH: 1142  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1043)..(1043)  
OTHER INFORMATION: n represents any one of a, c, t, and g.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1043)..(1043)  
OTHER INFORMATION: n represents any one of a, c, t, and g.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1114)..(1114)  
OTHER INFORMATION: n represents any one of a, c, t, and g.  
US-09-733-167A-2

Query Match 21.3%, Score 193.8; DB 4; Length 1142;

Best Local Similarity 52.9%; Pred. No. 1.7e-34;  
Matches 467; Conservative 0; Mismatches 407; Indels 9; Gaps 2;

QY 27 CCCGCTGAGGAG 86  
Db 54 CCGAGTGTGGCAG 113  
QY 87 GTTCAGAGTGTGGGCGGCGGAG 146  
Db 114 GTTCAGAGTGTGGGCGGAG 173  
QY 147 GAGTGTGGGCTCTGTGGGCGGAG 206  
Db 174 GTTCAGAGTGTGGGCGGAG 230  
QY 207 GCTGAGAGTGTGGGCGGCGGAG 266  
Db 231 ATTGGAGTGTGGGCGGAG 290  
QY 267 CTTGCGGCTGTGGGCGGCGGAG 326  
Db 291 GCTGCGGATATATCACTGGCAG 350  
QY 327 AGTGTCTCAG 386  
Db 351 TGTGTGCTGTGATCTTGTGAG 410  
QY 387 CTGCGGTGCGGCTGTGAG 446  
Db 411 CAGAGCTTCAAGTATCAAG 464  
QY 447 AGGCTTCCCGGAG 506  
Db 465 TCCCACTATCTGT 524  
QY 507 ACAGGCGGAG 566  
Db 525 AGCCGAG 584  
QY 567 CTTCAG 626  
Db 585 TCCCAAG 644  
QY 627 TGGGCGAGCTTGTGAG 686  
Db 645 TGAAGT 704  
QY 687 GAGAGT 746  
Db 705 TGAAGCTTGT 764  
QY 747 TGAAGT 806  
Db 765 TGAAGT 824  
QY 807 CGGCTGT 866  
Db 825 CTCTTATGT 884  
QY 867 CCGGAGAGCTGT 909  
Db 885 CCAAG 927

## RESULT 3

US-08-859-167-3

Sequence 3, Application US/08859167  
Patent No. 6037461  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emdad S.  
TITLE OF INVENTION: RADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

TITLE OF INVENTION: OF MAKING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461118  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,167  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1045 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..1044  
US-08-859-167-3

Query Match 21.1%; Score 192.2; DB 3; Length 1045;  
Best Local Similarity 52.8%; Pred No. 3.8e-34;  
Matches 466; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

QY 27 CCCGCTGCTGGAGAGAGTAGTGCCTTGACTACTAGCGGATGCTGCTTACCCGAT 86  
DB 114 CCAAGTGTGGCCAGAAAGCATGTAGAGAGAAACATGGGCTGTACAGCTGCACCGCAT 173  
QY 87 GTTGAGGTGTGGGGGGGCACTGACCGAGTCCAGCTGAGCTCTTCTGCT 146  
DB 174 GTTGTACATCGGGGCACTCATCTGACACACAGAGATGTGCGCGTCTTTCTTCTCT 233  
QY 147 GGATAGGCTCCTGGGCGCGCGGAGGCTTACCGGGCGCGCAGGGGCTAGAGCTCCT 206  
DB 234 TGTGTATGTCAATTATGACACGAGCTGTGAGCTC---ATCCGAATGACGTACTTCTT 290  
QY 207 GCTGAGCTGAGCGCCGCGGGCAGTGTGCGCGAGAGCAACTCTGCGGCTGTGGGCACT 266  
DB 291 ATTGCACTGTAGGCGCCAGGGCGCTGTGATGAAGTAATTTCGCGAGGTCTCTAGCT 350  
QY 267 CCTGGCGTGTGGCGCGGCAAGACTGTGCTGCGCACTGTGGGCGGAGCGCGCGCGC 326  
DB 351 GCTGGGCACTCATCATCTGCGCAGAGCTGTGCTTACGTCACCTTCAAGAGAGACGGGC 410  
QY 327 AGTGTCTCAGAAAGCTATAGCTATGAGCACTCCAGCTTCAAGAGAGAGAGAGGTAG 386  
DB 411 TGTGTGCTGTATCTTTGTAGACAGATATGTGAGAGACATCAATTCGCTATGTACCCC 470  
QY 387 CTGCGGTGCGCGCTGTGGCACTCAAGCAATTCTTCAAGAGAGGTCACTGTGAGAGAC 446  
DB 471 CAGAGCCCTCACTGATTCAGAACCAAGGCC-----TCCCAAGCCCTTAATAAACAGTGC 524  
QY 447 AGGCTTCCCCCAACCAAGCGGAGGCGGAGTGTGGGCGCGCCCAAGTGTGTGTCCAG 506  
DB 525 TCCCACTATCTGTGTGTGTGTGTGCCCCCACTTGGGCTCTCTGAGATGTGTAGCAAGCGGC 584

QY 507 ACGCGCGGAGAGAGGCGCCCGACCGGACCCAGACAGAGTCAAGCCCGCAGACTTC 566  
DB 585 AGCCGAGAGAGAGGCACTTGGAGGCAAGGAAAGCGCGGAAAGTCACTGACACAGCA 644  
QY 567 CTGTGAGGCAAGTGAAGCTGTGACATCCGGCTCGGGTTTGAAGAGTACTGTGAGACA 626  
DB 645 TCCCAAGGAGAGAGAGATGTGACATCAAGCTGGGGGTGGGCTGTGATCTGCAAGCA 704  
QY 627 TGGGCGAGCTTGGAGAGAGGCGTGGCATCCCGGCGGCCAGAGGCGTGGCGGCGACT 686  
DB 705 TGAAGCTCTCTGAGGGGCAATGTCTTTCTTAACAGAGAGAGCCACTTGAAGCGCAATT 764  
QY 687 GAGCTGTGTTGGGCGGACCGGACAGTGTGCTGCTCAAGGAGACTGTGGCTGTGTGG 746  
DB 765 TGAAGGCTTTAAGGAGGCAACACATCTCAAGTCCGGGAGCTGGGCTCATCATCTG 824  
QY 747 TGACATCAAGTTCTCAGAGCTCTCTATGTGAGAGCTTCTGGGGGCACTACTGATGTG 806  
DB 825 TGACATCAAGTTCTCTGAGCTCACTACCTGATGATCTGTGGCGTGACTACATCAATG 884  
QY 807 CGGCGTGTGAGAGGCGCGGGGCGTTCCTGCTGCTGAGAGGCGCTGAGAGAGGCTGTGG 866  
DB 885 CTCTTATTAGAGGCACTTAAGTGTCTTCAATCAAGACTTCTTCAAGCAAGCTGTGG 944  
QY 867 CCGGAGGCTGTTCGCTGTGTGCTCAGTGTGATGAGGCTGAC 909  
DB 945 CCATGAGCCATCAAGCTGTGTGTAAGTGAAGAGAGAGAC 987

RESULT 4  
US-09-109-273-3  
Sequence 3, Application US/09109273  
Patent No. 6063760  
GENERAL INFORMATION:  
APPLICANT: Alnemti, Emad S.  
APPLICANT: Fernandez-Alnemti, Teresa  
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 606376018  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,273  
FILING DATE:  
CLASSIFICATION:  
APPLICATION NUMBER: 08/859,167  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1045 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA

FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..1044  
US-09-109-273-3

Query Match 21.1%; Score 192.2; DB 3; Length 1045;  
Best Local Similarity 52.8%; Pred. No. 3.8e-34;  
Matches 466; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

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27 CCCGCTGCTGGAGAGAGATGAGTGCCTGAGCTACTACGAGATGCTGCTTCAACCGTAT 86
114 CCAAGTGTGGCCAGAAAGACATGTGAGAGAGACATGGGCTGTACAGCTGTGACCGCAT 173
87 GTTCAAGTGTGGGCGGCGCACTGACCGAGTGCAGCTGAGCTTCTGCT 146
174 GTTTACATCGTGGGCACTCATCTGACACACAGAGATGTGGCGCTTTCTTCTCTT 233
147 GGATGAGGCTCCTGGCGCGCGGAGGCTTACCGCGGCGCGACGCGCTAGACTCT 206
234 TGTGTATGTCAATTGATGACACAGAGCGTGTGACTC--ATCCGAAATGACGTGACTTCT 290
207 GCTGAGCTGAGAGCGCGCGGCGAGTGTGCGGCGAGACAACTGCGGCTGTGGGCAACT 266
291 ATTGCACTGAGAGCGCGCGGCGGCTGTGTGATGAAAGTAACTTTCCGCAAGTGTGAGCT 350
267 CTTGCGCTGTGGCGCGCGCACGACTGTGCTGCGCACTGTGCGCGCAAGCGCGCGCC 326
351 GCTGGCATCATCACTGCGCACGACCTGCTGCTTACGTCACCTCAAGAGAGACGCGGC 410
327 AGTGTCTCCAGAAAGCTATAGCTATAGGACCTCCAGCTCTTCAAGAGAGACAGAGGTAG 386
411 TGTGTGCTGTATCTTTGATGACAAATATCTGAGAGAGACATTAATTCGTATGTACCCC 470
387 CTGCGGTGCGCGTCCGAGTCAAGCAATTTCTGCAAGGCTCACTGGAGAC 446
471 CAGAGCCTCTCAGTATCCAGAACAAAGGC-----TCCGAGCGCTTAAACAGTGC 524
447 AGGCTCCCCCAACCAAGCGGCGAGGCGGAGTGTGGGCGCGGCAAGTGTGTGCGCAG 506
525 TCCCACTATCTCTGTGTGTGTGTGCCCCCACTTCGAGTCTCAGATGTATGACAGCGCC 584
507 ACGGCGGAGAGAGAGGCGCGCACGCCAGAGAGAGTCAAGAGCGCGCAGACTTC 566
585 AGCCGAGGAGAGAGACCACTTTGGAGAGCGCAAAACCGCGAAGTATGTACACCGA 644
567 CTCTGAAGCAAAAGTATGATCTGTATCCGCTCGGCTTCAAGAGATCTGCGACA 626
645 TCCCAAGAGAGAGACGATGTATGATCATGAGCTGGGCTTGGAGTGAATCTGCGACA 704
627 TGGGCGAGCTTGGAGAGAGGCGGTGGCATCCGCGCGCGCCAGGCGCTGTGGCGGAGCT 686
705 TGAAGCTGTCTGTGAGGCGCAATGTCTTCTTAAACAGAGAGACCACTTGAAGCGCACTT 764
687 GAGAGTGTGGGCGGCGCACCGGAGTGTGCGCTCAAGGAGCGTGGGCTGTGGTTG 746
765 TGAAGGCTTTAAACAGGCGCAACCATCTCAAGTCCGCGAAGCTGGGCTCATATCTG 824
747 TGAATCAAGTGTCTGAGAGCTCTCTATCTGAGCGCTTCTGGGCGGACTACTGAGTGG 806
825 TGAATCAAGTGTCTGAGCTCACTCACTCATCTGAGTCACTTGTGGGCTGATCATATG 884
807 CGCCCTGTGAGAGCGCTGGCGGCGGTCTTCTGACTGAGGCGCTGTGCGAGAGGCTGTGG 866
885 CTCTTATTTAAGGAGACTTAAAGGTCTTCTATCAACACTCCCTCAAGAGAGCTGTGGG 944
867 CCGGAGAGGCTGTGGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 909
945 CCAAGAGAGCAATCAAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 987
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RESULT 5  
US-09-276-993-3  
Sequence 3, Application US/09276993

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Patent No. 6207801
GENERAL INFORMATION:
APPLICANT: Alnemuri, Emad S.
APPLICANT: Fernandez-Alnemuri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801x18
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,993
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TCU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1044
US-09-276-993-3
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Query Match 21.1%; Score 192.2; DB 3; Length 1045;  
Best Local Similarity 52.8%; Pred. No. 3.8e-34;  
Matches 466; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

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27 CCCGCTGCTGGAGAGAGATGAGTGCCTGAGCTACTACGAGATGCTGCTTCAACCGTAT 86
114 CCAAGTGTGGCCAGAAAGACATGTGAGAGAGACATGGGCTGTACAGCTGTGACCGCAT 173
87 GTTCAAGTGTGGGCGGCGCACTGACCGAGTGCAGCTGAGCTTCTGCT 146
174 GTTTACATCGTGGGCACTCATCTGACACACAGAGATGTGGCGCTTTCTTCTCTT 233
147 GGATGAGGCTCCTGGCGCGCGGAGGCTTACCGCGGCGCGACGCGCTAGACTCT 206
234 TGTGTATGTCAATTGATGACACAGAGCGTGTGACTC--ATCCGAAATGACGTGACTTCT 290
207 GCTGAGCTGAGAGCGCGCGGCGAGTGTGCGGCGAGACAACTGCGGCTGTGGGCAACT 266
291 ATTGCACTGAGAGCGCGCGGCGGCTGTGTGATGAAAGTAACTTTCCGCAAGTGTGAGCT 350
267 CTTGCGCTGTGGCGCGCGCACGACTGTGCTGCGCACTGTGCGCGCAAGCGCGCGCC 326
351 GCTGCGATCATCACTGCGCACGACCTGCTGCTTACGTCACCTCAAGAGAGACGCGGC 410
327 AGTGTCTCCAGAAAGCTATAGCTATGAGACCTCCAGCTCTTCAAGAGAGACAGAGGTAG 386
411 TGTGTGCTGTATCTTTGATGACAAATATCTGAGAGAGACATTAATTCGTATGTACCCC 470
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NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 1142  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; US-09-733-167A-4

Query Match 21.0%; Score 190.6; DB 4; Length 1142;  
 Best Local Similarity 52.7%; Pred. No. 8.9e-34;  
 Matches 465; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

27 CCCGCTGCGAGAGAGATGAGTGCCTGAGTACTACAGGATGCTGTGCTTACCGTAT 86  
 Db 54 CCAAGTGTGGCCCGAAGAGCCGTGGAGACCAAGATGAGGCTCTACAGCTTCCACCGAT 113  
 Qy 87 GTTCGAGGTGTGGGCGGCAACTGACCGAGTGGAGGCTCTGGGCTTCTCTCT 146  
 Db 114 GTTCGACATCTGTGGGACCACTTAACACAGAGATGTCGAGTCTTCTTCTTCTT 173  
 Qy 147 GATGAGGCTCTGTGGCGCGCGAGGCTTACCCGCGCCGACGCGCTTACAGCTCT 206  
 Db 174 TGTGATGTATTATGACCAATGAACG--TGACTCATCCGAATGACCGTACTTCT 230  
 Qy 207 GCTGAGCTGAGAGCCCGCGGCACTGGCGGAGAGCACTGCGGCTGTGGGCAACT 266  
 Db 231 ATTGCACTGAGAGCCCGAGGCGCGCTGTGAGAGTAACTTCCCGAGTGTGCACT 290  
 Qy 267 CCTGCGCGTGTGGGCGGCAAGACTGTGCGGCACTGGGCGGCAAGCGCGCGCC 326  
 Db 291 GCTGCGCATCATCATCTGCGGCACTTCTGCTTCTTCTTCTTCTTCTTCTTCTT 350  
 Qy 327 AGTGTCTCAGAACGCTATGACTATGAGCACTTCAAGTCTTCAAGAGAGAGAGGTAG 386  
 Db 351 TGTGTCCCTGATCTTGTAGCAAGTATCTGAGAGAAATCAATTCCTATGTGACCC 410  
 Qy 387 CTGCGCTGCGGCTGGGCACTGAGCACTTGTCAAAATCTCAAGAGGCTGAGGAGAC 446  
 Db 411 CAGAGCCCTCAAGTACCAAGAGCCGAGGCG-----TCCCAAGCCCTTAAAGCAGTGCC 464  
 Qy 447 AGGCTCCCCCAACCAAGCGGAGCGGAGTGGGCGGCGGCGGCGGCGGCGGCGG 506  
 Db 465 TCCCACTATCTGT 524  
 Qy 507 AGCGCGGCGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 566  
 Db 525 AGCCGAGGAGAGAACCAACTTGGAGGCGGAGAAAGCGGGAAGTGGTGAACCGA 584  
 Qy 567 CTCTGAGAGCAAGTGAAGTGTGACATCCGCTCCGGGTTGAGAGAGATCTGCGAGCA 626  
 Db 585 CCCGAAGGAAAGACAGATGTGATTCAGGCTCCGAGTTGCGGCGGAAATCTGCCAGCA 644  
 Qy 627 TGGGCGAGCTTGGAGAGCGGCTGGGCACTCCGCGGCGGCGGCGGCGGCGGCGG 686  
 Db 645 TGAACGGCTTGAAGAGCAATGTCTTCTCAATTAAGAGAGCCACTTGTGAGCGCAG 704  
 Qy 687 GGAAGTGTGGGAGGCGGAGAGTGTGCTGCAAGGAGCTGGGCTGTGTGTGTGT 746  
 Db 705 TGAACGCTTAAACAGGCGCAACATCTCAAGTCCCGGAGCGTGGGCTCATCATCTG 764  
 Qy 747 TGAATCAAGTTCACAGCTCTCTATCTGAGAGGCTTCTGGGCGGCACTCAAGTGTG 806  
 Db 765 TGAATCAAGTTCCTGAGCTCACTTACCTGAGGCACTTCTGGGAGAGCTACATTAATG 824  
 Qy 807 CGGCTCTGAGAGCGGCGGCGGAGTGTCTTCTGAGAGGCGGCGGAGAGAGTGTGG 866  
 Db 825 CTGATTAATTAAGAGCACTGAAGGTGTCTTATACAGACTCTTCAAGCAAGCTGTGG 884  
 Qy 867 CGGAGAGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 909  
 Db 885 CCAATGAAGCATCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 927

## RESULT 8

US-08-859-167-5

Sequence 5, Application US/08859167

Patent No. 6037461

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF

TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

TITLE OF INVENTION: OF MAKING THE SAME

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461tris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: WINDOWS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/859,167

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: cdna

FEATURE:

NAME/KEY: CDS

LOCATION: 32..988

US-08-859-167-5

Query Match 21.0%; Score 190.6; DB 3; Length 1200;  
 Best Local Similarity 52.7%; Pred. No. 9e-34;  
 Matches 465; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

27 CCCGCTGCGAGAGAGATGAGTGCCTGAGTACTACAGGATGCTGTGCTTACCGTAT 86  
 Db 58 CCAAGTGTGGCCCGAAGAGCCGTGGAGACCAAGATGAGGCTCTACAGCTTCCACCGAT 117  
 Qy 87 GTTCGAGGTGTGGGCGGCAACTGACCGAGTGGAGGCTCTGGGCTTCTCTCTCT 146  
 Db 118 GTTCGACATCTGTGGGACCACTTAACACAGAGATGTCGAGTCTTCTTCTTCTT 177  
 Qy 147 GATGAGGCTCTGTGGCGCGCGAGGCTTACCCGCGCCGACGCGGCTTACAGCTCT 206  
 Db 178 TGTGATGTATTATGATATACATGAACG--TGACTCATCCGAATGAGAGCTGTGCT 234  
 Qy 207 GCTGAGCTGAGAGCGGCGGCGGAGTGTGCGGCGAGAGCACTTGGGCTGTGGGCACT 266  
 Db 235 ATTGCACTGAGAGGCGGAGGCGGCGGCTGTGAGAGAGTAACTTTCGAGGCTGTGAG 294  
 Qy 267 CTGCGGCTGTGGCGCGGCAAGACTGTGCGGCACTTGGGCGGCAAGCGGCGGCGG 326  
 Db 295 GCTGCGCATCATCATCTGCGGCAATGCTGTGCGGCTTACCTTCAAGAAAGAGAGC 354  
 Qy 327 AGTGTCTCAGAAAGCTATGACTATGAGCACTTCAAGTCTTCAAGAGAGAGGAGTAG 386  
 Db 355 TGTGTCCCTGATCTTGTAGCAAGTATCTGAGAGAAATCAATTCCTATGTGACCC 414



Oy	387	CTGCCGTGGCGGTGGGAGTCAGCAAGTTCGTGAATTCCTGACGACAGGTCAGTGGAGAC	446
Db	415	CAGAGCCCTCAGTAGACCCAGAACCGAGGCC-----TCCCGAGCCCTCTAAAACAGTGCC	468
Oy	447	AGGCTCCCCCCCACCAAGACGGGACGGGCGGAGTCGGGGCCGGCCCAAGTGATGTGCCAG	506
Db	469	TCCCACTATCTCTGTGTGTGTGCTGCCCCACCTTCGGGTTTCTCAATGTGTAGTAAGGGCC	528
Oy	507	ACGGCGGCGGAGAGGGGGCCCCAGCCGACCCCAAGCAGTCAGTCAGACCCCGCCAGACTTTC	566
Db	529	AGCCGAGGAGAACACACTTGGGAGCGACGAAACCGCCGGAAGTCGGTGAACAACGA	588
Oy	567	CTCTGAAGCAAAATGACCTGTGTACATCCGGCTCTCGGGTTTCAGACAGATGACTGCGAGCA	626
Db	589	CCCGAAGGAAAGCAGACATGTGATTCAGGGCTCCAGTTCGGGCGGAATATCTCGACGA	648
Oy	627	TGGGCGAGCCTTGGAGCAGGGCGGTGCATTCGCGGCGGGCCCCAGGCGCTGGCGGGGAGCT	686
Db	649	TGAGACGGCTCTGCAAGGCAATGTCTTCTTCATTAAGCAAGAACCCACTTGAGGGCCAGTT	708
Oy	687	GGACGCTGTTTTGGGACAGGCCACCGCAGTGTGCTCGCTCAAGGACCTTGGGCTCTGTGTTTTG	746
Db	709	TGAGGGCTTTAAACAGGCCAACACTATCTCTCAAGTCCCGGAGACTGGGCTCCATCACTCG	768
Oy	747	TGACATCAAGTTCCTAGAGCTCTCTATCTGACGGCTTCTGCGGCGACTACTCTGAAGTGG	806
Db	769	TGACATCAAGTTCCTGAGCTCACTACCTCGAGCATTTCTGGCGAGACTACATTAATGG	828
Oy	807	CGCCCTGCTGCAGGCCCTTGCGGGGCGTGTCTTGACTGAAGGCCCTTCGGAAGGCTGTGGG	866
Db	829	CTCATATTATTAAGAGGCACTCAAAAGTGTCTTTCATCAACAGACTCTCTCAAGCAAGACTGTGG	888
Oy	867	CGGGAGCGCTTTCGCTGCTGGTCAGTGTGATGAGGCTGAC	909
Db	889	CCATGAGCATTCAGCTGCTGTGTGAACGTGAGTAGAGAGAC	931

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1  RESULT 9
2  US-09-109-273-5
3  : Sequence 5, Application US/09109273
4  : Patent No. 6063760
5  : GENERAL INFORMATION:
6  : APPLICANT: Alnemrl, Enad S.
7  : APPLICANT: Fernandez-Alnemrl, Teresa
8  : TITLE OF INVENTION: PADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
9  : TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
10 : TITLE OF INVENTION: OF MAKING THE SAME
11 : NUMBER OF SEQUENCES: 17
12 : CORRESPONDENCE ADDRESS:
13 : ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760r1s
14 : STREET: One Liberty Place, 46th floor
15 : CITY: Philadelphia
16 : STATE: PA
17 : COUNTRY: USA
18 : ZIP: 19103
19 :
20 : COMPUTER READABLE FORM:
21 : MEDIUM TYPE: floppy disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: WINDOWS
24 : SOFTWARE: WordPerfect
25 : CURRENT APPLICATION DATA:
26 : APPLICATION NUMBER: US/09/109,273
27 : FILING DATE:
28 : CLASSIFICATION:
29 : PRIOR APPLICATION DATA:
30 : APPLICATION NUMBER: 08/859,167
31 : FILING DATE:
32 : ATTORNEY/AGENT INFORMATION:
33 : NAME: Deluca, Mark
34 : REGISTRATION NUMBER: 33,229
35 : REFERENCE/DOCKET NUMBER: TUI-
36 : TELECOMMUNICATION INFORMATION:
37 :

```

	TELEPHONE: (215) 568-3100	
	TELEFAX: (215) 568-3439	
	INFORMATION FOR SEQ ID NO: 5:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 1200 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: double	
	TOPOLOGY: both	
	MOLECULE TYPE: cDNA	
	FEATURE:	
	NAME/KEY: CDS	
	LOCATION: 32..988	
	US-09-109-273-5	
Query Match	21.0%; Score 190.6; DB 3; Length 1200;	
Best Local Similarity	52.7%; Pred. No. 9e-34;	
Matches 465; Conservative	0; Mismatches 409; Indels 9; Gaps 2;	
Qy	27	CCCGTGCCTGGAGAGAGATGATGCTCGAATCTATACGGAGATGCTGTCCTTCAACCGAT 86
Db	58	CCAGGTGTGGCCCAAGAGCCTGGGGAGCAAGAACATGAGCTTACACGCTTCCACCGAT 117
Qy	87	GTTGAGGCTGTGGGCGGGCAACTGACCGAGTGCAGCTGGAGCTCTGAGCTTTCGCT 146
Db	118	GTTGACATCTGGGGACACCCACTACACACAGAGATGTCCGAGTGCCTTCTCTTT 177
Qy	147	GGATGAGCTCTGAGCCCGCCGAGAGCTTACCCCGGGCCCGACAGCGGCTTAGACTCT 206
Db	178	TGTTGATGTATTGATGACCATGAACG--TGACCTCATCCGAATGAGCCTGACTTCT 234
Qy	207	GCTGAGCTGGAGAGGCGCGGGCAGTGGGGAGAGCAACCTGGGGCTGCTGGGGCACT 266
Db	235	ATTGACATGGAGGCGCACGGCCGCTGTGAGAGAGTAACTTTGGCCAGGTGCTGACT 294
Qy	267	CCTGGCGCTGTGGCCCGCCGACGACTGCTGCCGACCTGGCGGCAAGCGCGCGGCC 326
Db	295	GCTGGCATCATCACTGCGCACTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 354
Qy	327	AGTGTCTTCAGAAAGCTATAGCTATGAGCACTCCAGCTTTCAAGAGGAGCAGAGGTTA 386
Db	355	TGTGTGCTGATCTTGTGAGCAAGTATCTGAGAGAAATCAATTCGCTATGTGACCCC 414
Qy	387	CTGCCGTGCGGTGCGGACGTAAAGCAGTTTTCGCAATTCTACAGAGGTCAGTGGAGAC 446
Db	415	CAGAGCCCTTCAGTGCACCAAGAACGAGGCC-----TCCCAAGCCCTTAAACAGTCC 468
Qy	447	AGGCTCCCCCCCAACCAAGCGGCAAGCGGAGTGGGGCGGCGCCAGTGGTGGCCAG 506
Db	469	TCCCACTATCTGT 528
Qy	507	ACGGCGGCGAGAGAGGGGCCCAAGCGGCAACCCAGCAGCAGTCAAGACC CGCAGACTTC 566
Db	529	AGCCGAGAGGAGAACCAACACTTTGGGAGCGAGGAGAAACCGCGGAAAGTGGTGAACAC 588
Qy	567	CTCTGAAGGCAAGTGAACCTTGACATCCGGCTCCGGGTTTGAAGAGTACTGGGACCA 626
Db	589	CCCGAAGAAAGAGCAGATGTGATCAAGGCTCCGAAATTTGGGGGGAATCTGACACA 648
Qy	627	TGGGCGACGCTTGGAGCAAGGGGCTGGGACATCCCGGCGGCGCCAGCGGCTGGCGGCACT 686
Db	649	TGAGAGCGGCTCTGCAAGCAATGTCTTCTCAATAGCAGAGACCACTTGAAGCGCAGTT 708
Qy	747	TGACATCAAGTTCTCAGAGCTCTCTTATCTGAAGGCTTTCTGGGGCAGCTTACTGAAGTG 806
Db	769	TGACATCAAGTTCTCTGAGCTTCACTTACCTGACGCACTTGGCGGAGACTCATATTAAGG 828
Qy	807	CGCCCTGCGCAGGCGCTGGGGGGGCTGTTCTGTAAGGCGCTTGGAGAGGCTGTGGG 866
Db	829	CTCATATTAGAGGACTGAAGAGGTGTCTTATACAGACTCTCTCAAGCAGACTGTGGG 888

QY 867 CCGGAGGCTGTTCCCTGCTGTCAGTGTGATGAGGCTGAC 909  
DB 889 CCATGAAGCATCAAGCTGCTGTGTAACGTGATGAGGAGAC 931

## RESULT 10

US-09-276-993-5  
Sequence 5, Application US/09216993  
Patent No. 6207801

## GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF

TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801r1s

STREET: One Liberty Place, 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: WINDOWS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/276,993

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/859,167

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 32..988

US-09-276-993-5

Query Match 21.0%; Score 190.6; DB 3; Length 1200;

Best Local Similarity 52.7%; Pred. No. 9e-34;

Matches 465; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

QY 27 CCCGCTGGGAGAGATGAGTGCCTGACTACTAAGGATGCTGTGCTTCAACCGAT 86  
DB 58 CCAAGTGTGGCCCGAAGAGCTGGGAGCAAGACATGGCTCTTACAGCTCCACCGAT 117  
QY 87 GTTGGAGTGTGGCCGGGCAACTGACCGAGTGCAGTGCAGTGCCTGTGCTTTTGTCT 146  
DB 118 GTTGCACATCTGTGGCAACCACTTACACACAGAGATGCTCCGAGTCTTTCTTCTTTT 177  
QY 147 GGATGAGGCTCTTGGCCGCGGAGGCTTACCCCGGCGCGCAGCGGCTTACAGCTCTT 206  
DB 178 TGTGATGTATTATGATGACATGAACG---TGAATCAATCCGAATGAGACGTGACTTCTT 234  
QY 207 GCTGAGCTGAGAGGCGCGGCGGAGTGGCGGAGAGCAACTCTGGGCTGTGGGCAACT 266

DB 235 ATTGCACTGAGACGCCAGGCGCGCTGTGACGAGATTACTTTGCCAGTGTCTGACCT 294  
QY 267 CTTGCGGCTGTGGCCCGCCAGACCTGCTGCGCCACCTGGCGGCAAGCGCGCGCC 326  
DB 295 GCTGGCATCATCACTGCGCCATGACTTCTGCTCCCTACCTTACTCTCAAGAAAGACGAGC 354  
QY 327 AGTGTCTCAGAACGCTTATGACTATGGCACTTCCAGCTCTTCAAGAGAGACAGAGGTAG 386  
DB 355 TGTGTGCCCTGATCTTTGAGCAAGTATCTGGAGGAACATCAATTCCTATGTGACCCC 414  
QY 387 CTGCGCTGCGCGTGGGAGTCAAGACATTTCTGCAATTTCTCAAGAGGCTGATGGGAAAC 446  
DB 415 CAGAGCCCTTCAAGTACCAAGAACCGAGGCG-----TCCCAAGCCCTTCAAAACAGTGC 468  
QY 447 AGGCTCCCCCAACCAAGCGGAGCGGAGTGGGCGGCGCCAGTGTGTGGCCAG 506  
DB 469 TCCCACTATCTGTGTGTGTCTGCCCACTTGGGTTCTCAATGTGTATTAAGCGGCC 528  
QY 507 ACGGCGGCGAGAGGCGGCCCGAGCCGCAAGCCAGACGATCAAGAGCCGCGACCTTC 566  
DB 529 AGCCGAGGAGAAACCACTTGGGAGCCAGGAAAGCGCGAAGTGTGACACAGA 588  
QY 567 CTCTGAAGCAAAATGACCTGTGACATCCGCTCGGGTTGAGACAGATGATCTGGAGCA 626  
DB 589 CCCAAGGAAAGACAGACATGTATCAAGGCTCCGATTTGGGCGGAATCTGCGACGA 648  
QY 627 TGGGCGAGCTTGGAGCAGGCGGTGGCATCCGCGCGGCCAGCGCTGCGCGAGACT 686  
DB 649 TGAAGCGCTGTGCAAGCAATGCTTCTCCAATTAAGAGAACCACTTGAAGCGCGACT 708  
QY 687 GAGCGTGTGGGAGGCGCACCGAGTGTGCGCTCAAGGAGCCTGGGCTGTGTGTTG 746  
DB 709 TGAAGCGCTTAAACAGGCGCAACTATCTCAAGTCCCGGAGCTGCGGCTCATATCTG 768  
QY 747 TGACATCAAGTTCTCAAGGCTCTCTTAATGAGAGCCTTGGGCGCACTTCAAGTGTG 806  
DB 769 TGACATCAAGTTCTCAAGGCTCTCTTAATGAGAGCCTTGGGCGCACTTCAATTAATG 828  
QY 807 CGCCCTGTGAGGCGCTGCGGCGGCTGTGCTGATGATGATGAGGCTGAC 909  
DB 829 CTCAATTATTAAGGACCTGAAGAGTGTCTTATCAAGACTCTTCAAGCAAGCTGTGG 888  
QY 867 CCGGAGGCTGTTGCTGCTGCTGTGATGATGATGAGGCTGAC 909  
DB 889 CCATGAAGCATCAAGCTGTGTGAAGTGAAGAGAGGAC 931

## RESULT 11

US-09-723-450-5

Sequence 5, Application US/09723450

Patent No. 6576751

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An

FILE REFERENCE: T02445

CURRENT APPLICATION NUMBER: US/09/723,450

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/276,993

PRIOR FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: 08/859,167

PRIOR FILING DATE: 1997-05-20

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 1200

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURES:

NAME/KEY: misc feature

OTHER INFORMATION: No. 6576751el Sequence

NAME/KEY: CDS

LOCATION: (32)..(988)

US-09-723-450-5

Query Match 21.0%; Score 190.6; DB 4; Length 1200;  
Best Local Similarity 52.7%; Pred. No. 98-34; Indels 9; Gaps 2;  
Matches 465; Conservative 0; Mismatches 409;

```
27 CCGCTGCTGGAGAGAGATGAGTGCCTGACTACTACGAGATGCTGTGCTTACCGTAT 86
28 CCAAGTGTGGCCGGAAGAGCGTGGAGGACAGAAACATGGGCTCTACAGCTTCAACGCT 117
87 GTTCGAGGTGTGGCGGCGCACTGACCGAGTGCAGCTGAGCTCTGCGCTTCTGCT 146
118 GTTCGACATCTGGCGCACCCACTTAACACAGAGATGCTCCAGTCTTCTTCTTCTT 177
147 GGATGAGCTCTGCTGGCGCGCGGAGGCTTGGCGGCGCGGCGGCGGCTGAGACTCT 206
178 TGTGTATTTATTGATGACATGAAAG--TGTACTATTCGAAATGAGCGTGACTTCTT 234
207 GCTGAGCTGGAGCGCGCGGCGGAGTGGCGGAGAGACAACTGCGGCTGTGGGCAACT 266
225 ATTTGACATGGAGCGCGCGGCGGCTGTGAGAGAGTAACTTCCGCGAGTGTGCAAGT 294
267 CCTGCGCTGTGCGCGCGGCGGAGCTGTGCGCACTGCGCGGCGGAGCGCGGCGG 326
295 GCTGCGCATCATCACTGCGCATGACTGTGCTGCTTACGTTACTCTCAAGAAAGACGAGC 354
327 AGTGTCTCAGAAAGCTATAGCTATGAGCACTCCAGCTCTTCAAGAGAGACAGAGGTAG 386
355 TGTGTGCTCTGATCTTTGATGACAGATATCTGAGAGAAACATATTCGTTATGTACCCC 414
387 CTGCGCTGCGCGCTCGGCGAGTCAAGCAATCTGCAATTTCTCAGCAGAGCTCACTGGAGAC 446
415 CAGAGCCTCACTGAGCCGAGAACGAGAGC-----TCCGAGCCTCTTAAAGAGTGC 468
447 AGGCTCCCCCAACCAAGCGGAGCGGCGGAGTGGGCGGCGGCGGCGGCGGCGGCGG 506
469 TCCCACTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 528
507 ACGGCGGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 566
529 AGCGGAGGAGAACCAACCTTGGAGCGGAGGAAACCGCGGAGTGGTGAACACGAGA 588
567 CTCTGAGGCAAGTGTGAGTGTGAGATCGGCTCGGCGGTTGAGAGAGATACCTGAGAGA 626
589 CCGGAGAGAGAAAGCAGACATGTGATATCAGGCTCCGAGTTCCGCGGAGATATCTGCAAGA 648
627 TGGGCAAGCTTGGAGCAGGCGGCGGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGG 686
649 TGAGACGCGCTGTGCAAGGCAATGTCTTCTCAATAAGCAGAGCCCACTTGAAGCGCAGTT 708
687 GGAAGCTGTTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 746
709 TGAGCGCTTTAAACAGGCGGCAACATATCTCAAGTCCGCGGCGGCGGCGGCGGCGG 768
747 TGACATCAAGTGTGAGAGCTCTCTATCTGAGAGCGCTTCTGCGGCGGCACTACCTGAGTGG 806
769 TGACATCAAGTGTCTGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 828
807 CGCCCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 866
829 CTCAATTATTAGAGGCACTGAAAGGTGTCTTATCAACAGACTCTTCAACAGACTGTGG 888
867 CCGGAGAGCTGTTCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 909
889 CCATGAAGCATCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 931
```

RESULT 12  
US-09-733-167A-8  
; Sequence 8, Application US/09733167A  
; Patent No. 6696547  
; GENERAL INFORMATION:  
; APPLICANT: Peter, Marcus

APPLICANT: Krammer, Peter  
; TITLE OF INVENTION: Protein for Regulation of Apoptosis  
; FILE REFERENCE: 4121-120  
; CURRENT APPLICATION NUMBER: US/09/733,167A  
; CURRENT FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: PCT/DE99/01712  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3  
; PRIOR FILING DATE: 1998-06-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Truncated segment of the DNA sequence encoding human DEBD, compri  
US-09-733-167A-8

Query Match 16.1%; Score 146.2; DB 4; Length 630;  
Best Local Similarity 60.4%; Pred. No. 88-24; Indels 0; Gaps 0;  
Matches 241; Conservative 0; Mismatches 158;

```
511 CGGCGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 570
178 CGAGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 630
571 GAGGCGAAGTGTGAGCTGTGAGATCTGCGGCTCGGCGGTTGAGAGAGTACTGCGAGATGG 630
238 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
631 CGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
298 ACTGCTCTGAGGCGGAGATGTCTTCTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAG 750
691 GTGTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
358 CGCTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
751 ATCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 810
418 ATCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
811 CTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
478 TTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 937
871 GAGGCTGTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 909
538 GAGGCTATCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 976
```

RESULT 13  
US-09-733-167A-7  
; Sequence 7, Application US/09733167A  
; Patent No. 6696547  
; GENERAL INFORMATION:  
; APPLICANT: Peter, Marcus  
; APPLICANT: Krammer, Peter  
; TITLE OF INVENTION: Protein for Regulation of Apoptosis  
; FILE REFERENCE: 4121-120  
; CURRENT APPLICATION NUMBER: US/09/733,167A  
; CURRENT FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: PCT/DE99/01712  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Truncated segment of the DNA sequence encoding human DEBD, compr  
US-09-733-167A-7

Query Match 9.7%; Score 88.4; DB 4; Length 342;  
Best Local Similarity 57.3%; Pred. No. 7.5e-11;  
Matches 180; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

OY 27 CCCGCTGGAGAGAGATGAGTGCCTGACTACTACGGAGATGCTGTGCTTACACGGAT 86  
DB 27 CCAGGTGTGGCCAGAGAGATGAGTGCAGAGAAACAGGCTGTACAGCTTGCACCGCAT 86  
OY 87 GTTCAGAGTGTGGCGGAGCACTGACCGAGTGCAGCTGAGCTCTTGTCTCT 146  
DB 87 GTTTCACATGTGGGCACTCATCTGACACAGAGATGTGGCGTCTTCTTCTCT 146  
OY 147 GGATAGGCTCTGTGGCGCGCGGAGGCTTAGCCCGGCGCGGAGGCTTAGAGCTCT 206  
DB 147 TGTGTATGTTCATGTATGACCAAGAGCTGACTCAT--CCGAAATGAGACGTGACTTCT 203  
OY 207 GCTGAGCTGAGAGCGCGCGGAGTGTGGCGGAGCAACCTGTGGGCACT 266  
DB 204 ATTGCACTGAGAGCGCCAGGCGCTGTGATGAAGTAACTTTCGCGAGGCTGCACT 263  
OY 267 CTTGGCGGTGTGGCGCGGAGCACTGTCTGCGGACCTGTGGCGGAGCGGCGGCG 326  
DB 264 GCTGCGCATTCATCATCTCGCAGACCTGTGCTTACGTACCTCAAGAGAGAGCGG 323  
OY 327 AGTGTCTCCAGAAC 340  
DB 324 TGTGTCCCTGATC 337

## RESULT 14

US-07-704-288C-2

Sequence 2, Application US/07704288C  
Patent No. 539680  
GENERAL INFORMATION:  
APPLICANT: LAMB, CHRISTOPHER J.  
APPLICANT: ZHU, QUN  
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY  
ELEMENTS  
TITLE OF INVENTION: ELEMENTS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: United States  
ZIP: 90071-2921  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07704,288C  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P31 8899  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 546-4737  
TELEFAX: (619) 546-9392  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1151 base pairs  
TYPE: nucleic acid

STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 55..1062  
US-07-704-288C-2

Query Match 5.6%; Score 50.8; DB 1; Length 1151;  
Best Local Similarity 57.6%; Pred. No. 0.03;  
Matches 91; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

OY 159 TGGCGCGCGGAGGCTTACCTCCGCGCGGAGCGGCTTACGCTCTGTGAGCTGGA 218  
DB 71 TGTGTGCGCATGTGTGCGGAGGCGCTTCTGTGCGGCGCGGCTGATGCCAGAGTGGCGCA 130  
OY 219 GCGCGCGGAGGAGGCGGCGGAGCAACCTGCGGCTGTGAGGGAACCTTGGCGGCT 278  
DB 131 GCGAGGCGGCGGCGGAGTGTGCGGCAACTCTCTGTGAGGCAAGTTCGCTGTGCGG 190  
OY 279 GAGCGCGGAGGCTGTGCGGCACTGTGCGGAGCGGAGC 316  
DB 191 GCTCCACTCCGACTTACTGCGGCGCGGATGCCAGAGC 228

## RESULT 15

US-08-093-372-1

Sequence 1, Application US/08093372  
Patent No. 5530187  
GENERAL INFORMATION:  
APPLICANT: Lamb, Christopher J.  
APPLICANT: Zhu, Qun  
APPLICANT: Maher, Eileen A.  
APPLICANT: Dixon, Richard A.  
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 90071-2921  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,372  
FILING DATE: 16-JUL-1993  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9391  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1151 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 55..1062  
OTHER INFORMATION: /product= "RICE CHITINASE"  
US-08-093-372-1

Query Match 5.6%; Score 50.8; DB 1; Length 1151;  
 Best Local Similarity 57.6%; Pred. No. 0.03;  
 Matches 91; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Oy	159	TGGCCCGCCGAGGCTTAGCCCGGAGCCGCGACCGGCTTAGAGCTCTGAGCTGGA	218
Db	71	TGGTGGCCATGGTGGCCAGGCGCCCTTCTCTGCGCGCGCCCGTCATGCGGAGCAGTGGGCA	130
Oy	219	GCGCCGCGGCGAGTGGCGGAGAGCAACCTGCGGCTGCTGAGGCAACTCTGCGGCTGCT	278
Db	131	GCCAGGCCGCGCGCGGCGGCTGCTCCCACTGCTCTGCTGCAAGCAATTGCGCTGAGCG	190
Oy	279	GCGCCGCGCAGACCTGCTGCGCGCACTGCGCGCAAGC	316
Db	191	GCTCCACCTCCGACTACTGCGCGCGGATGCCAGAGC	228

Search completed: February 12, 2005, 12:44:46  
 Job time : 151 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:58:57 / Search time 424 Seconds  
(without alignments)  
12691.144 Million cell updates/sec

Title: US-10-030-271-1

Perfect score: 909

Sequence: 1 atgcgcctatccgcggctgcac.....tcagtcgagatgagctgac 909

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16dec04:\*

- 1: genebegn19808:\*
- 2: genebegn19908:\*
- 3: genebegn20008:\*
- 4: genebegn20018:\*
- 5: genebegn20028:\*
- 6: genebegn20038:\*
- 7: genebegn20048:\*
- 8: genebegn20058:\*
- 9: genebegn20068:\*
- 10: genebegn20078:\*
- 11: genebegn20088:\*
- 12: genebegn20098:\*
- 13: genebegn20108:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	909	5	AAf27407 Human apo
2	909	100.0	1883	5	AAf27408 Human apo
3	907.4	99.8	981	10	ADc79259 Human DED
4	907.4	99.8	1230	6	ABA94362 Human APR
5	907.4	99.8	1924	6	AAa40080 Human DED
6	907.4	99.8	1924	6	AAa59062 Human DED
7	907.4	99.8	1979	12	ADa86891 Human tum
8	907.4	99.8	2045	3	AAa95790 Apoptosis
9	907.4	99.8	2045	3	AAa95790 Apoptosis
10	907.4	99.8	2045	3	AAa95790 Apoptosis
11	825.8	90.8	1106	6	ABU39692 Human NS
12	825.8	90.8	1106	6	ABU39692 Human NS
13	799.4	87.9	1966	6	AAa62603 cDNA sequ
14	581.2	63.9	1570	4	AAa99646 Human pro
15	541	59.5	1067	4	AAa58961 Human pol
16	541	59.5	1067	4	AAa58961 Human pol
17	541	59.5	1067	4	AAa58961 Human pol
18	529	58.2	1042	4	AAa60747 Human pol
19	528	58.1	626	4	AAa70725 Human pol
20	346.2	38.1	603	5	AAa93937 Primer sp

C	21	326.6	35.9	111084	12	ADQ18808	Adq18808 Human sof
	22	301.4	33.2	303	6	AAa40075	AAa40075 Human DED
	23	301.4	33.2	303	6	AAa59057	AAa59057 Human DED
	24	193.8	21.3	1139	3	AAa43923	AAa43923 Human DED
	25	193.8	21.3	1830	4	AAa15765	AAa15765 Human CN
	26	193.8	21.3	2261	4	AAa14367	AAa14367 Human CN
	27	193.8	21.3	2261	6	AAa46133	AAa46133 cDNA enco
	28	192.2	21.1	1045	5	AAa43203	AAa43203 Human FLA
	29	192.2	21.1	1045	5	AAa43203	AAa43203 Human FLA
	30	192.2	21.1	2079	5	AAa24761	AAa24761 Human pro
	31	190.6	21.0	1142	3	AAa43924	AAa43924 Murine DE
	32	190.6	21.0	1200	2	AAa74138	AAa74138 Mouse FLA
	33	190.6	21.0	1200	6	AAa43204	AAa43204 Mouse FLA
	34	157.2	17.3	484	9	AAa43205	AAa43205 Human adu
	35	152.4	16.8	451	9	AAa41209	AAa41209 Human foe
C	36	119.2	13.1	769	10	ADa34431	ADa34431 Mouse mit
	37	114.6	12.6	525	10	ADa34432	ADa34432 Mouse mit
	38	112	12.3	553	9	AAa23692	AAa23692 Human adu
	39	111	12.2	278	11	ADa79498	ADa79498 Colton can
	40	111	12.2	422	8	AAa218661	AAa218661 Group III
	41	86.8	9.5	669	4	AAa05181	AAa05181 Human CN
	42	83.8	9.2	523	4	AAa06261	AAa06261 Human CN
	43	56.6	6.2	114955	2	AAa53491	AAa53491 Human ade
	44	54.8	6.0	980	8	ADa71128	ADa71128 Rice gene
	45	52.8	5.8	2073	8	AAa42664	AAa42664 Human Lp3

## ALIGNMENTS

RESULT 1	AAf27407	standard; cDNA; 909 BP.
ID	AAf27407	standard; cDNA; 909 BP.
XX	AAf27407	
AC	AAf27407	
DT	24-APR-2001	(first entry)
XX		
DE	Human apoptosis-associated factor NT2RM1000558 partial cDNA, SEQ ID NO.1.	
XX		
KW	Human, apoptosis-associated factor; NT2RM1000558; death effector domain; DED; caspase family cleavage domain; pro-apoptotic; drug screening; cell proliferation; ischaemic disease; chronic viral disease; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200104300-A1.	
XX		
PD	18-JAN-2001.	
XX		
PF	06-JUL-2000; 2000WO-JP004516.	
XX		
PR	08-JUL-1999; 99JP-00194179.	
XX		
PR	18-OCT-1999; 99US-0159586P.	
XX		
PI	(HELI-) HELIX RES INST.	
XX		
DR	Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;	
XX		
DR	WPI; 2001-138348/14.	
XX		
PF	P-PSDB; AAB60386.	
XX		
PT	Polynucleotide encoding an apoptosis-associated factor protein with death effector domain and caspase family-cleavage domain, useful in regulating diseases with cell proliferation.	
XX		
PS	Claim 1; Page 41-43; 53pp; Japanese.	
XX		
CC	The invention relates to a novel human apoptosis-associated factor (AAB60386, AAB60387), designated NT2RM1000558, which contains a death effector domain (DED) and a caspase family cleavage domain and is capable of inducing apoptosis in cells. The invention also relates to nucleic acids encoding the protein (AAf27407, AAf27408); variants of the protein	
CC		



CC (particularly dominant negative variants); vectors and host cells  
 CC comprising a nucleic acid which encodes an apoptosis-associated factor  
 CC of the invention; the recombinant production of the protein; an antibody  
 CC against the protein; and methods of screening for compounds which can  
 CC regulate apoptosis. The apoptosis-related factor is useful in regulating  
 CC diseases associated with cell proliferation and in screening drug  
 CC candidates e.g., for regulating cell proliferation or cell death in  
 CC ischaemic diseases and chronic viral diseases. The present sequence  
 CC represents cDNA encoding a substantial proportion of the human apoptosis-  
 CC associated factor NT2RM1000558

XX Sequence 909 BP; 139 A; 284 C; 332 G; 154 T; 0 U; 0 Other;

Query Match 100.0%; Score 909; DB 5; Length 909;

Best Local Similarity 100.0%; Pred. No. 2.1e-171;  
 Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGGGCGTATCCGGGTCGACCCCGGCTGTGGGAGAGATGAGTCCCTGACATAC 60
DB 1 ATGGGCGTATCCGGGTCGACCCCGGCTGTGGGAGAGATGAGTCCCTGACATAC 60
QY 61 TACGGGATGCTGTCCCTTCAACCGTATGTTGAGTGTGGGCGGCAACTGACCGAGTGC 120
DB 61 TACGGGATGCTGTCCCTTCAACCGTATGTTGAGTGTGGGCGGCAACTGACCGAGTGC 120
QY 121 GAGCTGAGACTCTCTGACCTTTCTGTGTGATGAGGCTCTGCGCGCGGAGGCTTAAACC 180
DB 121 GAGCTGAGACTCTCTGACCTTTCTGTGTGATGAGGCTCTGCGCGCGGAGGCTTAAACC 180
QY 181 CGGGGCGCGAGCGGCTGTGAGCTCCTGTGTGAGCTGTGAGCGCGCGGAGTGTGGCGAG 240
DB 181 CGGGGCGCGAGCGGCTGTGAGCTCCTGTGTGAGCTGTGAGCGCGCGGAGTGTGGCGAG 240
QY 241 AGCAACTGCTGCGGCTGTGGGCAACTCTCTGCGGCTGTGGCGCGGCAACTGCTGTGGCG 300
DB 241 AGCAACTGCTGCGGCTGTGGGCAACTCTCTGCGGCTGTGGCGCGGCAACTGCTGTGGCG 300
QY 301 CACCTGGGCGCGAGCGGCGCGGCGGCAAGTGTCTCAAGAACGCTATAGCTATGCACTTCC 360
DB 301 CACCTGGGCGCGAGCGGCGCGGCGGCAAGTGTCTCAAGAACGCTATAGCTATGCACTTCC 360
QY 361 AGCTTTCAAGAGAGACAGAGGTTAGCTGCGCGCTGCGCGGCAAGTGTCTCAAGAACGCT 420
DB 361 AGCTTTCAAGAGAGACAGAGGTTAGCTGCGCGCTGCGCGGCAAGTGTCTCAAGAACGCT 420
QY 421 AATTCTCAGCAGGCTCAGTGTGAGACAGGCTCTCCCGCAACCGGACGGCGGCGAGT 480
DB 421 AATTCTCAGCAGGCTCAGTGTGAGACAGGCTCTCCCGCAACCGGACGGCGGCGAGT 480
QY 481 CGGGGCGCGGCGGCTGTGTGTGCTCAAGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGG 540
DB 481 CGGGGCGCGGCGGCTGTGTGTGCTCAAGCGGCGGCGGAGGCGGCGGCGGCGGCGGCGG 540
QY 541 CAGGAGTCAAGAGCGGCGGCGGCAAGTCTCTGTAAGGCAAGTGAAGTGTGACATCCGGGCTC 600
DB 541 CAGGAGTCAAGAGCGGCGGCGGCAAGTCTCTGTAAGGCAAGTGAAGTGTGACATCCGGGCTC 600
QY 601 CGGGTTCAGCAGAGTACTGTCAGACATGAGGCGGCGGCTGTGAGCAGGCGGCGGCGGCGG 660
DB 601 CGGGTTCAGCAGAGTACTGTCAGACATGAGGCGGCGGCTGTGAGCAGGCGGCGGCGGCGG 660
QY 661 CGGGTTCAGCAGAGTACTGTCAGACATGAGGCGGCGGCTGTGAGCAGGCGGCGGCGGCGG 720
DB 661 CGGGTTCAGCAGAGTACTGTCAGACATGAGGCGGCGGCTGTGAGCAGGCGGCGGCGGCGG 720
QY 721 TCAAGGAGCTGGGCTGTGTGTGTTGTGACATCAAGTCTCTGAGACTCTCCATCTGAGAC 780
DB 721 TCAAGGAGCTGGGCTGTGTGTGTTGTGACATCAAGTCTCTGAGACTCTCCATCTGAGAC 780
QY 781 GCTTCTGAGGAGGAGCTGAGTGTGAGGCGGCGGCTGTGAGGCGGCGGCGGCGGCGGCGG 840
DB 781 GCTTCTGAGGAGGAGCTGAGTGTGAGGCGGCGGCTGTGAGGCGGCGGCGGCGGCGGCGG 840

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QY 841 ACTGAGGCGCTTCCGAGAGGCTGTGTGGCGCGGAGGCTGTTCCTGCTGTGATGTGAT 900
DB 841 ACTGAGGCGCTTCCGAGAGGCTGTGTGGCGCGGAGGCTGTTCCTGCTGTGATGTGAT 900
QY 901 GAGGCTGAC 909
DB 901 GAGGCTGAC 909

```

RESULT 2  
 AAF27408  
 ID AAF27408 standard; cDNA; 1883 BP.

XX AAF27408;

DT 24-APR-2001 (first entry)

DE Human apoptosis-associated factor NT2RM1000558 cDNA, SEQ ID NO.3.

KM Human; apoptosis-associated factor; NT2RM1000558; death effector domain;

KM DED; caspase family cleavage domain; pro-apoptotic; drug screening;

OS Homo sapiens.

PI WO200104300-A1.

PD 18-JAN-2001.

PE 06-JUL-2000; 2000WO-JP004516.

PR 08-JUL-1999; 99JP-00194179.

PR 18-OCT-1999; 99US-0159586P.

PA (HELI-) HELIX RES INST.

PI Ota T, Ito T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;

DR WPI; 2001-138348/14.

DR P-PSDB; AAB60387.

PT Polynucleotide encoding an apoptosis-associated factor protein with death

PT effector domain and caspase family-cleavage domain, useful in regulating

PT diseases with cell proliferation.

PS Claim 3; Page 44-47; 53pp; Japanese.

CC The invention relates to a novel human apoptosis-associated factor

CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death

CC effector domain (DED) and a caspase family cleavage domain and is capable

CC of inducing apoptosis in cells. The invention also relates to nucleic

CC acids encoding the protein (AAF27407, AAF27408); variants of the protein

CC (particularly dominant negative variants); vectors and host cells

CC comprising a nucleic acid which encodes an apoptosis-associated factor

CC of the invention; the recombinant production of the protein; an antibody

CC against the protein; and methods of screening for compounds which can

CC regulate apoptosis. The apoptosis-related factor is useful in regulating

CC diseases associated with cell proliferation and in screening drug

CC candidates e.g., for regulating cell proliferation or cell death in

CC ischaemic diseases and chronic viral diseases. The present sequence

CC represents a full-length cDNA encoding the human apoptosis-associated

CC factor NT2RM1000558

XX Sequence 1883 BP; 343 A; 595 C; 588 G; 357 T; 0 U; 0 Other;

Query Match 100.0%; Score 909; DB 5; Length 1883;

Best Local Similarity 100.0%; Pred. No. 2.2e-171;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGGCGTATCCGGGTCGACCCCGGCTGTGGGAGAGATGAGTCCCTGACATAC 60
DB 124 ATGGGCGTATCCGGGTCGACCCCGGCTGTGGGAGAGATGAGTCCCTGACATAC 183

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QY 61 TACGGGATGCTGCTTCAACCGTATGTTGAGGTGTGGGCGGCACTGACCGAGTGC 120
DB 184 TACGGGATGCTGCTTCAACCGTATGTTGAGGTGTGGGCGGCACTGACCGAGTGC 243
QY 121 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGCGCGGAGCTTTAGCC 180
DB 244 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGCGCGGAGCTTTAGCC 303
QY 181 CGGGCCCGGAGGCGCTAGAGCTCTGCTGAGGCTGTGAGAGCGCGCGGAGGCTGTGCGGCGAG 240
DB 304 CGGGCCCGGAGGCGCTAGAGCTCTGCTGAGGCTGTGAGAGCGCGCGGAGGCTGTGCGGCGAG 363
QY 241 AGCAACTGTGGCTGTGGGAGCACTCTGCGCGTGTGCTGAGCGCGCGGAGGCTGTGCGGCGAG 300
DB 364 AGCAACTGTGGCTGTGGGAGCACTCTGCGCGTGTGCTGAGCGCGCGGAGGCTGTGCGGCGAG 423
QY 301 CACCTGGCGCGCAAGCGGCGCGCGCGGAGTGTCTCCAGAACGCTATAGCTATGCACTTCC 360
DB 424 CACCTGGCGCGCAAGCGGCGCGCGCGGAGTGTCTCCAGAACGCTATAGCTATGCACTTCC 483
QY 361 AGCTTTCAAGAGAGGAGAGAGGAGTGTGCTGCGCGTGTGCTGAGCGAGTCAAGCTTCTGCA 420
DB 484 AGCTTTCAAGAGAGGAGAGAGGAGTGTGCTGCGCGTGTGCTGAGCGAGTCAAGCTTCTGCA 543
QY 421 AATTCTCAGCAGAGGTCAGTGGAGAGCAGGCTCCCGCCCAACAGCGGAGCGGCGGAGT 480
DB 544 AATTCTCAGCAGAGGTCAGTGGAGAGCAGGCTCCCGCCCAACAGCGGAGCGGCGGAGT 603
QY 481 CGGGGCGGCGCAAGTGTGTGTGTCAGAGCGCGCGGAGAGGAGGAGGCGCGGAGCGGAG 540
DB 604 CGGGGCGGCGCAAGTGTGTGTGTCAGAGCGCGCGGAGAGGAGGAGGCGCGGAGCGGAG 663
QY 541 CAGCAGTCAGAGCGCGCGGAGAGCTTCTCTGAAGGAGAGGAGGAGGAGGAGGAGGAGGAG 600
DB 664 CAGCAGTCAGAGCGCGCGGAGAGCTTCTCTGAAGGAGAGGAGGAGGAGGAGGAGGAGGAG 723
QY 601 CGGGGTCAGAGAGTGTGTGTGTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
DB 724 CGGGGTCAGAGAGTGTGTGTGTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783
QY 661 CGGGCCCGGAGGCGCTGCGCGGCGGAGGAGTGTGTTGGGAGGAGGAGGAGGAGGAGGAG 720
DB 784 CGGGCCCGGAGGCGCTGCGCGGCGGAGGAGTGTGTTGGGAGGAGGAGGAGGAGGAGGAG 843
QY 721 TCAAGGAGAGCTGAGGCTGTGAGTTTGTGATCATCAAGTTTCAAGGCTCTATCTAGAG 780
DB 844 TCAAGGAGAGCTGAGGCTGTGAGTTTGTGATCATCAAGTTTCAAGGCTCTATCTAGAG 903
QY 781 GCTTCTGAGGAGGAGTCACTGAGTGTGAGGCGCTGTGCTGAGAGGCGCTGTGCTGTG 840
DB 904 GCTTCTGAGGAGGAGTCACTGAGTGTGAGGCGCTGTGCTGAGAGGCGCTGTGCTGTG 963
QY 841 ACTGAGAGGCTGTGAGAGGCTGTGAGGCGGAGAGGCTGTGCTGTGCTGTGCTGTGAGT 900
DB 964 ACTGAGAGGCTGTGAGAGGCTGTGAGGCGGAGAGGCTGTGCTGTGCTGTGCTGTGAGT 1023
QY 901 GAGGCTGAC 909
DB 1024 GAGGCTGAC 1032

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RESULT 3  
ADCT9259 standard; cDNA; 981 BP.

ADCT9259;

01-JAN-2004 (first entry)

Human DEDD2 encoding cDNA SEQ ID NO:1.

human; death effector domains containing DNA-binding protein;

DEAD-containing DNA-binding protein; DEDD2; cell death; gene therapy;

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KW cytosolic; cancer; chronic myeloid leukaemia; gene; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX CDS 1..981
XX FT /tag= a
XX FT /product= "DEDD2"
XX PN
XX MO0003054195-A1.
XX PD
XX 03-JUL-2003.
XX PF
XX 20-DEC-2002; 2002MO-JP013371.
XX PR
XX 20-DEC-2001; 2001JP-00387854.
XX PR
XX 18-JUL-2002; 2002JP-00209458.
XX PA
XX (MORG ) MORINAGA MILK IND CO LTD.
XX PI
XX Suzu S, Hageshita H, Nomaguchi K, Yamada M, Hayasawa H;
XX DR
XX WPI; 2003-569246/53.
XX DR
XX P-PSDB; ADC79260.
XX PT
XX DNA encoding cell death proteins for treatment of kidney, large intestine
XX PS
XX and prostate cancers and leukemia.
XX Claim 2; Page 18-20; 26pp; Japanese.
XX CC
XX The present sequence encodes a human death effector domains (DED)
XX containing DNA-binding protein (DEDD) protein, designated DEDD2, that
XX causes cell death. Also described: (1) primer and probe for investigation
XX of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has
XX cytostatic activity. DEDD2 can be used in the diagnosis and treatment of
XX CC
XX cancers of the kidney, large intestine and prostate, and acute and
XX chronic myeloid leukaemia.
XX SQ
XX Sequence 981 BP; 151 A; 303 C; 363 G; 164 T; 0 U; 0 Other;
XX
XX Query Match 99.8%; Score 907.4; DB 10; Length 981;
XX Best Local Similarity 99.9%; Pred. No. 4,4e-171;
XX Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGAGTATCCGGGTCGACCCCGGCGCGCTGTGCTGAGAGAGAGTATGCTTGAAGTAC 60
DB 1 ATGGGAGTATCCGGGTCGACCCCGGCGCGCTGTGCTGAGAGAGAGTATGCTTGAAGTAC 60
QY 61 TACGGGATGCTGCTTCAACCGTATGTTGAGGTGTGGGCGGCACTGACCGAGTGC 120
DB 61 TACGGGATGCTGCTTCAACCGTATGTTGAGGTGTGGGCGGCACTGACCGAGTGC 120
QY 121 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGCGCGGAGCTTTAGCC 180
DB 121 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGCGCGGAGCTTTAGCC 180
QY 181 CGGGCCCGGAGGCGCTAGAGCTCTGCTGAGGCTGTGAGAGCGCGCGGAGGCTGTGCGGCGAG 240
DB 181 CGGGCCCGGAGGCGCTAGAGCTCTGCTGAGGCTGTGAGAGCGCGCGGAGGCTGTGCGGCGAG 240
QY 241 AGCAACTGTGGCTGTGGGAGCACTCTGCGCGTGTGCTGAGCGCGCGGAGGCTGTGCGGCGAG 300
DB 241 AGCAACTGTGGCTGTGGGAGCACTCTGCGCGTGTGCTGAGCGCGCGGAGGCTGTGCGGCGAG 300
QY 301 CACCTGGCGCGCAAGCGGCGCGCGGAGTGTCTCCAGAACGCTATAGCTATGCACTTCC 360
DB 301 CACCTGGCGCGCAAGCGGCGCGCGGAGTGTCTCCAGAACGCTATAGCTATGCACTTCC 360
QY 361 AGCTTTCAAGAGAGGAGAGGAGTGTGCTGCGCGTGTGCTGAGCGAGTCAAGCTTCTGCA 420
DB 361 AGCTTTCAAGAGAGGAGAGGAGTGTGCTGCGCGTGTGCTGAGCGAGTCAAGCTTCTGCA 420
QY 421 AATTCTCAGCAGAGGTCAGTGGAGAGCAGGCTCCCGCCCAACAGCGGAGCGGCGGAGT 480

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Db 421 AATTCTCAGACGGTCTAGTGGAGACAGGCTCCCCCAACCAAGCGAGCGGAGT 480  
 Qy 481 CGGGGCGGCGGAGTGGTGGTCCAGACGGCGCGAGAGAGGGGCCCAACCGCCAGCCAG 540  
 Db 481 CGGGGCGGCGGAGTGGTGGTCCAGACGGCGCGAGAGAGGGGCCCAACCGCCAGCCAG 540  
 Qy 541 CAGCAGTACAGAGCCCGGAGACCTTCTCTGAAAGGCAAGTACCTGTGACATCCGGCTC 600  
 Db 541 CAGCAGTACAGAGCCCGGAGACCTTCTCTGAAAGGCAAGTACCTGTGACATCCGGCTC 600  
 Qy 601 CGGGTTCAGACAGATCTGACAGATGGGCGAGGCTTGGAGCAGAGGGGTGGCATCCGG 660  
 Db 601 CGGGTTCAGACAGATCTGACAGATGGGCGAGGCTTGGAGCAGAGGGGTGGCATCCGG 660  
 Qy 661 CGGGCCGAGCGCTGCGCGAGAGTGAACGTGTTGGGCGAGCCACCGCAGTGTGCGC 720  
 Db 661 CGGGCCGAGCGCTGCGCGAGAGTGAACGTGTTGGGCGAGCCACCGCAGTGTGCGC 720  
 Qy 721 TCAGAGGACCTGGGCTGTGTGTGTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780  
 Db 721 TCAGAGGACCTGGGCTGTGTGTGTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780  
 Qy 781 GCTTCTGGGCGGACCTACCTGAGTGGCGGCTGCTGACAGGCGCTGGGGGCGTGTCCG 840  
 Db 781 GCTTCTGGGCGGACCTACCTGAGTGGCGGCTGCTGACAGGCGCTGGGGGCGTGTCCG 840  
 Qy 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGCGAGGCTGTTCGCTGCTGTCAGTGTGAT 900  
 Db 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGCGAGGCTGTTCGCTGCTGTCAGTGTGAT 900  
 Qy 901 GAGGCTGAC 909  
 Db 901 GAGGCTGAC 909

## RESULT 4

ABA94362  
 ID ABA94362 standard; DNA; 1230 BP.

AC ABA94362;  
 XX

DT 26-MAR-2002 (first entry)  
 XX

DE Human APRG polypeptide (Incyte ID. 3102521CD1) encoding cDNA.  
 XX

KW APRG; apoptosis regulator; cytosolic; antiatherosclerotic; osteopathic;  
 KW antiarteriosclerotic; hepatotropic; antipsoriatic; antihelmintic; human;  
 KW antiatherogenic; antiatherogenic; antiatherogenic; anti-HIV; cancer;  
 KW antiinflammatory; antidiabetic; antihypertensive; nephrotropic; ophthalmological;  
 KW immunosuppressive; dermatological; antitumor; antithrombotic; fungicide;  
 KW antiatherogenic; antibacterial; antiviral; antiparasitic; protozoicide;  
 KW tranquilizer; valnerary; gynecological; vasotropic; gene therapy; ss.  
 XX

OS Homo sapiens.  
 XX

FH Key Location/Qualifiers  
 FT 127..1107  
 FT CDS /tag= a  
 FT /product= "APRG polypeptide"  
 XX

PN W020192527-A2.  
 XX

PD 06-DEC-2001.  
 XX

PF 30-MAY-2001; 2001WO-US017581.  
 XX

PR 01-JUN-2000; 2000US-0209407P.  
 PR 30-NOV-2000; 2000US-0250326P.  
 XX

PA (INCY-) INCYTE GENOMICS INC.  
 XX

PI Tang YT, Azimzal Y, Yue H, Burford N, Ding L, Elliott VS;

PI Paterson C, Baughn MR;  
 XX  
 DR WPI; 2002-114350/15.  
 DR P-PSDB; ABB07263.  
 XX  
 PT Novel human apoptosis regulator polypeptides and polynucleotides for  
 PT diagnosing, preventing, treating cell proliferative, immunological and  
 PT reproductive disorders and for identifying modulators of therapeutic use.  
 PS Claim 5; Page 101; 103pp; English.

The invention provides human apoptosis regulator (APRG) polypeptides and polynucleotides. The APRG polypeptides, polynucleotides and modulators are useful for diagnosing, preventing and treatment of cell proliferative, immunological and reproductive disorders. The cell proliferative disorders include cancers, actinic keratosis, arteriosclerosis, atherosclerosis, burns, cirrhosis, hepatitis, psoriasis, and immunological disorders include acquired immunodeficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, ankylosing spondylitis, amyloidosis, allergies, anemia, osteoporosis, autoimmune hemolytic anemia, asthma, autoimmune thyroiditis, Crohn's disease, contact dermatitis, diabetes mellitus, gout, Graves' disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, hemodialysis, urethritis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma. Reproductive disorders include disorders of prolactin production, infertility, endometriosis, polycystic ovary syndrome, ectopic pregnancies, galactorrhea, abnormal sperm physiology, disruptions of spermatogenesis, cancer of testis and prostate, impotence, carcinoma of male breast and gynecoma. The APRG polynucleotides are useful for creating knock-in humanized animals or transgenic animals to model human disease and to detect and quantify gene expression in biopsied tissues in which expression of APRG is correlated with disease. APRG fragments of it and antibodies specific for APRG are useful as elements on a microarray which is useful to monitor or measure protein-protein interactions, drug-target interactions and gene expression profiles. The present sequence represents a human APRG polypeptide encoding cDNA.

SO Sequence 1230 BP; 205 A; 382 C; 433 G; 210 T; 0 U; 0 Other;

Query Match 99.8%; Score 907.4; DB 6; Length 1230;  
 Best Local Similarity 99.9%; Pred. No. 4.4e-111;  
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGCTATCCGGATGACCCCGCCGCTGGAGAGAGATGAGTCTGAGTAC 60  
 Db 127 ATGGCGCTATCCGGATGACCCCGCCGCTGGAGAGAGATGAGTCTGAGTAC 186  
 Qy 61 TACGGAGTCTGTGCTTACCGTATGTTGAGGTGGCGGCAACTGACGAGTGC 120  
 Db 187 TACGGAGTCTGTGCTTACCGTATGTTGAGGTGGCGGCAACTGACGAGTGC 246  
 Qy 121 GAGCTGAGCTCCCTGGCTTCTGCTGATGAGGCTCTGCGCGCGGAGGCTTGGCC 180  
 Db 247 GAGCTGAGCTCCCTGGCTTCTGCTGATGAGGCTCTGCGCGCGGAGGCTTGGCC 306  
 Qy 247 GAGCTGAGCTCCCTGGCTTCTGCTGATGAGGCTCTGCGCGCGGAGGCTTGGCC 306  
 Db 307 CGGGCCGAGCGGCTGAGAGCTCTGCTGAGAGTGAAGCGCGCGGCACTGAGCAG 366  
 Qy 181 CGGGCCGAGCGGCTGAGAGCTCTGCTGAGAGTGAAGCGCGCGGCACTGAGCAG 366  
 Db 307 CGGGCCGAGCGGCTGAGAGCTCTGCTGAGAGTGAAGCGCGCGGCACTGAGCAG 366  
 Qy 241 AGCAACTGCGGCTGCTGGGCGCACTCTGCGCGTGGCGCGCAGACTGCTGCGG 300  
 Db 367 AGCAACTGCGGCTGCTGGGCGCACTCTGCGCGTGGCGCGCAGACTGCTGCGG 426  
 Qy 301 CACCTGGCGGCGAGCGGCGCGCGCGAGTCTTCCAGAAAGCTATGAGCACTGCC 360  
 Db 427 CACCTGGCGGCGAGCGGCGCGCGCGAGTCTTCCAGAAAGCTATGAGCACTGCC 486  
 Qy 361 AGCTCTTCAAGAGAGAGAGAGAGTGTGCGCGCTGCGGAGTCAAGAGTCTTGA 420  
 Db 487 AGCTCTTCAAGAGAGAGAGAGTGTGCGCGCTGCGGAGTCAAGAGTCTTGA 546

Qy	421	AATTCAGAGAGGGCTAGTGGGAGCAGGCTCCCCCAACAGAGGGACGGCGAGT	480
Db	547	AATTCAGAGAGGGCTAGTGGGAGCAGGCTCCCCCAACAGAGGGACGGCGAGT	606
Qy	481	CGGGGCGGGCCAGTGGTGTGCCAGACGGCGGCGAGAGGGGGCCCGACGCCAG	540
Db	607	CGGGGCGGGCCAGTGGTGTGCCAGACGGCGGCGAGAGGGGGCCCGACGCCAG	666
Qy	541	CAGCAGTACAGAGCCCGCCAGACTTTCCTGAAAGCAAATGACCTGTGACATCCGGTTC	600
Db	667	CAGCAGTACAGAGCCCGCCAGACTTTCCTGAAAGCAAATGACCTGTGACATCCGGTTC	726
Qy	601	CGGGTTCAGAGAGAGTACTGCGAGCATGGGCGAGCCTTGAGACAGAGGGCGTGACATCCCGG	660
Db	727	CGGGTTCAGAGAGAGTACTGCGAGCATGGGCGAGCCTTGAGACAGAGGGCGTGACATCCCGG	786
Qy	661	CGGCCCCCAGGGCGCTGGCGCGGACGTGGAAGTGTGGGCAAGGCCACCGCAGTGTGGCC	720
Db	787	CGGCCCCCAGGGCGCTGGCGCGGACGTGGAAGTGTGGGCAAGGCCACCGCAGTGTGGCC	846
Qy	721	TCAAGGAGACTGGGCTGTGGTGTGACATCAAGTTCCTAGAGCTCTCTATCTGGAC	780
Db	847	TCAAGGAGACTGGGCTGTGGTGTGACATCAAGTTCCTAGAGCTCTCTATCTGGAC	906
Qy	781	GCTTCTGGGGGACTACCTGAGTGGCGCCCTGTGCAGGCGCCCTGGGGGCGTGTCTTG	840
Db	907	GCTTCTGGGGGCGACTACCTGAGTGGCGCCCTGTGCAGGCGCCCTGGGGGCGTGTCTTG	966
Qy	841	ACTGAGGCCCTGCGAGAGAGCTGTGGGCGGGAGAGCTGTTCGCTGCTGTCAGTGTGAT	900
Db	967	ACTGAGGCCCTGCGAGAGAGCTGTGGGCGGGAGAGCTGTTCGCTGCTGTCAGTGTGAT	1028
Qy	901	GAGGCTGAC 909	
Db	1027	GAGGCTGAC 1035	

RESULT 5  
AAD40080  
ID AAD40080 standard; DNA; 1924 BP.

AC AAD40080;

DT 22-OCT-2002 (first entry)

DE Human DED4 (death effector domain) gene.

KM Human, death domain, DD, death effector domain, DED; Chlamydia infection;  
KM NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
KM inflammation; allergy; autoimmunity; allograft rejection; cell division;  
KM immune-based pathology; fibrosis; arthritis; graft versus host disease;  
KM immunosuppressive; gene therapy; antiense therapy; gene; ds-

OS Homo sapiens.

FH	Key	Location/Qualifiers

FT / \*tag= a

FT	/note= "No stop codon"
----	------------------------

```
FT m18c_feature 157. .222
```

```
FT      /note= "Nuclear localisation sequence"
```

PN WO200240680-A2

PD 23-MAY-2002.

PF 15-NOV-2001; 2001WO-US044844.

PR 17-NOV-2000; 2000US-00715893

XX  
PA (BURN-) BURNHAM INST.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

XX

DR P-PSDB; AAE24860.

PT New polypeptide c

PT allergy, sepsis, autoimmunity, allograft rejection and other diseases

PS Claim 19; Page 184-186; 209pp; English.

The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug, that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTMD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SP, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FFA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTMD DD of *C. trachomatis*, *C. muridarum*, *C. pneumoniae*, and *C. psittaci* or a nucleic acid encoding the CTMD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human DED4 gene

Query Match 99.8%; Score 907.4; DB 6; Length 1924;

```

Best local similarity  22.26;  E-Value: 3.00E-111;
Matches  908;  Conservative  0;  Mismatches  1;  Indels  0
Gaps  0

```

QY 1 ATGGCGTATCCGGGTCGACCCCGGCCGTCGTGGAGGAGGATGAGTGCCCTGACTAC 60

Db 91 ATGGCGCTATCCGGGTCGACCCCCGGCCGTCGTGGAGAGGATGAGTGCCTGACTAC 150

QY 61 TACGGATGCTGTCCGTTACCCGATGTTCCAGGTGGTGGCGGCACTGACCGAGTGC 120

Db 151 TACGGATGCTGTCGCTTCAACCGTATGTTCCGAGGTGGTGGCGGCACTGACCGAGTGC 210

121 GAGCTGAGCTCCTGGCCTTCTGCTGATGAGGCTCCTGGCCGCCGAGGCTTAGCC 180

Db 211 GAGCTGAGCTCCTGGCCTTCTGCTGGATGAGGCTCCTGGCGCCCGAGGCTTAGCC 270

QY 181 CGGGCCCGCAGCGGCTAGAGCTCCTGCTGGAGCTGGAGCGCCGCGGCA GTGCCGAG 240

Db 271 CGGGCCCGCAGCGGCTAGAGCTCCTGCTGGAGCTGGAGCGCCGCGGCAGTGCACGAG 330

241 AGCAACCTGCGGCTGCTGGGCACTCCTGCGCGTGTGGCCCGCACGACCTGTGCCG 300

Db 331 AGCAACCTGGGCTGCTGGGGCACTCCTGCGCGTGTGCTGGCCCGCACGACCTGCTGCCG 390

301 CACCTGGCGCGCAGCGCGCCGCGCAGTGTCTCCAGAACGCTATAGCTATGGCACCTCC 360

Db 391 CACCTGGCGCGCAGCGCGCGGCAGTGTCTCCAGAACGCTATAGCTATGGCACTCC 450

361 AGCTCTCAAGAGGACAGAGGGTAGCTGCCGTCGCCGTGGCAGTCAAGCAGTCTGCA 420

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Db 451 AGCTTTCAAAAGAGACAGAGGATGCTCCGCTCGCGAGTCAAGCAGTTCTGGA 510
Oy 421 AATTTCAGCAGAGGTCAGTGGAGACAGAGCTCCCCCAACCAAGCGAGCGGAGT 480
Db 511 AATTTCAGCAGAGGTCAGTGGAGACAGAGCTCCCCCAACCAAGCGAGCGGAGT 570
Oy 481 CGGGGCGCGGCGGAGTGTGTGTGTCAGACGCGCGGAGAGGGGCGCCAGCGCCAG 540
Db 571 CGGGGCGCGGCGGAGTGTGTGTGTCAGACGCGCGGAGAGGGGCGCCAGCGCCAG 630
Oy 541 CAGCAGTCAAGAGCCGCGGAGACCTTCTCTGAAGGCAAGTGTGATCTCGGCTC 600
Db 631 CAGCAGTCAAGAGCCGCGGAGACCTTCTCTGAAGGCAAGTGTGATCTCGGCTC 690
Oy 601 CGGGTTGAGCAGAGTACTGCGAGCATGAGCGCCAGCTTGTGAGCAGAGCGCTGCA 660
Db 691 CGGGTTGAGCAGAGTACTGCGAGCATGAGCGCCAGCTTGTGAGCAGAGCGCTGCA 750
Oy 661 CGGCGCCAGCGGCTGTGGCGGAGCTGGAAGTGTGGGAGGCAAGCGAGTGTGCG 720
Db 751 CGGCGCCAGCGGCTGTGGCGGAGCTGGAAGTGTGGGAGGCAAGCGAGTGTGCG 810
Oy 721 TCAAGGAGCCTGTGTGTGTGTGTGATCATGAGTTCTGAGAGCTCTCATCTGAG 780
Db 811 TCAAGGAGCCTGTGTGTGTGTGTGATCATGAGTTCTGAGAGCTCTCATCTGAG 870
Oy 781 GCGTTCTGGGGGAGCCTGACCTGAGTGGCGGCTGTGTCAGAGCGCCGCGGAGCT 840
Db 871 GCGTTCTGGGGGAGCCTGACCTGAGTGGCGGCTGTGTCAGAGCGCCGCGGAGCT 930
Oy 841 ACTGAGGCGGCTGTGCGAGAGGCTGTGGCGGCGGAGGCTGTTCCTGTGTGATG 900
Db 931 ACTGAGGCGGCTGTGCGAGAGGCTGTGGCGGCGGAGGCTGTTCCTGTGTGAT 990
Oy 901 GAGGCTGAC 909
Db 991 GAGGCTGAC 999

```

RESULT 6  
AADS9062  
ID AADS9062 standard; cDNA; 1924 BP.

AADS9062;  
18-DEC-2003 (first entry)  
Human DED4 full length gene.

Human DED4 full length gene.  
Human; death Domain; DD; death effector domain; DED; cell proliferation;  
Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;  
neural growth factor receptor-interacting protein; cell adhesion;  
vasotrophic; microbial infection; inflammation; allograft rejection; CTRD;  
cell stress response; benign prostatic hypertrophy; antibacterial; NIDP;  
apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;  
neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;  
keloid; gene; ss.

Homo sapiens.  
Location/Qualifiers  
Key 91..1044  
CDS /\*tag= a  
/\*product= "Human DED4 protein"  
/\*note= "No stop codon"  
FT /partial  
FT 157..222  
FT misc\_signal  
FT /\*tag= b  
FT /\*note= "Nuclear localisation sequence"  
XX US2003049702-A1.  
XX

```

PD 13-MAR-2003.
XX
PF 15-NOV-2001; 2001US-00001254.
XX
PR 17-NOV-2000; 2000US-00715893.
PR 17-NOV-2000; 2000US-0367360P.
PR 29-JUN-2001; 2001US-0301889P.
XX
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (LEES/) LEE S H.
PA (ROTH/) ROTH W.
PA (STEN/) STENNER-LIEWEN F.
XX
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI Stenner-Liewen F;
XX
DR WPI; 2002-500222/53.
DR P-PsDB; AAE38903.
XX
PT New polypeptide comprising a death domain or death effector domain,
PT useful for discovery of drugs that suppress infection, inflammation,
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
PS Claim 19; Page 42-44; 99pp; English.
XX

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The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDP) DD and neural growth factor receptor-interacting death domain (NIDP) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTRD, DED4 or NIDP with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein CC that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human DED4 full length gene. The DED4 gene is located on chromosome 19

Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;

Query Match 99.8%; Score 907.4; DB 6; Length 1924;  
Best Local Similarity 99.9%; Pred. No. 4,6-111;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy 1 ATGGGCTATCCGGGTGACCCCGCCGCTGGAGAGAGATGAGTCTGAGCTAC 60
Db 91 ATGGGCTATCCGGGTGACCCCGCCGCTGGAGAGAGATGAGTCTGAGCTAC 150
Oy 61 TACGGATGCTGTGCTTCAACCGATGTTGAGAGTGTGGCGGCAACTGACGAGTGC 120
Db 151 TACGGATGCTGTGCTTCAACCGATGTTGAGAGTGTGGCGGCAACTGACGAGTGC 210
Oy 121 GAGCTGAGCTCTGCGCTTCTGCTGATGAGGCTCTCGGCGCGGAGGCTTACCC 180
Db 211 GAGCTGAGCTCTGCGCTTCTGCTGATGAGGCTCTCGGCGCGGAGGCTTACCC 270
Oy 181 CGGGCCGCGGCGGCTTGAAGCTCTGCTGAGAGCGCGCGGCGGCTGTGGCGAG 240
Db 271 CGGGCCGCGGCGGCTTGAAGCTCTGCTGAGAGCGCGCGGCGGCTGTGGCGAG 330

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OY	241	AGCAACCTGGCGGCTGTGGGGGCAACCTCGGCGGAGCTGGCCCGGCGACGACCTGGCTGGCG	300
Db	331	AGCAACCTGGCGGCTGTGGGGGCAACCTCTGTCGGCTGCTGGCCCGGCGACGACCTGGCTGGCG	390
OY	301	CACCTGGCGCGAAGCGGGCGCGGCCGACGATGTCTCCAGAACGCTATAGCTATAGCACCTCC	360
Db	391	CACCTGGCGCGAAGCGGGCGCGGCCGACGATGTCTCCAGAACGCTATAGCTATAGCACCTCC	450
OY	361	AGCTCTTCAAAAGAGCAGAGGGTAGCTGCGCGCGCGCTGGCGGAGTCAAGCAATTCGTGA	420
Db	451	AGCTCTTCAAAAGAGCAGAGGGTAGCTGCGCGCGCGCTGGCGGAGTCAAGCAATTCGTGA	510
OY	421	AATTTCTCAGCAGGGGTCAGTGGGAGACAGGCTCCCCCGCCAAACAAAGCGGACGCGCGAGT	480
Db	511	AATTTCTCAGCAGGGGTCAGTGGGAGACAGGCTCCCCCGCCAAACAAAGCGGAGCGCGGAGT	570
OY	481	CGGGGCGCGGCCCAAGTGTGTGTGCAGACGGCGCGGAGAGAGGGGCCCAAGCTCCGACCCCGAG	540
Db	571	CGGGGCGCGGCCCAAGTGTGTGTGCAGACGGCGCGGAGAGAGGGGCCCAAGCTCCGACCCCGAG	630
OY	541	CAGCAGTCAAGACCCCGCCAGACCTTCTCTGAAGGAGAAAGTAGCTGTGACATCCGAGCTC	600
Db	631	CAGCAGTCAAGACCCCGCCAGACCTTCTCTGAAGGAGAAAGTAGCTGTGACATCCGAGCTC	690
OY	601	CGGGTTTCGAGCAGAGTACTGCGAGCAATGAGGAGCGCAGCTTTGAGACGAGGAGCGGTGACATCCGG	660
Db	691	CGGGTTTCGAGCAGAGTACTGCGAGCAATGAGGAGCGCAGCTTTGAGACGAGGAGCGGTGACATCCGG	750
OY	661	CGGGCCCGCAGGGCGCTGGCGCGGAGCGTGAAGCTGTTGGCGAGGCGCACCGGAGTGGCTGGCG	720
Db	751	CGGGCCCGCAGGGCGCTGGCGCGGAGCGTGAAGCTGTTGGCGAGGCGCACCGGAGTGGCTGGCG	810
OY	721	TCAAGGGAACCTGGGCTGTGTGTGTGTGAATCAACAATTCTCAGAGCTCTCTCAATCTGGAC	780
Db	811	TCAAGGGAACCTGGGCTGTGTGTGTGTGAATCAACAATTCTCAGAGCTCTCTCAATCTGGAC	870
OY	781	GGCTTCTGGGGGAGCACTACCTGAGTGGCGGCTGCTGTCAGAGGCCCTGGGGGGCGTGTCTCG	840
Db	871	GGCTTCTGGGGGAGCACTACCTGAGTGGCGGCTGCTGTCAGAGGCCCTGGGGGGCGTGTCTCG	930
OY	841	ACTGAGGCGCTTCGAGAGGCTGTGGGCGGGGAGGCTGTTGCGCTGTGATCAATGTGGAT	900
Db	931	ACTGAGGCGCTTCGAGAGGCTGTGGGCGGGGAGGCTGTTGCGCTGTGATCAATGTGGAT	990
OY	901	GAGGCTGAC	909
Db	991	GAGGCTGAC	999

RESULT 7  
ADQ86891  
ID ADQ86891 standard; cDNA; 1979 BP.

DT	07-OCT-2004	(first entry)
XX		
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #3766.	
XX		
KW	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;	
KW	cancer; cell proliferative disorder; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004060270-A2.	
XX		
PD	22-JUL-2004.	
XX		
PF	15-OCT-2003; 2003WO-US029126.	
XX		
PR	18-OCT-2002; 2002US-0418988P.	
XX		

PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
XX  
XX  
P1 Wu TD, Zhou Y;  
XX  
XX  
DR WPI; 2004-534300/51.  
XX  
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.  
XX  
XX Claim 1, SEQ ID NO 3766, 5504bp, English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytotoxic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 1979 BP; 365 A; 617 C; 627 G; 370 T; 0 U; 0 Other;

Query Match	99.8%;	Score 907.4;	DB 12;	Length 1979;
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Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	ATGAGCGCTATCCGGAGTCGACCCCGAGCCCCGCTGCTGGAGAGAGATGATGTCCTGGACTAC	60
Db	ATGAGCGCTATCCGGAGTCGACCCCGAGCCCCGCTGCTGGAGAGAGATGATGTCCTGGACTAC	220
Qy	TACGGAGATCTGTCGCTTCAACCGTATGTTTCGAGGTGTGGAGCGAGCAACTGACCCGAGTGC	120
Db	TACGGAGATCTGTCGCTTCAACCGTATGTTTCGAGGTGTGGAGCGAGCAACTGACCCGAGTGC	280
Qy	GAGCTGAGACTCTCTGGCCCTTTCCTGCTGAGATGAGGCTCTCTGGAGCGCGCGGAGGCTTAAGCC	180
Db	GAGCTGAGACTCTCTGGCCCTTTCCTGCTGAGATGAGGCTCTCTGGAGCGCGCGGAGGCTTAAGCC	340
Qy	CGAGCCCGGAGCGGAGCTTAAGGCTCTCTGCTGAGAGCTGAGAGCGCCCGCGGAGCATGTGGCGAG	240
Db	CGAGCCCGGAGCGGAGCTTAAGGCTCTCTGCTGAGAGCTGAGAGCGCCCGCGGAGCATGTGGCGAG	400



QY	241	AGCAACCTGCGCTGCTGGGGCAAACTCTGCGGATGCTGACCGGACAGACCTGCTGCCG	300
Db	401	AGCAACCTGCGCTGCTGGGGCAAACTCTGCGGATGCTGACCGGACAGACCTGCTGCCG	460
QY	301	CACCTGGCGCGCAAGCGGCGCCGCGCAGTGTCTCCAGAAAGCTATATGACATCTCC	360
Db	461	CACCTGGCGCGCAAGCGGCGCCGCGCAGTGTCTCCAGAAAGCTATATGACATCTCC	520
QY	361	AGCTTTTCAAAAGAGACAGAGGGTATGCTGCTGCGCGCTGCGGACATGACAGTTTCTGA	420
Db	521	AGCTTTTCAAAAGAGACAGAGGGTATGCTGCTGCGCGCTGCGGACATGACAGTTTCTGA	580
QY	421	AATTCTCAGCAGAGGTTCAGTGGAGACAGGCTCCCGCCCAACCAAGCGGAGCGGCGAGT	480
Db	581	AATTCTCAGCAGAGGTTCAGTGGAGACAGGCTCCCGCCCAACCAAGCGGAGCGGCGAGT	640
QY	481	CGGGGCGCGGCCAGATGTGTGTCCAGACGCGCGCGAGAGGSGGCCCAAGCCGACCCGAG	540
Db	641	CGGGGCGCGGCCAGATGTGTGTCCAGACGCGCGCGAGAGGSGGCCCAAGCCGACCCGAG	700
QY	541	CAGCAGTCAGAGCCCGCGCAGACCTTCCCTGTGAAGGCAAGTGAACCTGTGACATCCGGCTC	600
Db	701	CAGCAGTCAGAGCCCGCGCAGACCTTCCCTGTGAAGGCAAGTGAACCTGTGACATCCGGCTC	760
QY	601	CGGGTTCGAGCAGAGTATCTGCGAGATGGGCGCAGCCTTGAGACAGGCGCTGACATCCCGG	660
Db	761	CGGGTTCGAGCAGAGTATCTGCGAGATGGGCGCAGCCTTGAGACAGGCGCTGACATCCCGG	820
QY	661	CGGCCCCAGCGCGCTGGCGCGGCGAGCTGGAAGTGTGTTGGGAGGCGCAACGCAAGTGTGCGC	720
Db	821	CGGCCCCAGCGCGCTGGCGCGGCGAGCTGGAAGTGTGTTGGGAGGCGCAACGCAAGTGTGCGC	880
QY	721	TCAAGGAGCCTGGGCGCTGTGTGTTGTGACATCAAGTTCAGAGCTCTCCATCTGAC	780
Db	881	TCAAGGAGCCTGGGCGCTGTGTGTTGTGACATCAAGTTCAGAGCTCTCCATCTGAC	940
QY	781	GCTTCTTGGGGGCGACTACCTGAGTGGCGCGCTGTCGACAGGCCCTGCGGAGCGTGTCTCG	840
Db	941	GCTTCTTGGGGGCGACTACCTGAGTGGCGCGCTGTCGACAGGCCCTGCGGAGCGTGTCTCG	1000
QY	841	ACTGAGGCGCTTCGCGAGGCGTGTGGGCGGGAGGCGTGTTCGCTGCTGATGAT	900
Db	1001	ACTGAGGCGCTTCGCGAGGCGTGTGGGCGGGAGGCGTGTTCGCTGCTGATGAT	1060
QY	901	GAGGCTGAC 909	
Db	1061	GAGGCTGAC 1069	
RESULT 8			
AAA95790			
ID	AAA95790 standard; cDNA, 2045 BP.		
XX	AAA95790;		
XX	28-FEB-2001 (first entry)		
DE	Apoptosis related gene 1 clone HLDK36.		
KM	Cytostatic; antiinflammatory; immunosuppressive; antisclerotic; cardiant;		
KM	virucidal; anti-AIDS; vasotropic; anti-ischaemic; antiparkinsonian; ss;		
KM	anti-12lzheimer; gene therapy; human; apoptosis; fusion protein; cancer;		
KM	colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;		
KM	autoimmune disorder; multiple sclerosis; viral infection.		
OS	Homo sapiens.		
XX	W0200056752-A2.		
XX	28-SEP-2000.		
PD	15-MAR-2000; 2000WO-US006642.		
XX	PF		

XX 24-MAR-1999; 99US-0126018P.  
PR 17-JUN-1999; 99US-0139638P.  
PR 18-AUG-1999; 99US-0149449P.  
XX XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, N1 J, Young PA;  
DR WPI; 2000-587660/55.  
XX P-PSDB; AAB15551.  
PT Nucleic acids encoding human apoptosis associated protein, useful for then  
PT prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's  
PT disease, inflammation and ischemic injury.  
XX  
PS Claim 1; Page 244-245; 273pp; English.  
XX  
XX The invention relates to the isolation of genes encoding 9 human  
CC apoptosis-related proteins. The nucleotide sequences AA95790-A95798  
CC encode the human apoptosis related proteins AAB15551-B15559. The genes  
CC can be used to generate fusion proteins by linking to the gene for the  
CC human immunoglobulin G Fc (IgG Fc) portion (AA95799) for increasing the  
CC stability of the fusion protein as compared to the human protein only.  
CC The gene and encoded protein may be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate apoptosis associated  
CC protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,  
CC melanomas and lymphomas), inflammation, autoimmune disorders (e.g.  
CC multiple sclerosis) and viral infections (e.g. herpes)  
XX  
XX Sequence 2045 BP; 457 A; 620 C; 604 G; 364 T; 0 U; 0 Other;

Query Match	Best Local Similarity	99.8%; 99.9%;	Score 907.4; 99.9%;	DB 3; 17;	Length 2045;				
Matches	908;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0
Qy	1	ATGCGCTATCCGGGTGCA	CCCCCGGCCCCGCTGGGAGAGATGAGTGCCTTGAAC	TAC	60				
Db	121	ATGGCGCTATCCGGGTGCA	CCCCCGGCCCCGCTGGGAGAGATGAGTGCCTTGAAC	TAC	180				
Qy	61	TACGGGATGCTATCCGCTTCA	CCGTATGTTTCAGAGTGTGTGGGCGGGGCACTGACCCGATGC		120				
Db	181	TACGGGATGCTATCCGCTTCA	CCGTATGTTTCAGAGTGTGTGGGCGGGGCAACTGACCCGATGC		240				
Qy	121	GAGCTGGAAGCTCTGTGGCTT	CTGTCTGTGATAGAGCTCTGTGGCGCGCGGAGGCTTAGCC		180				
Db	241	GAGCTGGAAGCTCTGTGGCTT	CTGTCTGTGATAGAGCTCTGTGGCGCGCGGAGGCTTAGCC		300				
Qy	181	CGGGCCCGCAGCGGCTTAGAGCT	CTCTGTGTGAGCTGAGCGCGCGGCGAGTGGCGGCGAG		240				
Db	301	CGGGCCCGCAGCGGCTTAGAGCT	CTCTGTGTGAGCTGAGCGCGCGGCGAGTGGCGGCGAG		360				
Qy	241	AGGAACCTGCGGCTCTATGGGCGA	ACTCCTGGGCGGTGTGGCCCGGCGACGACTTGGCGCG		300				
Db	361	AGGAACCTGCGGCTCTATGGGCGA	ACTCCTGGGCGGTGTGGCCCGGCGACGACTTGGCGCG		420				
Qy	301	CACTTGCGCGGAGAGCGGCGCGG	CGAGTGTCTTCAGAGGCTTAGCTTAGCACTCC		360				
Db	421	CACTTGCGCGGAGAGCGGCGCGG	CGAGTGTCTTCAGAGGCTTAGCTTAGCACTCC		480				
Qy	361	AGCTCTTCAAGAGAGACAGAGG	GTAGCTGTCCGTGCGGATGACAGTTCGCA		420				
Db	481	AGCTCTTCAAGAGAGACAGAGG	GTAGCTGTCCGTGCGGATGACAGTTCGCA		540				
Qy	421	AATTTTCAGAGAGGTGCA	TGGGAGACAGGCTCCCCCGCAACCAAGCGGAGCGCGGAGT		480				
Db	541	AATTTTCAGAGAGGTGCA	TGGGAGACAGGCTCCCCCGCAACCAAGCGGAGCGCGGAGT		600				
Qy	481	CGGGGCGGGCCCA	GTGTGTGTGCGAGACGCGGCGGAGAGGGGCCCAACCGCAG		540				
Db	601	CGGGGCGGGCCCA	GTGTGTGTGCGAGACGCGGCGGAGAGGGGCCCAACCGCAG		660				
Qy	541	CAGCAGTCAGAGCCCGCAGAC	CTTCTCTTGAAAGCAAGTGA	CTGTGACATCGGCTC	600				



Db 661 CAGAGTCAGAGCCCGCCAGACTTCTCTGAAGGCAAGTGAAGTGAATCCGAGTCC 720  
Qy 601 CGGGTTCCAGAGAGTACTGCGAGATGAGCCAGCTTGGAGAGAGGGTGGCATCCCGG 660  
Db 721 CGGGTTCCAGAGAGTACTGCGAGATGAGCCAGCTTGGAGAGAGGGTGGCATCCCGG 780  
Qy 661 CGGGCCCAAGGCGCTGGCGGAGCTGAGACGTGTTGGGCAAGGCCAGAGTGTGGGC 720  
Db 781 CGGGCCCAAGGCGCTGGCGGAGCTGAGACGTGTTGGGCAAGGCCAGAGTGTGGGC 840  
Qy 721 TCAAGGAGCTGGGCTGTGTGTTGTGACATCAAGTTCTCAGAGCTTCTATCTGAGC 780  
Db 841 TCAAGGAGCTGGGCTGTGTGTTGTGACATCAAGTTCTCAGAGCTTCTATCTGAGC 900  
Qy 781 GCTTTCTGGGCGAGTACTGATGAGGCGCCCTGCTGCAAGCCCTGCGGGGCGTGTCCG 840  
Db 901 GCTTTCTGGGCGAGTACTGATGAGGCGCCCTGCTGCAAGCCCTGCGGGGCGTGTCCG 960  
Qy 841 ACTGAGGCGCTGGCGAGGCTGTGGGCGGAGGCGTGTCCCTGCTGAGTGTGAT 900  
Db 961 ACTGAGGCGCTGGCGAGGCTGTGGGCGGAGGCGTGTCCCTGCTGAGTGTGAT 1020  
Qy 901 GAGGCTGAC 909  
Db 1021 GAGGCTGAC 1029

RESULT 9  
AAH33283  
ID AAH33283 standard; cDNA; 2045 BP.  
XX  
AC AAH33283;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.  
XX  
DE Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KM colorectal carcinoma; 88.  
XX  
OS Homo sapiens.  
XX  
PV WO200122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-US026524.  
XX  
PR 29-SEP-1999; 99US-0157137P.  
PR 03-NOV-1999; 99US-0163280P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
DR WPI; 2001-233537/24.  
DR P-PSDB; AAG73852.  
XX  
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
XX useful for preventing, diagnosing and/or treating colorectal cancers.  
PS Claim 1; Page 2451; 9803bp; English.  
XX  
XX AAH32943 to AAH37195 and AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytosolic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to

CC supplement the patients own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922  
XX  
SQ Sequence 2045 BP; 457 A; 620 C; 604 G; 364 T; 0 U; 0 Other;

Query Match 99.8%; Score 907.4; DB 4; Length 2045;  
Best Local Similarity 99.9%; Pred. No. 4.6e-171;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGTATCCGGTCAACCCCGCCCGCTGGGAGAGATGATGCTTGAATAC 60  
Db 121 ATGGCGTATCCGGTCAACCCCGCCCGCTGGGAGAGATGATGCTTGAATAC 180  
Qy 61 TACGGGATGCTGTGCTTACCGTATGTTGAGGTGTGGGCGGCACTGACGAGTGC 120  
Db 181 TACGGGATGCTGTGCTTACCGTATGTTGAGGTGTGGGCGGCACTGACGAGTGC 240  
Qy 121 GAGCTGAGACTCTTGCCCTTCTGCTGATGAGGCTCTTGCGCGCCGAGAGCTTAAGC 180  
Db 241 GAGCTGAGACTCTTGCCCTTCTGCTGATGAGGCTCTTGCGCGCCGAGAGCTTAAGC 300  
Qy 181 CGGGCCCGAGCGGCTTGAAGCTCTGCTGATGAGGCTCTTGCGCGCCGAGAGCTTAAGC 240  
Db 301 CGGGCCCGAGCGGCTTGAAGCTCTGCTGATGAGGCTCTTGCGCGCCGAGAGCTTAAGC 360  
Qy 241 AGCAACCTGGGCTGCTGGGCGAATCCTGGGCGGCTGGGCGGCAAGCTGCTGCCG 300  
Db 361 AGCAACCTGGGCTGCTGGGCGAATCCTGGGCGGCTGGGCGGCAAGCTGCTGCCG 420  
Qy 301 CACTTGAGCGGCAAGCGGCGGCGAGTGTCTCCAGAAAGCTATAGTATGCACTTC 360  
Db 421 CACTTGAGCGGCAAGCGGCGGCGAGTGTCTCCAGAAAGCTATAGTATGCACTTC 480  
Qy 361 AGCTTTCAAGAGGACAGAGGATGCTGCGCTGCCCTTGAGCTCAAGCACTTCTGCA 420  
Db 481 AGCTTTCAAGAGGACAGAGGATGCTGCGCTGCCCTTGAGCTCAAGCACTTCTGCA 540  
Qy 421 AATTCTCAGCGAGGCTCACTGGGAGACAGGCTCCCCCAACCAAGCGGAGGGAGT 480  
Db 541 AATTCTCAGCGAGGCTCACTGGGAGACAGGCTCCCCCAACCAAGCGGAGGGAGT 600  
Qy 481 CGGGCCCGGCGGAGTGTGTGTCAGACGCGCGGAGAGGGGCCCAAGCCCAAGCCGAG 540  
Db 601 CGGGCCCGGCGGAGTGTGTGTCAGACGCGCGGAGAGGGGCCCAAGCCCAAGCCGAG 660  
Qy 541 CAGAGTCAAGAGCCCGGAGACTTCTCTGTAAGGCAAGTGAAGCTGTGACATCCGGCTC 600  
Db 661 CAGAGTCAAGAGCCCGGAGACTTCTCTGTAAGGCAAGTGAAGCTGTGACATCCGGCTC 720  
Qy 601 CGGGTTCCAGAGAGTACTGCGAGATGAGCCAGCTTGGAGAGAGGGTGGCATCCCGG 660  
Db 721 CGGGTTCCAGAGAGTACTGCGAGATGAGCCAGCTTGGAGAGAGGGTGGCATCCCGG 780  
Qy 661 CGGGCCCAAGGCGCTGGCGGAGCTGAGACGTGTTGGGCAAGGCCAGAGTGTGGGC 720  
Db 781 CGGGCCCAAGGCGCTGGCGGAGCTGAGACGTGTTGGGCAAGGCCAGAGTGTGGGC 840  
Qy 721 TCAAGGAGCTGGGCTGTGTGTTGTGACATCAAGTTCTCAGAGCTTCTATCTGAGC 780  
Db 841 TCAAGGAGCTGGGCTGTGTGTTGTGACATCAAGTTCTCAGAGCTTCTATCTGAGC 900  
Qy 781 GCTTTCTGGGCGAGTACTGATGAGGCGCCCTGCTGCAAGCCCTGCGGGGCGTGTCCG 840  
Db 901 GCTTTCTGGGCGAGTACTGATGAGGCGCCCTGCTGCAAGCCCTGCGGGGCGTGTCCG 960  
Qy 841 ACTGAGGCGCTGGAGGCTGTGGGCGGAGGCGTGTCCCTGCTGAGTGTGAT 900

Db 961 ACTGAGCCCTTCGAGAGGCTGTGGCCCGGAGGCTGTGCTGTGTCAGTGGAT 1020  
QY 901 GAGGCTGAC 909  
Db 1021 GAGGCTGAC 1029

RESULT 10  
AAFI8296  
ID AAFI8296 standard; DNA; 2044 BP.  
XX  
AC AAFI8296;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Lung cancer associated polynucleotide sequence SEQ ID 315.  
XX  
KW Human; lung cancer associated protein; neuroprotective; cytostatic;  
KW cardiostatic; immunomodulatory; muscular active; vulnerary;  
KW gastrointestinal; nephrotoxic; antiinfective; gynecological;  
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
KW proliferative disorder; wound healing; infectious disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO20005180-A2.  
XX  
PD 21-SEP-2000.  
XX  
PE 08-MAR-2000; 2000WO-US005918.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PA (ROSE/) ROSEN C A.  
XX  
PI Ruben SM;  
XX  
DR WPI; 2000-587514/55.  
DR P-PSDB; AAB58420.  
XX  
PT Lung cancer associated gene sequences, referred to as lung cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as lung cancer.  
XX  
PS Claim 1; Page 772-773; 1425bp; English.

Polynucleotide sequences AAFI7982 - AAFI8424 encode human lung cancer  
associated proteins represented in AAB58106 - AAB58548. Lung cancer  
associated proteins and polynucleotide sequences, their agonists, and  
antagonists may have neuroprotective; cytostatic; cardiostatic;  
immunomodulatory; muscular active general; vulnerary; gastrointestinal  
activity; nephrotoxic; antiinfective; gynecological; or antibacterial  
activity. The invention also includes antibodies specific for the protein  
or polynucleotide sequences. The lung cancer associated polynucleotide  
sequences may be used for detection of lung cancer, chromosome  
identification, as chromosome markers, and for numerous other diagnostic  
or research purposes. The proteins may be used to treat disorders such as  
neural, immune, muscular, reproductive, gastrointestinal, pulmonary,  
cardiovascular, renal, and proliferative disorders. The proteins may also  
be used in the treatment of wounds and infectious diseases.  
Polynucleotide sequences AAFI8425 - AAFI8433 and peptide AAB58549 are  
used in the course of the invention for the identification and  
characterisation of the polynucleotide and protein sequences

Sequence 2044 BP; 457 A; 620 C; 603 G; 364 T; 0 U; 0 Other;  
XX  
XX

Query Match 98.5%; Score 895.4; DB 3; Length 2044;  
Best Local Similarity 99.8%; Pred.No. 1.1e-168;  
Matches 907; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 ATGGCGTATCCGGGTGACCCCGGCGGCTGTGGAGAGAGTGTGCTGACTTAC 60

Db 121 ATGGCGTATCCGGGTGACCCCGGCGGCTGTGGAGAGAGTGTGCTGACTTAC 180  
QY 61 TACGGATGTGTGCTTACCGATGTGTCAGAGGTGAGGCGGCACTGACGAGTGC 120  
Db 181 TACGGATGTGTGCTTACCGATGTGTCAGAGGTGAGGCGGCACTGACGAGTGC 240  
QY 121 GAGCTGAGCTCTTGAGCTTTCTGTGATGAGGCTCTTGAGGCGGCGGAGGCTTAC 180  
Db 241 GAGCTGAGCTCTTGAGCTTTCTGTGATGAGGCTCTTGAGGCGGCGGAGGCTTAC 300  
QY 181 CGGGCCCCAGCGGCTTGAAGCTCTTGCTGAGAGCTGAGCGCCGCGGCGAGTGCAG 240  
Db 301 CGGGCCCCAGCGGCTTGAAGCTCTTGCTGAGAGCTGAGCGCCGCGGCGAGTGCAG 360  
QY 241 AGCAACCTGCGGCTGCTGGGCACTCTGAGCGGCTGAGCGGCGGCACTGCTGCG 300  
Db 361 AGCAACCTGCGGCTGCTGGGCACTCTGAGCGGCTGAGCGGCGGCACTGCTGCG 420  
QY 301 CACCTGCGCGCAAGCGGCGCGGCGAGTGTCTCAGAGAGCTATAGCTATGCGACCTCC 360  
Db 421 CACCTGCGCGCAAGCGGCGCGGCGAGTGTCTCAGAGAGCTATAGCTATGCGACCTCC 480  
QY 361 AGCTTTTAAAGAGAGACAGAGGTAAGTCTGCGGCTGCGGAGTCAAGATTCTGCA 420  
Db 481 AGCTTTTAAAGAGAGACAGAGGTAAGTCTGCGGCTGCGGAGTCAAGATTCTGCA 540  
QY 421 AATTCTGAGAGGCTGATGAGAGACAGGCTCCCGGCAACCAAGCGGCAAGCGGAGT 480  
Db 541 AATTCTGAGAGGCTGATGAGAGACAGGCTCCCGGCAACCAAGCGGCAAGCGGAGT 600  
QY 481 CGGGGCGGCGCAAGTGTGTGTCAGACGCGCGGCGAGAGGCGGCGGCAAGCGGCGAG 540  
Db 601 CGGGGCGGCGCAAGTGTGTGTCAGACGCGCGGCGAGAGGCGGCGGCAAGCGGCGAG 660  
QY 541 CAGCAGTCAAGAGCCCGGCAAGCTTCTGTAAGGCAAGTGAAGTGTGATCTCGGCTC 600  
Db 661 CAGCAGTCAAGAGCCCGGCAAGCTTCTGTAAGGCAAGTGAAGTGTGATCTCGGCTC 720  
QY 601 CGGGTTGAGAGAGTCTGAGAGATGAGGCGGCGGCTTGAAGAGAGGCGGCTGCA 660  
Db 721 CGGGTTGAGAGAGTCTGAGAGATGAGGCGGCGGCTTGAAGAGAGGCGGCTGCA 780  
QY 721 TCAAGGAGCTGAGGCTGTGTGTTTGTGATCAAGTTCTCAGAGCTCTCTATCTGAC 780  
Db 841 TCAAGGAGCTGAGGCTGTGTGTTTGTGATCAAGTTCTCAGAGCTCTCTATCTGAC 900  
QY 781 GCTTCTGAGGCGAGCTGAGAGGCGGCGGCTGAGAGGCGGCGGAGGCTGCTG 840  
Db 901 GCTTCTGAGGCGAGCTGAGAGGCGGCGGCTGAGAGGCGGCGGAGGCTGCTG 959  
QY 841 ACTGAGCGCTGTCAGAGGCTGTGAGCGGCGGAGGCTTGTGCTGTGATGTGAGAT 900  
Db 960 ACTGAGCGCTGTCAGAGGCTGTGAGCGGCGGAGGCTTGTGCTGTGATGTGAGAT 1019  
QY 901 GAGGCTGAC 909  
Db 1020 GAGGCTGAC 1028

RESULT 11  
ABL39692  
ID ABL39692 standard; cDNA; 1084 BP.  
XX  
AC ABL39692;  
XX  
DT 10-MAY-2002 (first entry)  
XX  
DE Human NS cDNA sequence SEQ ID NO:2.





PD 18-OCT-2001.  
 XX 29-WAR-2001; 2001WO-US010485.  
 PF 06-APR-2000; 2000US-0195604P.  
 PR (GENY ) GENETICS INST INC.  
 XX  
 PA  
 PI Wong GG, Clark HP, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
 PI Gulukota K, Graham JR;  
 DR WPI; 2002-010900/01.  
 PT New polynucleotides encoding secreted proteins useful for treating e.g.  
 PT asthma, HIV and Crohn's disease.  
 XX  
 XX  
 XX Claim 1; Page 280; 391p; English.  
 CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides a  
 CC method for producing proteins from these polynucleotide sequences. The  
 CC proteins are useful for identifying compounds that modulate their  
 CC activity and production, and the cell is also useful for identifying  
 CC compounds that modulate expression of the polynucleotide sequences  
 CC encoding the secreted proteins. The sequences of the invention are useful  
 CC for treating diseases such as hyperproliferative disorders (e.g. cancer),  
 CC immune deficiency disorders (e.g. severe combined immunodeficiency  
 CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders  
 CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and  
 CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of  
 CC the invention are also useful in gene therapy. AAS62214-AAS62838  
 CC represent the cDNA sequences of the invention that encode for novel human  
 CC secreted proteins  
 XX  
 SQ Sequence 1966 BP; 356 A; 618 C; 614 G; 378 T; 0 U; 0 Other;

Query Match 87.9%; Score 799.4; DB 6; Length 1966;  
 Best Local Similarity 90.2%; Pred. No. 1.3e-149;  
 Matches 908; Conservative 0; Mismatches 1; Indels 99; Gaps 1;

QY 1 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGATGAGTCCCTGAGCTAC 60  
 DB 50 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGATGAGTCCCTGAGCTAC 109  
 DB 61 TACGGGATCTCTGCTTACCGTATGTTGAGGTGGGCGGCACTGACCGAGTGC 120  
 DB 110 TACGGGATCTCTGCTTACCGTATGTTGAGGTGGGCGGCACTGACCGAGTGC 169  
 QY 121 GAGCTGAGGCTCTGGGCTTTTGGCGATGAGGCTCGGCGCGCGGAGAGGCTTACGC 180  
 DB 170 GAGCTGAGGCTCTGGGCTTTTGGCGATGAGGCTCGGCGCGCGGAGAGGCTTACGC 229  
 QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGCGAGTGGCGGAG 240  
 DB 220 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGCGAGTGGCGGAG 289  
 QY 241 AGCAACCTGCGGCTGCTGGGGCACTCTGCGCGTGTGGCGCGGCACTGCTGCGCG 300  
 DB 290 AGCAACCTGCGGCTGCTGGGGCACTCTGCGCGTGTGGCGCGGCACTGCTGCGCG 349  
 QY 301 CACCTGGCGGCAAGGCGGCGCGGCGGCGAGTGTCCGAGAGCGGTATGATGGACCTGC 360  
 DB 350 CACCTGGCGGCAAGGCGGCGGCGGCGGCGGCGAGTGTCCGAGAGCGGTATGATGGACCTGC 409  
 QY 361 AGCTCTTCAAGAGGACAGAGGGTATGCTGCGTGGCGCTGCGGCACTGAGCACTTCTGCA 420  
 DB 410 AGCTCTTCAAGAGGACAGAGGGTATGCTGCGTGGCGCTGCGGCACTGAGCACTTCTGCA 469  
 QY 421 AATTCTCAGCAGGCTATGTTGGAGAGAGGCTCCCCCAACCAAGGCGGCGGAGT 480  
 DB 470 AATTCTCAGCAGGCTATGTTGGAGAGAGGCTCCCCCAACCAAGGCGGCGGAGT 529

QY 481 CGGGCCCGGCGGCTGAGTGTGTCGAGACGCGGCGGAGAGGAGGCGCCAGCCGCA 540  
 DB 530 CGGGCCCGGCGGCTGAGTGTGTCGAGACGCGGCGGAGAGGAGGCGCCAGCCGCA 589  
 QY 541 CAGCAGTCAAGAGCCCGGCGGCACTCTTCTGTAAGGCAAGTGAACCTG----- 587  
 DB 590 CAGCAGTCAAGAGCCCGGCGGCACTCTTCTGTAAGGCAAGTGAACCTGCTGTACAGA 649  
 QY 588 ----- 587  
 DB 650 AGCAGGTCGACGATCTGCTTCTGTGAGGACCTCCGGAAGCTTCAATTAGTGTGAA 709  
 QY 588 -----TGACATCCGCGCTCCGCGTTTGAAGAGTACTGCG 622  
 DB 710 GGGCAAGGAGGAGAGGCTTGTCAATGACATCCGCGCTCCGCGTTGAGCAGATCTGCG 769  
 QY 623 AGCAGGTCGACGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 682  
 DB 770 AGCAGGTCGACGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 829  
 QY 683 AGCTGAGGTCGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 742  
 DB 830 AGCTGAGGTCGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 889  
 QY 743 TTTGTGATCAATGATCTCAGAGCTCTCTATCTGAGAGGCTTCTGAGGAGGAGGAGGAG 802  
 DB 890 TTTGTGATCAATGATCTCAGAGCTCTCTATCTGAGAGGCTTCTGAGGAGGAGGAGGAG 949  
 QY 803 GTGGCGGCTCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 862  
 DB 950 GTGGCGGCTCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1009  
 QY 863 TGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 909  
 DB 1010 TGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1056

RESULT 14  
 AAH99646  
 ID AAH99646 standard; cDNA, 1570 BP.  
 XX  
 XX AAH99646;  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human protein encoding cDNA sequence SEQ ID NO:481.  
 XX  
 KW Human; cancer; HIV infection; human immunodeficiency virus;  
 KW antineoplastic; antineoplastic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiac; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimetabolite; cardiovascular; anaemia;  
 KW antiaggregant; haemostatic; antidiabetic; osteoporosis; eczema;  
 KW dermatological; antiallergic; antiaesthetic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153455-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 22-DEC-2000; 2000WO-US035017.  
 XX  
 XX 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.





CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification

XX Sequence 1067 BP; 191 A; 349 C; 328 G; 199 T; 0 U; 0 Other;

Query Match 59.5%; Score 541; DB 4; Length 1067;

Best Local Similarity 95.8%; Pred. No. 3e-98;

Matches 572; Conservative 0; Mismatches 10; Indels 15; Gaps 1;

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QY 1 ATGGCGCTATCCGGGTCGACCCCGGCCGCTGCTGGAGAGAGATAGTCCCTGAGCTAC 60
DB 151 ATGGCGCTATCCGGGTCGACCCCGGCCGCTGCTGGAGAGAGATAGTCCCTGAGCTAC 210
QY 61 TACGGGATGCTGCTGCTTCACTGATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC 120
DB 211 TACGGGATGCTGCTGCTTCACTGATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC 270
QY 121 GAGCTGAGAGCTCTGGGCTTTTGTGCTGATGAGGCTCTGGGCGCGCGGAGGCTTAGCC 180
DB 271 GAGCTGAGAGCTCTGGGCTTTTGTGCTGATGAGGCTCTGGGCGCGCGGAGGCTTAGCC 330
QY 181 CGGGCCCGCAGCGGCTAGAGCTCTGTGCTGAGCTGAGCGCGCGCGGCACTGCGCGAG 240
DB 331 CGGGCCCGCAGCGGCTTAGAGCTCTGTGCTGAGCTGAGCGCGCGCGGCACTGCGCGAG 390
QY 241 AGCAACTGCGGCTGTGGGGCAACTCTGTGCGGTGCTGCGCCCGCACTGCTGCGG 300
DB 391 AGCAACTGCGGCTGTGGGGCAACTCTGTGCGGTGCTGCGCCCGCACTGCTGCGG 450
QY 301 CACCTGGGCGGCAAGGGCGCGCGCGGCAAGTCTCCAGAAAGCTATAGCTATAGGCACTCC 360
DB 451 CACCTGGGCGGCAAGGGCGCGCGCGGCAAGTCTCCAGAAAGCTATAGCTATAGGCACTCC 510
QY 361 AGCTCTTCAAGAGAGCAGAGGGTAGCTCCGTCGCGCTCGGCACTCAAGCAGTTCTGCA 420
DB 511 AGCTCTTCAAGAGAGCAGAGGGTAGCTCCGTCGCGCTCGGCACTCAAGCAGTTCTGCA 570
QY 421 AATTCTCAGCAGGCTCAGTGGAGAGGCTCCCCCAACCAAGCGGCGAGCGGAGT 480
DB 571 AATTCTCAGCAG-----GGCTCCCCCAACCAAGCGGCGAGCGGAGT 615
QY 481 CGGGGCGGGCCAGTGTGTGTGTCAGACGCGCGGCGGAGAGGGGCGCCAGCCGACCCGAG 540
DB 616 CGGGGCGGGCCAGTGTGTGTGTCAGACGCGCGGCGGAGAGGGGCGCCAGCCGACCCGAG 675
QY 541 CAGCAGTCAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAACCTGTGACATCCGG 597
DB 676 CAGCAGTCAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAACCAACCAACTCG 732
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Search completed: February 12, 2005, 11:11:16  
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 12:44:53 / Search time 2935 Seconds  
(without alignments)  
15007.084 Million cell updates/sec

Title: US-10-030-271-1

Perfect score: 909  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
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13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	909	6	BD093311 Apoptosis
2	909	100.0	1883	6	BD093312 Apoptosis
3	909	100.0	1883	6	BD093312 Apoptosis
4	858	94.4	981	6	CQ119642 Sequence
5	858	94.4	981	6	AF443591 Homo sapi
6	858	94.4	1230	6	AX322754 Sequence
7	858	94.4	1230	6	AX322754 Sequence
8	756	83.2	1951	9	BC027930 Homo sapi
9	603	66.3	981	9	AF457575 Homo sapi
10	411	45.2	2012	9	AY125488 Homo sapi
11	383	42.1	2005	9	BC013372 Homo sapi
12	334	36.7	626	6	BD149917 Primer fo
13	334	36.7	626	6	AX869855 Sequence
14	322	35.4	1659	9	AX130203 Homo sapi
15	321	35.3	95663	9	AC010247 Homo sapi
16	281	30.9	1067	6	AR339362 Sequence
17	277	30.5	111084	9	AC006486 Homo sapi
18	252	27.7	303	6	AX431298 Sequence
19	187	20.6	1084	6	AX364851 Sequence

20	187	20.6	1106	6	AX364852 Sequence
21	177	19.5	603	6	AX136449 Sequence
22	177	19.5	603	6	BD123689 Secretory
23	144	15.8	167108	2	AC068283 Homo sapi
24	56	6.2	993	10	AF457576 Mus muscu
25	56	6.2	993	10	AF457576 Mus muscu
26	56	6.2	1540	10	AF543541 Mus muscu
27	56	6.2	1540	10	BC037043 Mus muscu
28	27	6.2	190669	2	AC120393 Mus muscu
29	27	6.2	226909	5	AC079949 Mus muscu
30	23	2.5	1821	5	BC075935 Mus muscu
31	23	2.5	125523	5	BC248385 Zebrafish
32	22	2.4	838	6	CQ411697 Sequence
33	22	2.4	141272	9	AP001976 Homo sapi
34	21	2.3	154937	2	AP002382 Homo sapi
35	21	2.3	323	6	CQ406469 Sequence
36	21	2.3	1553	8	AK060228 Oryza sat
37	21	2.3	66135	1	AP006840_35 Continuation (36 o
38	21	2.3	110000	1	AP006840_00 Continuation (10 o
39	21	2.3	110000	1	AP006840_09 Continuation (10 o
40	21	2.3	110000	1	AP006840_12 Continuation (13 o
41	21	2.3	110000	1	AP006840_16 Continuation (17 o
42	21	2.3	110000	1	AP006840_18 Continuation (19 o
43	21	2.3	110000	1	AP006840_21 Continuation (22 o
44	21	2.3	110000	1	AP006840_21 Continuation (22 o
45	21	2.3	110000	1	AP006840_27 Continuation (28 o
46	21	2.3	110000	1	AP006840_31 Continuation (34 o
47	21	2.3	11841	8	AP005190 Oryza sat
48	21	2.3	164263	8	AP005515 Oryza sat
49	21	2.3	250084	2	AC117545 Mus muscu
50	21	2.3	347786	1	BX640438 Bordetell
51	21	2.3	347786	1	BX640424 Bordetell
52	21	2.3	349146	1	BD093317 Apoptosis
53	20	2.2	23	6	BD093320 Apoptosis
54	20	2.2	547	11	BV043023 S212P6545
55	20	2.2	614	8	AK072505 Oryza sat
56	20	2.2	945	10	RATRA15X Mus muscu
57	20	2.2	1083	10	MUSHROX AK104164 Oryza sat
58	20	2.2	1148	8	AK060329 Oryza sat
59	20	2.2	1166	8	AK071358 Oryza sat
60	20	2.2	1117	8	AK071358 Oryza sat
61	20	2.2	3880	1	AVIHUPABYC X63650 A.vinelandi
62	20	2.2	6008	1	AVDHODNA AE004546 Pseudomon
63	20	2.2	10417	1	AE004546 Pseudomon
64	20	2.2	13914	1	AVIHOXHP L23970 Azotobacter
65	20	2.2	90976	2	AC147595 Mus muscu
66	20	2.2	110000	1	AE017282_31 Continuation (32 o
67	20	2.2	110000	2	BX255276_11 Continuation (12 o
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69	20	2.2	110892	9	AP000633 Homo sapi
70	20	2.2	125217	8	AC097627 Genomic s
71	20	2.2	14457	2	AP004631 Oryza sat
72	20	2.2	148947	8	AP004397 Oryza sat
73	20	2.2	156933	8	AC125411 Genomic s
74	20	2.2	161424	8	AC1018367 Homo sapi
75	20	2.2	162941	2	AF485811 Oryza sat
76	20	2.2	162945	2	AC015647 Homo sapi
77	20	2.2	162945	2	AC015647 Homo sapi
78	20	2.2	166042	9	AP006289 Homo sapi
79	20	2.2	173877	10	AC099624 Mus muscu
80	20	2.2	182619	1	AC127591 Mus muscu
81	20	2.2	189050	1	AL646069 Ralstonia
82	20	2.2	192020	2	AC102311 Mus muscu
83	20	2.2	193777	10	AC104324 Mus muscu
84	20	2.2	202212	9	CNSO1RGF AL157957 Human chr
85	20	2.2	222830	2	AC134899 Mus muscu
86	20	2.2	229035	2	AC117925 Ratius no
87	20	2.2	230318	2	AC123468 Ratius no
88	20	2.2	234247	2	AC130866 Ratius no
89	20	2.2	251186	2	AC120750 Ratius no
90	20	2.2	25557	2	AC098609 Ratius no
91	20	2.2	258285	2	AC095235 Ratius no
92	20	2.2	270654	2	AC096084 Ratius no

C 93	20	2.2	277000	1	SC0939109	AL939109 Streptomy	C 166	19	2.1	102151	9	HS979N1	AL035659 Human DNA
C 94	20	2.2	300029	1	AE016787	AE016787 Pseudomon	C 167	19	2.1	105522	9	AC021080	AC021080 Homo sapi
C 95	20	2.2	301925	1	AP005046	AP005046 Streptomy	C 168	19	2.1	103480	2	AC007905	AC007905 Homo sapi
C 96	20	2.2	346259	1	BX640435	BX640435 Bordetell	C 169	19	2.1	110000	1	AP006618	AP006618_32
C 97	20	2.2	346287	1	BX640450	BX640450 Bordetell	C 170	19	2.1	110000	1	AY305378	AY305378_0
C 98	19	2.1	360	6	AX794353	AX794353 Sequence	C 171	19	2.1	110000	2	AC091343	AC091343_6
C 99	19	2.1	360	6	AX803613	AX803613 Sequence	C 172	19	2.1	110000	2	LMFLCHR25_02	LMFLCHR25_02
C 100	19	2.1	377	11	G48211	G48211 SHGC-60419	C 173	19	2.1	110000	2	LMFLCHR31_19	LMFLCHR31_19
C 101	19	2.1	553	10	AF299351	AF299351 Cavia por	C 174	19	2.1	110000	2	LMFLCHR36_32	LMFLCHR36_32
C 102	19	2.1	606	6	AX119213	AX119213 Sequence	C 175	19	2.1	110931	9	AC008512	AC008512
C 103	19	2.1	759	6	CO730798	CO730798 Sequence	C 176	19	2.1	111714	2	AL359432	AL359432
C 104	19	2.1	878	6	ARS22606	ARS22606 Sequence	C 177	19	2.1	112065	8	AC109596	AC109596
C 105	19	2.1	906	6	CQ769320	CQ769320 Sequence	C 178	19	2.1	114285	8	AP001870	AP001870
C 106	19	2.1	943	6	AX574584	AX574584 Sequence	C 179	19	2.1	122322	9	AC008850	AC008850
C 107	19	2.1	943	6	AY358178	AY358178 Homo sapi	C 180	19	2.1	132636	2	AC108369	AC108369 Homo sapi
C 108	19	2.1	988	6	ARS06943	ARS06943 Sequence	C 181	19	2.1	135983	2	AC134767	AC134767
C 109	19	2.1	1536	5	BC067160	BC067160 Dario rer	C 182	19	2.1	138009	2	CR759952	CR759952
C 110	19	2.1	1641	8	BC004932	BC004932 Homo sapi	C 183	19	2.1	138740	2	AC009113	AC009113
C 111	19	2.1	1660	8	AK069852	AK069852 Oryza sat	C 184	19	2.1	141320	2	AC017833	AC017833
C 112	19	2.1	1680	3	AY070936	AY070936 Drosophi1	C 185	19	2.1	146578	9	AC012468	AC012468
C 113	19	2.1	1870	3	AK024551	AK024551 Homo sapi	C 186	19	2.1	147651	8	AC099774	AC099774
C 114	19	2.1	1871	6	CO798278	CO798278 Sequence	C 187	19	2.1	148667	9	HS1018E9	HS1018E9
C 115	19	2.1	1871	6	AY676494	AY676494 Homo sapi	C 188	19	2.1	150184	2	AC134554	AC134554
C 116	19	2.1	1871	10	AB057765	AB057765 Mus muscu	C 189	19	2.1	151796	2	AC096995	AC096995
C 117	19	2.1	2089	9	HSN802333	HSN802333	C 190	19	2.1	152050	2	ML067213	ML067213
C 118	19	2.1	2225	5	AF014368	AF014368 Dario rer	C 191	19	2.1	152050	5	EX005316	EX005316
C 119	19	2.1	2247	5	AF128112	AF128112 Drosophi1	C 192	19	2.1	154333	5	AL157711	AL157711
C 120	19	2.1	2247	6	CO614409	CO614409 Sequence	C 193	19	2.1	154818	2	EX927374	EX927374
C 121	19	2.1	2317	5	AF014369	AF014369 Dario rer	C 194	19	2.1	156552	2	AP005004	AP005004
C 122	19	2.1	2403	5	AF014367	AF014367 Dario rer	C 195	19	2.1	156812	8	AC110724	AC110724
C 123	19	2.1	2528	6	BD237550	BD237550 Dario rer	C 196	19	2.1	159420	2	AC009017	AC009017
C 124	19	2.1	2528	6	BD237550	BD237550 Novel BAG	C 197	19	2.1	163377	9	AC087714	AC087714
C 125	19	2.1	2533	6	AR477557	AR477557 Sequence	C 198	19	2.1	163377	9	AC026409	AC026409
C 126	19	2.1	2533	6	AX794344	AX794344 Sequence	C 199	19	2.1	164737	2	AC118967	AC118967
C 127	19	2.1	2533	6	AX803611	AX803611 Sequence	C 200	19	2.1	165902	2	AC023721	AC023721
C 128	19	2.1	2534	6	BD237557	BD237557 Novel BAG	C 201	19	2.1	167213	2	AC146379	AC146379
C 129	19	2.1	2534	6	AR477564	AR477564 Sequence	C 202	19	2.1	167508	10	CR354750	CR354750
C 130	19	2.1	2534	9	AF071218	AF071218 Homo sapi	C 203	19	2.1	167962	2	AC073484	AC073484
C 131	19	2.1	2534	9	AF095193	AF095193 Homo sapi	C 204	19	2.1	168799	2	AC009531	AC009531
C 132	19	2.1	2536	6	CO729403	CO729403 Sequence	C 205	19	2.1	169091	2	AC025852	AC025852
C 133	19	2.1	2550	6	AF127139	AF127139 Homo sapi	C 206	19	2.1	170606	2	EX957335	EX957335
C 134	19	2.1	2586	9	BC006418	BC006418 Homo sapi	C 207	19	2.1	172427	5	AL923392	AL923392
C 135	19	2.1	2700	10	BC003913	BC003913 Mus muscu	C 208	19	2.1	172434	8	AC090486	AC090486
C 136	19	2.1	2739	6	AX654352	AX654352 Sequence	C 209	19	2.1	172435	2	AL159984	AL159984
C 137	19	2.1	3785	1	AF105060	AF105060 Riffia pa	C 210	19	2.1	175039	2	AC118633	AC118633
C 138	19	2.1	4688	1	RCNAHUP	RCNAHUP Rhodobacter	C 211	19	2.1	175039	9	AC092447	AC092447
C 139	19	2.1	4697	3	CELTRA1A	CELTRA1A Caenorhadi	C 212	19	2.1	175547	2	AC005826	AC005826
C 140	19	2.1	4756	6	CO574955	CO574955 Sequence	C 213	19	2.1	177750	9	AC005874	AC005874
C 141	19	2.1	4850	10	BC051383	BC051383 Mus muscu	C 214	19	2.1	177864	9	AF134471	AF134471
C 142	19	2.1	4856	10	BC052326	BC052326 Mus muscu	C 215	19	2.1	177883	2	AC046159	AC046159
C 143	19	2.1	5082	10	BC082331	BC082331 Mus muscu	C 216	19	2.1	178073	1	SC059046	SC059046
C 144	19	2.1	5268	6	CO614408	CO614408 Sequence	C 217	19	2.1	178239	3	AC009367	AC009367
C 145	19	2.1	5760	6	AX616761	AX616761 Sequence	C 218	19	2.1	180270	3	AC007923	AC007923
C 146	19	2.1	7781	1	AF298190	AF298190 Sinorhizo	C 219	19	2.1	180387	3	AC009378	AC009378
C 147	19	2.1	9937	1	AE004563	AE004563 Pseudomon	C 220	19	2.1	182312	2	AC087709	AC087709
C 148	19	2.1	11103	1	AE001944	AE001944 Pseudomon	C 221	19	2.1	182445	2	AC132717	AC132717
C 149	19	2.1	11974	1	AE007247	AE007247 Sinorhizo	C 222	19	2.1	184062	4	AC149232	AC149232
C 150	19	2.1	12753	1	AE007233	AE007233 Sinorhizo	C 223	19	2.1	184661	9	AC124156	AC124156
C 151	19	2.1	32492	10	MUSPACOL	MUSPACOL Mouse pro-a	C 224	19	2.1	185398	10	AC121926	AC121926
C 152	19	2.1	38516	1	AF540992	AF540992 Pseudomon	C 225	19	2.1	186495	2	AC147081	AC147081
C 153	19	2.1	44653	9	HS38085	HS38085 Human DNA	C 226	19	2.1	186632	10	AC140047	AC140047
C 154	19	2.1	51729	9	AC118276	AC118276 Homo sapi	C 227	19	2.1	187006	2	AC120295	AC120295
C 155	19	2.1	66696	9	AL359743	AL359743 Human DNA	C 228	19	2.1	188095	4	AC091505	AC091505
C 156	19	2.1	69348	2	AC020525	AC020525 Drosophi1	C 229	19	2.1	188389	2	AC024199	AC024199
C 157	19	2.1	72895	2	AC116400	AC116400 Mus muscu	C 230	19	2.1	189537	2	AC113444	AC113444
C 158	19	2.1	77740	1	AF540993	AF540993 Pseudomon	C 231	19	2.1	190287	2	AC134249	AC134249
C 159	19	2.1	79884	9	AC109440	AC109440 Homo sapi	C 232	19	2.1	191783	2	AC139604	AC139604
C 160	19	2.1	81931	10	AL611987	AL611987 Mouse DNA	C 233	19	2.1	191966	9	AC150280	AC150280
C 161	19	2.1	88588	9	AC010453	AC010453 Homo sapi	C 234	19	2.1	192203	3	AC034102	AC034102
C 162	19	2.1	90348	1	AF497482	AF497482 Micromono	C 235	19	2.1	194308	3	AC009377	AC009377
C 163	19	2.1	91468	2	AP002334	AP002334 Homo sapi	C 236	19	2.1	195964	2	AC018879	AC018879
C 164	19	2.1	95477	9	AC007076	AC007076 Homo sapi	C 237	19	2.1	196903	2	AC068424	AC068424
C 165	19	2.1	100976	9	HS1005F21	HS1005F21 Human DNA	C 238	19	2.1	199814	3	CEY47D3A	CEY47D3A

239	19	2.1	200109	9	CNS07EBZ	AL451071 Human chr	312	18	2.0	918	6	C0817218	C0817218 Sequence
240	19	2.1	201060	10	AL929382	AL929382 Mouse DNA	313	18	2.0	918	6	C0817221	C0817221 Sequence
241	19	2.1	202157	4	AC124907	AC124907 Equus cab	314	18	2.0	918	6	C0817223	C0817223 Sequence
242	19	2.1	204684	10	AC127581	AC127581 Mus muscu	315	18	2.0	1023	11	G10653	G10653 human STS C
243	19	2.1	207974	10	AL831771	AL831771 Mouse DNA	316	18	2.0	1023	8	AB107992	AB107992 Tricium
244	19	2.1	210886	2	AC017051	AC017051 Homo sapi	317	18	2.0	1032	4	AF497260	AF497260 Vombat
245	19	2.1	212030	2	AC019148	AC019148 Homo sapi	318	18	2.0	1056	6	AR156614	AR156614 Sequence
246	19	2.1	223040	2	AC128102	AC128102 Rattus no	319	18	2.0	1056	6	BS1749	BS1749 Xylitol deh
247	19	2.1	226416	10	AC092752	AC092752 Genomic B	320	18	2.0	1105	9	CR533526	CR533526 Homo sapi
248	19	2.1	227682	2	AC122603	AC122603 Rattus no	321	18	2.0	1179	6	C0801209	C0801209 Sequence
249	19	2.1	230263	2	AC111787	AC111787 Rattus no	322	18	2.0	1287	6	CQ736225	CQ736225 Sequence
250	19	2.1	230930	2	AC130854	AC130854 Rattus no	323	18	2.0	1314	6	BD269207	BD269207 Vaccine
251	19	2.1	232415	2	AC095640	AC095640 Rattus no	324	18	2.0	1314	6	AX028478	AX028478 Sequence
252	19	2.1	232945	2	AC103156	AC103156 Rattus no	325	18	2.0	1317	6	CQ717442	CQ717442 Sequence
253	19	2.1	234065	2	AC140765	AC140765 Rattus no	326	18	2.0	1328	9	AK057774	AK057774 Homo sapi
254	19	2.1	234950	2	AC094003	AC094003 Rattus no	327	18	2.0	1355	6	BS3699	BS3699 Human prote
255	19	2.1	236774	10	AC124516	AC124516 Mus muscu	328	18	2.0	1355	6	BD095394	BD095394 Human pro
256	19	2.1	237974	2	AC094771	AC094771 Rattus no	329	18	2.0	1360	9	BC000788	BC000788 Homo sapi
257	19	2.1	238367	2	AC094187	AC094187 Rattus no	330	18	2.0	1366	9	AK000578	AK000578 Homo sapi
258	19	2.1	238937	2	AC094926	AC094926 Rattus no	331	18	2.0	1400	9	BC006244	BC006244 Homo sapi
259	19	2.1	243661	5	CR392340	CR392340 Zebrafish	332	18	2.0	1409	6	AK025970	AK025970 Homo sapi
260	19	2.1	247887	2	AC110342	AC110342 Rattus no	333	18	2.0	1409	6	BD276508	BD276508 FULL-LENG
261	19	2.1	251533	2	AC125364	AC125364 Rattus no	334	18	2.0	1409	6	AK048072	AK048072 Sequence
262	19	2.1	251710	2	AC117065	AC117065 Rattus no	335	18	2.0	1422	6	CQ726719	CQ726719 Sequence
263	19	2.1	253184	2	AC137219	AC137219 Rattus no	336	18	2.0	1447	6	AX086256	AX086256 Sequence
264	19	2.1	253746	2	AC135747	AC135747 Rattus no	337	18	2.0	1473	3	AJ831833	AJ831833 Drosophill
265	19	2.1	256354	2	AC150070	AC150070 Gallus ga	338	18	2.0	1630	8	AK072181	AK072181 Oryza sat
266	19	2.1	257692	3	AE003517	AE003517 Drosophill	339	18	2.0	1767	9	AF007791	AF007791 Homo sapi
267	19	2.1	258193	10	AC101221	AC101221 Mus muscu	340	18	2.0	1815	8	AK105585	AK105585 Oryza sat
268	19	2.1	258786	2	AC125773	AC125773 Rattus no	341	18	2.0	1861	10	AY033912	AY033912 Mus muscu
269	19	2.1	258829	2	AC073771	AC073771 Mus muscu	342	18	2.0	1922	6	AX336103	AX336103 Sequence
270	19	2.1	260468	2	AC109419	AC109419 Rattus no	343	18	2.0	1922	6	AX336178	AX336178 Sequence
271	19	2.1	263399	2	AC111251	AC111251 Rattus no	344	18	2.0	1922	6	AX336456	AX336456 Sequence
272	19	2.1	269739	10	AC139108	AC139108 Mus muscu	345	18	2.0	1922	6	AX336717	AX336717 Sequence
273	19	2.1	274560	2	AC099390	AC099390 Rattus no	346	18	2.0	1922	6	AX337648	AX337648 Sequence
274	19	2.1	279011	9	AE006467	AE006467 Homo sapi	347	18	2.0	1922	6	AX337648	AX337648 Sequence
275	19	2.1	284913	2	AC129698	AC129698 Rattus no	348	18	2.0	1922	6	AX409454	AX409454 Sequence
276	19	2.1	291799	3	AE003489	AE003489 Drosophill	349	18	2.0	1944	9	HSM801815	HSM801815 Human (clon
277	19	2.1	292145	2	AC091459	AC091459 Mus muscu	350	18	2.0	1953	10	AF013145	AF013145 Rattus no
278	19	2.1	292900	2	AC097763	AC097763 Rattus no	351	18	2.0	2005	10	AF116896	AF116896 Rattus no
279	19	2.1	300029	8	AE017076	AE017076 Oryza sat	352	18	2.0	2015	10	BC078788	BC078788 Rattus no
280	19	2.1	302300	1	AP005034	AP005034 Streptomy	353	18	2.0	2098	5	BC076738	BC076738 Xenopus 1
281	19	2.1	303774	2	AC105878	AC105878 Rattus no	354	18	2.0	2192	10	AF233646	AF233646 Mus muscu
282	19	2.1	308050	1	SC0939124	SC0939124 Streptomy	355	18	2.0	2199	9	BC001522	BC001522 Homo sapi
283	19	2.1	314746	2	AC106421	AC106421 Rattus no	356	18	2.0	2283	10	BC026539	BC026539 Mus muscu
284	19	2.1	322635	2	AC095310	AC095310 Rattus no	357	18	2.0	2283	6	C0843341	C0843341 Sequence
285	19	2.1	323222	2	AC112459	AC112459 Rattus no	358	18	2.0	2283	9	AK124305	AK124305 Homo sapi
286	19	2.1	344805	1	BX640434	BX640434 Bordetell	359	18	2.0	2334	9	BC062549	BC062549 Homo sapi
287	19	2.1	348074	1	BX640449	BX640449 Bordetell	360	18	2.0	2395	1	AF123492	AF123492 Pseudomon
288	19	2.1	348134	1	BX640420	BX640420 Bordetell	361	18	2.0	2412	6	AX835205	AX835205 Sequence
289	19	2.1	348866	1	BX640426	BX640426 Bordetell	362	18	2.0	2412	9	AK098120	AK098120 Homo sapi
290	19	2.1	349008	1	BX640444	BX640444 Bordetell	363	18	2.0	2487	9	BC035506	BC035506 Homo sapi
291	18	2.0	142	6	AX927406	AX927406 Sequence	364	18	2.0	2569	9	HUMSCNA421	HUMSCNA421
292	18	2.0	142	6	AJ718774	AJ718774 Nicotiana	365	18	2.0	2745	9	AF301906	AF301906 Homo sapi
293	18	2.0	142	8	AJ718775	AJ718775 Nicotiana	366	18	2.0	2753	6	AX554768	AX554768 Sequence
294	18	2.0	204	4	CATPES03	M16667 Feline c-fe	367	18	2.0	2823	6	BD180452	BD180452 Highly th
295	18	2.0	251	11	BV168193	BV168193 sqmm7640	368	18	2.0	2906	9	AB188491	AB188491 Homo sapi
296	18	2.0	303	11	BV034559	BV034559 S212P6009	369	18	2.0	2946	14	FCGCAONC	FCGCAONC
297	18	2.0	324	6	CQ727703	CQ727703 Sequence	370	18	2.0	2977	9	AB032993	AB032993 Homo sapi
298	18	2.0	339	6	CQ734705	CQ734705 Sequence	371	18	2.0	2996	8	AK101081	AK101081 Oryza sat
299	18	2.0	397	6	AX918678	AX918678 Sequence	372	18	2.0	2997	6	AX960776	AX960776 Sequence
300	18	2.0	397	6	BD054211	BD054211 Sequence	373	18	2.0	3063	4	S80649	S80649 SP-B-pulmon
301	18	2.0	475	6	CQ739992	CQ739992 Sequence	374	18	2.0	3069	3	AF219383	AF219383 Drosophill
302	18	2.0	497	11	BV180580	BV180580 sqmm1017	375	18	2.0	3120	9	AB089939	AB089939 Homo sapi
303	18	2.0	500	4	AF201724	AF201724 Sus scrof	376	18	2.0	3175	10	MM062907	MM062907 Homo sapi
304	18	2.0	513	6	AX437028	AX437028 Sequence	377	18	2.0	3181	9	HSM806774	HSM806774 Homo sapi
305	18	2.0	612	11	GS5269	GS5269 SHGC-81470	378	18	2.0	3181	10	AF251347	AF251347 Mus muscu
306	18	2.0	618	6	AX432088	AX432088 Sequence	379	18	2.0	3257	9	HSM807947	HSM807947 Homo sapi
307	18	2.0	698	5	HS4316514	AJ316514 Homo sapi	380	18	2.0	3257	8	HSM807950	HSM807950 Homo sapi
308	18	2.0	706	5	AB098253	AB098253 Echis mul	381	18	2.0	3307	8	AF340030	AF340030 Apterigill
309	18	2.0	788	5	CR407323	CR407323 Gallus ga	382	18	2.0	3399	6	BD183250	BD183250 Walker fo
310	18	2.0	885	5	CR390901	CR390901 Gallus ga	383	18	2.0	3403	6	C0609945	C0609945 Sequence
311	18	2.0	894	5	AF071874	AF071874 Gallus ga	384	18	2.0	3468	9	HUMSCNA22	HUMSCNA22 Human type

385	18	2.0	3505	10	EC060248	BC060248 Mus muscu	458	18	2.0	102148	2	AP000597	AP000597 Homo sapi
386	18	2.0	3515	9	AK123604	AK123604 Homo sapi	459	18	2.0	103216	2	AL080251	AL080251 Human DNA
387	18	2.0	3539	9	LC0579911	AJ579911 Lotus cor	460	18	2.0	103636	8	AP004940	AP004940 Lotus cor
388	18	2.0	3777	10	AK173086	AK173086 Mus muscu	461	18	2.0	105940	9	AC010606	AC010606 Homo sapi
389	18	2.0	3994	10	AL626766	AL626766 Mouse DNA	462	18	2.0	107655	2	AC084840	AC084840 Homo sapi
390	18	2.0	4210	8	AK103401	AK103401 Oryza sat	463	18	2.0	108523	9	AC000159	AC000159 Homo sapi
391	18	2.0	4507	5	BC078008	BC078008 Xenopus l	464	18	2.0	108727	8	AP004020	AP004020 Oryza sat
392	18	2.0	4856	9	AK024480	AK024480 Homo sapi	465	18	2.0	110000	1	AE016822	AE016822_01
393	18	2.0	5164	9	AB058719	AB058719 Homo sapi	466	18	2.0	110000	1	AE017333	AE017333_03
394	18	2.0	5197	9	RLFI1XKL	Z70305 R. leguminos	467	18	2.0	110000	1	AE017333	AE017333_33
395	18	2.0	5768	6	AX329625	AX329625 Sequence	468	18	2.0	110000	1	CP000002	CP000002_03
396	18	2.0	5768	6	HUMAN1	J04982 Human heart	469	18	2.0	110000	1	CP000002	CP000002_33
397	18	2.0	6032	6	AB074880	AB074880 Chlamydom	470	18	2.0	110000	2	AC091352	AC091352_2
398	18	2.0	6222	6	CQ609944	CQ609944 Sequence	471	18	2.0	110000	2	AC106675	AC106675_0
399	18	2.0	7819	6	CQ730498	CQ730498 Sequence	472	18	2.0	110000	2	AC114021	AC114021 Rat
400	18	2.0	7823	8	AY289797	M81758 Homo sapien	473	18	2.0	110000	2	AC141330	AC141330_1
401	18	2.0	8177	8	AY289797	AY289797 Chlamydom	474	18	2.0	110000	2	AP006501	AP006501_02
402	18	2.0	10029	1	AE012267	AE012267 Xanthomon	475	18	2.0	110000	2	LMF1CHR3	LMF1CHR3_15
403	18	2.0	10081	1	AE004512	AE004512 Pseudomon	476	18	2.0	110000	2	LMF1CHR3	LMF1CHR3_31
404	18	2.0	10094	1	AE012871	AE012871 Chlamydom	477	18	2.0	110000	3	AC125735	AC125735_2
405	18	2.0	10147	1	AE004900	AE004900 Pseudomon	478	18	2.0	110000	3	AC125735	AC125735_1
406	18	2.0	10412	1	AE012064	AE012064 Xanthomon	479	18	2.0	110794	9	AL133268	AL133268 Human DNA
407	18	2.0	10789	1	AE009051	AE009051 Agrobacte	480	18	2.0	111568	2	AC083908	AC083908 Homo sapi
408	18	2.0	10866	1	AE008017	AE008017 Agrobacte	481	18	2.0	111865	2	AL355883	AL355883 Homo sapi
409	18	2.0	11064	1	AE012296	AE012296 Xanthomon	482	18	2.0	112961	9	HS322112	HS322112
410	18	2.0	11653	1	AE012442	AE012442 Xanthomon	483	18	2.0	113049	10	AL591675	AL591675 Mouse DNA
411	18	2.0	15658	4	MWRK3	Y07749 M. vison mRN	484	18	2.0	113733	9	AP003159	AP003159 Homo sapi
412	18	2.0	22810	9	AB009668	AB009668 Homo sapi	485	18	2.0	115407	2	HS1000N6	HS1000N6
413	18	2.0	30943	6	CQ801140	CQ801140 Sequence	486	18	2.0	115431	9	AC010880	AC010880 Homo sapi
414	18	2.0	32229	9	CQ868646	CQ868646 Sequence	487	18	2.0	117612	8	AC104427	AC104427 Oryza sat
415	18	2.0	33847	1	AY233211	AY233211 Streptomy	488	18	2.0	117927	8	AC013416	AC013416 Homo sapi
416	18	2.0	35026	1	BPHEPCRD	Y13383 Bordetella	489	18	2.0	118828	9	AP006333	AP006333 Homo sapi
417	18	2.0	36888	1	AY046057	AY046057 Escherich	490	18	2.0	119304	8	AP004255	AP004255 Oryza sat
418	18	2.0	37115	2	AC139098	AC139098 Homo sapi	491	18	2.0	120000	10	AC132084	AC132084 Mus muscu
419	18	2.0	37909	1	AP005232	AP005232 Homo sapi	492	18	2.0	120926	2	AC127673	AC127673 Telhmani
420	18	2.0	38188	9	AY120852	AY120852 Synchoco	493	18	2.0	122000	2	AC133008	AC133008 Oryza sat
421	18	2.0	38957	9	AC144899	AC144899 Homo sapi	494	18	2.0	123149	2	AC008655	AC008655 Homo sapi
422	18	2.0	39576	3	AC008054	AC008054 Leishmani	495	18	2.0	123430	9	AP001824	AP001824 Homo sapi
423	18	2.0	40327	9	AP005379	AP005379 Homo sapi	496	18	2.0	126368	2	AC104742	AC104742 Mus muscu
424	18	2.0	40592	9	HS1191F1	Z68756 Human DNA s	497	18	2.0	126592	5	BX649211	BX649211 Zebrafish
425	18	2.0	41303	9	AC005175	AC005175 Homo sapi	498	18	2.0	126766	9	HS154513	HS154513 Homo sapi
426	18	2.0	41831	7	BPHE50940	AJ550940 Bacteriop	499	18	2.0	126803	9	AC007032	AC007032 Homo sapi
427	18	2.0	42271	9	AC020952	AC020952 Homo sapi	500	18	2.0	126982	9	AC117515	AC117515 Homo sapi
428	18	2.0	44566	2	AC139088	AC139088 Homo sapi	501	18	2.0	127098	8	AC144426	AC144426 Oryza sat
429	18	2.0	46024	2	AC100659	AC100659 Mus muscu	502	18	2.0	128501	9	AC012614	AC012614 Homo sapi
430	18	2.0	46077	2	AC137289	AC137289 Rat	503	18	2.0	128600	9	AC005192	AC005192 Homo sapi
431	18	2.0	46391	9	HSAS54C12	AL080242 Human DNA	504	18	2.0	132803	2	AC011051	AC011051 Homo sapi
432	18	2.0	47077	9	AL161648	AL161648 Human DNA	505	18	2.0	134163	2	AY331134	AY331134 Homo sapi
433	18	2.0	48177	7	AY369265	AY369265 Burtholde	506	18	2.0	135237	2	AP000814	AP000814 Homo sapi
434	18	2.0	48764	2	AC101107	AC101107 Mus muscu	507	18	2.0	135569	2	AC073997	AC073997 Homo sapi
435	18	2.0	53352	2	AC083369	AC083369 Homo sapi	508	18	2.0	136773	5	CR392330	CR392330 Zebrafish
436	18	2.0	52687	2	AC068390	AC068390 Homo sapi	509	18	2.0	137367	2	AC150200	AC150200 Papio anu
437	18	2.0	55307	2	AC014684	AC014684 Drosophil	510	18	2.0	138033	2	AP002339	AP002339 Homo sapi
438	18	2.0	58143	2	AC137177	AC137177 Rat	511	18	2.0	138376	8	AP002578	AP002578 Homo sapi
439	18	2.0	59314	2	AC099864	AC099864 Mus muscu	512	18	2.0	138390	14	AY261359	AY261359 Bovine he
440	18	2.0	60914	2	AC135246	AC135246 Rat	513	18	2.0	138824	8	AC051633	AC051633 Oryza sat
441	18	2.0	66615	2	AC091112	AC091112 Homo sapi	514	18	2.0	138966	2	AC008803	AC008803 Homo sapi
442	18	2.0	66615	2	AL831709	AL831709 Homo sapi	515	18	2.0	139444	8	AP004878	AP004878 Oryza sat
443	18	2.0	72207	9	AL592947	AL592947 Homo sapi	516	18	2.0	139953	8	HSBA5043	HSBA5043 Homo sapi
444	18	2.0	74279	9	AL592444	AL592444 Human DNA	517	18	2.0	140513	8	AP007253	AP007253 Oryza sat
445	18	2.0	75015	5	AP0091626	AP0091626 Datto rer	518	18	2.0	142272	2	AL513474	AL513474 Homo sapi
446	18	2.0	77204	2	AP000724	AP000724 Homo sapi	519	18	2.0	142402	2	CR847574	CR847574 Datto rer
447	18	2.0	80772	2	AC010449	AC010449 Homo sapi	520	18	2.0	143223	9	AL162725	AL162725 Human DNA
448	18	2.0	83715	2	AC138269	AC138269 Mus muscu	521	18	2.0	143701	8	HS29C18	HS29C18 Human DNA
449	18	2.0	84107	2	HS248B1	AL023578 Human DNA	522	18	2.0	145491	8	AP002883	AP002883 Oryza sat
450	18	2.0	86000	2	AC136951	AC136951 Leishmani	523	18	2.0	147640	5	EX323035	EX323035 Zebrafish
451	18	2.0	88973	6	CQ870090	CQ870090 Sequence	524	18	2.0	147788	9	AP005360	AP005360 Homo sapi
452	18	2.0	90243	3	AC084449	AC084449 Caenorhab	525	18	2.0	147788	9	AL596225	AL596225 Human DNA
453	18	2.0	92724	3	AP006074	AP006074 Lotus cor	526	18	2.0	148803	2	BX510998	BX510998 Homo sapi
454	18	2.0	93134	8	BX908807	BX908807 Neutropor	527	18	2.0	148891	9	AL162274	AL162274 Human DNA
455	18	2.0	95648	8	AC090214	AC090214 Homo sapi	528	18	2.0	149095	2	AC022683	AC022683 Homo sapi
456	18	2.0	101396	9	AC131182	AC131182 Homo sapi	529	18	2.0	149200	9	AL355645	AL355645 Human DNA
457	18	2.0	101990	9	AC127029	AC127029 Homo sapi	530	18	2.0	149316	10	AC123791	AC123791 Mus muscu



C 677	18	2.0	201543	2	AC1233914	Mus muscu	C 750	18	2.0	237992	2	AC102617	AC102617 Mus muscu
C 678	18	2.0	202239	2	CR759882	Danio rer	C 751	18	2.0	238297	2	AC126703	AC126703 Rattus no
C 679	18	2.0	202539	2	AC132505	Rattus no	C 752	18	2.0	238543	2	AC133701	AC133701 Rattus no
C 680	18	2.0	203042	2	AC116261	Rattus no	C 753	18	2.0	240059	2	AC108769	AC108769 Mus muscu
C 681	18	2.0	203132	8	AP004071	Oryza sat	C 754	18	2.0	240350	2	AC124154	AC124154 Rattus no
C 682	18	2.0	203492	2	AC107626	Mus muscu	C 755	18	2.0	240809	2	AC098059	AC098059 Rattus no
C 683	18	2.0	203566	2	AC092179	Homo sapi	C 756	18	2.0	241681	2	AC094546	AC094546 Rattus no
C 684	18	2.0	203710	2	AC107762	Mus muscu	C 757	18	2.0	242984	2	AC130775	AC130775 Rattus no
C 685	18	2.0	203710	2	AC107762	Mus muscu	C 758	18	2.0	244105	2	AC098897	AC098897 Rattus no
C 686	18	2.0	203905	2	AC073720	Mus muscu	C 759	18	2.0	244220	10	AC122941	AC122941 Mus muscu
C 687	18	2.0	204782	2	AC011168	Homo sapi	C 760	18	2.0	244856	2	AC094026	AC094026 Rattus no
C 688	18	2.0	205222	10	AC123534	Mus muscu	C 761	18	2.0	245499	2	AC107173	AC107173 Rattus no
C 689	18	2.0	205350	2	AC078946	Mus muscu	C 762	18	2.0	245828	2	AC098403	AC098403 Rattus no
C 690	18	2.0	206123	2	AC017106	Homo sapi	C 763	18	2.0	246173	2	AC110096	AC110096 Rattus no
C 691	18	2.0	206310	9	AY371697	Homo sapi	C 764	18	2.0	246517	2	AC125601	AC125601 Rattus no
C 692	18	2.0	206373	5	AL954133	Zebrafish	C 765	18	2.0	246913	2	AC113620	AC113620 Rattus no
C 693	18	2.0	206500	2	AC150823	Callithr	C 766	18	2.0	246970	2	AC121035	AC121035 Rattus no
C 694	18	2.0	206512	2	AC135435	Rattus no	C 767	18	2.0	247084	2	AC125034	AC125034 Mus muscu
C 695	18	2.0	206509	9	AC016397	Homo sapi	C 768	18	2.0	247200	2	AC123570	AC123570 Rattus no
C 696	18	2.0	207304	4	AC125499	Equus cab	C 769	18	2.0	247910	2	AB017307	AB017307 Thermus t
C 697	18	2.0	207304	4	AC125499	Equus cab	C 770	18	2.0	247910	2	AC112533	AC112533 Rattus no
C 698	18	2.0	207743	4	AC121066	Oryctolag	C 771	18	2.0	247936	2	AC093475	AC093475 Mus muscu
C 699	18	2.0	207791	2	AC116771	Mus muscu	C 772	18	2.0	250277	2	AC122757	AC122757 Mus muscu
C 700	18	2.0	210784	2	AC119293	Rattus no	C 773	18	2.0	251021	2	AC129763	AC129763 Rattus no
C 701	18	2.0	210842	2	AC140748	Rattus no	C 774	18	2.0	251533	2	AC125364	AC125364 Rattus no
C 702	18	2.0	211583	9	AC069025	Homo sapi	C 775	18	2.0	251710	2	AC117065	AC117065 Rattus no
C 703	18	2.0	211585	10	AL626784	Mouse DNA	C 776	18	2.0	251872	2	AC125998	AC125998 Rattus no
C 704	18	2.0	212178	2	AC131482	Rattus no	C 777	18	2.0	253184	2	AC137219	AC137219 Rattus no
C 705	18	2.0	213033	2	AC131482	Rattus no	C 778	18	2.0	253358	2	AC138303	AC138303 Mus muscu
C 706	18	2.0	213745	2	BX469890	Homo sapi	C 779	18	2.0	260639	2	AC134258	AC134258 Rattus no
C 707	18	2.0	213853	2	AC150608	Callithr	C 780	18	2.0	260963	2	AC105828	AC105828 Rattus no
C 708	18	2.0	213967	2	AC121595	Rattus no	C 781	18	2.0	263706	2	AC120895	AC120895 Rattus no
C 709	18	2.0	214911	2	AC010537	Homo sapi	C 782	18	2.0	263901	2	AC115371	AC115371 Rattus no
C 710	18	2.0	215087	2	AC113594	Mus muscu	C 783	18	2.0	264464	2	AC107410	AC107410 Rattus no
C 711	18	2.0	215087	2	CR847847	Danio rer	C 784	18	2.0	264501	2	AC136579	AC136579 Rattus no
C 712	18	2.0	216069	2	AC122086	Rattus no	C 785	18	2.0	271975	2	AC111856	AC111856 Rattus no
C 713	18	2.0	216340	2	AC073754	Mus muscu	C 786	18	2.0	272400	2	AC110146	AC110146 Rattus no
C 714	18	2.0	216345	4	AC122153	Oryctolag	C 787	18	2.0	273684	2	AC113630	AC113630 Rattus no
C 715	18	2.0	216410	2	AC148046	AP004168	C 788	18	2.0	274560	2	AC099390	AC099390 Rattus no
C 716	18	2.0	217205	8	AP004168	Oryza sat	C 789	18	2.0	275200	10	AC116392	AC116392 Mus muscu
C 717	18	2.0	217514	2	AC145779	Sus scrof	C 790	18	2.0	276079	2	AC117102	AC117102 Rattus no
C 718	18	2.0	217584	2	AC113399	Mus muscu	C 791	18	2.0	277993	2	AC055705	AC055705 Mus muscu
C 719	18	2.0	217636	10	AC127411	Mus muscu	C 792	18	2.0	279449	2	AC126636	AC126636 Rattus no
C 720	18	2.0	217722	5	BX284621	Zebrafish	C 793	18	2.0	282148	2	AC097022	AC097022 Rattus no
C 721	18	2.0	217794	2	AC111124	Mus muscu	C 794	18	2.0	282148	2	AC112576	AC112576 Rattus no
C 722	18	2.0	218602	2	AC145072	Mus muscu	C 795	18	2.0	283299	2	AC108628	AC108628 Rattus no
C 723	18	2.0	221545	10	AL844855	Mouse DNA	C 796	18	2.0	294461	2	AC118895	AC118895 Rattus no
C 724	18	2.0	222175	2	AC094189	Mus muscu	C 797	18	2.0	295117	2	AL499603	AL499603 Homo sapi
C 725	18	2.0	222429	2	AC148419	Melagris	C 798	18	2.0	296116	3	AE003782	AE003782 Homo sapi
C 726	18	2.0	222658	10	AC055766	Mus muscu	C 799	18	2.0	299700	1	AP006571	AP006571 Gloeobact
C 727	18	2.0	223061	2	AC098658	Rattus no	C 800	18	2.0	299800	1	AP005028	AP005028 Streptomy
C 728	18	2.0	223992	2	AC134196	Rattus no	C 801	18	2.0	299925	1	AP005039	AP005039 Streptomy
C 729	18	2.0	225087	10	AL845277	Mouse DNA	C 802	18	2.0	299925	1	AP005048	AP005048 Streptomy
C 730	18	2.0	225395	2	AC130267	Rattus no	C 803	18	2.0	300150	1	AP005945	AP005945 Bradyrhiz
C 731	18	2.0	226256	10	AC125082	Mus muscu	C 804	18	2.0	300242	1	AE016790	AE016790 Pseudomon
C 732	18	2.0	226503	2	AC112067	Rattus no	C 805	18	2.0	300242	1	AE017229	AE017229 Pseudomon
C 733	18	2.0	226712	2	AC115423	Rattus no	C 806	18	2.0	300750	1	AP006576	AP006576 Gloeobact
C 734	18	2.0	227221	2	AC137438	Rattus no	C 807	18	2.0	300950	1	AP005940	AP005940 Bradyrhiz
C 735	18	2.0	227452	2	AC105558	Rattus no	C 808	18	2.0	300957	8	AE017116	AE017116 Oryza sat
C 736	18	2.0	227570	2	AC117132	Rattus no	C 809	18	2.0	301399	1	AE017233	AE017233 Pseudomon
C 737	18	2.0	228548	2	BX119889	Danio rer	C 810	18	2.0	302101	1	AE016784	AE016784 Pseudomon
C 738	18	2.0	228687	2	AC111862	Rattus no	C 811	18	2.0	305250	1	AE016780	AE016780 Pseudomon
C 739	18	2.0	229506	2	AL161933	Homo sapi	C 812	18	2.0	305584	2	AE016920	AE016920 Chromodac
C 740	18	2.0	229797	2	AC133348	Rattus no	C 813	18	2.0	305838	2	AC118433	AC118433 Rattus no
C 741	18	2.0	232972	2	AC093991	Rattus no	C 814	18	2.0	310325	1	AE016864	AE016864 Pseudomon
C 742	18	2.0	233196	2	BX511086	Danio rer	C 815	18	2.0	310550	1	SC093913	SC093913 Streptomy
C 743	18	2.0	233861	2	AC127851	Rattus no	C 816	18	2.0	314750	2	AC106421	AC106421 Rattus no
C 744	18	2.0	234560	2	AC097419	Rattus no	C 817	18	2.0	323450	2	SME591790	SME591790 Simorhizo
C 745	18	2.0	235435	2	AC094124	Rattus no	C 818	18	2.0	324430	2	AC118529	AC118529 Rattus no
C 746	18	2.0	235792	2	AC094908	Rattus no	C 819	18	2.0	334520	1	AP003588	AP003588 Nosroc sp
C 747	18	2.0	236640	2	AC126854	Rattus no	C 820	18	2.0	344321	1	BX640429	BX640429 Bordetell
C 748	18	2.0	236660	2	AC097934	Rattus no	C 821	18	2.0	348134	1	BX640420	BX640420 Bordetell
C 749	18	2.0	237233	10	AC141643	Mus muscu	C 822	18	2.0	348624	1	BX640441	BX640441 Bordetell



C 823	18	2.0	348753	2	AC109063	AC109063 Rattus no	C 896	17	1.9	466	11	G39199	G39199 Z15431 Zebir
C 824	18	2.0	348934	1	BX640417	BX640417 Bordetell	C 897	17	1.9	477	5	CQ607761	CQ607761 Sequence
C 825	18	2.0	349305	1	BX640433	BX640433 Bordetell	C 898	17	1.9	508	5	CR387553	CR387553 Gallus ga
C 826	18	2.0	349497	1	BX640440	BX640440 Bordetell	C 899	17	1.9	511	11	G07079	G07079 human STS M
C 827	17	1.9		36	A08028	A08028 Oligonucleo	C 900	17	1.9	515	11	G62600	G62600 SHGC-140100
C 828	17	1.9		36	A13195	A13195 Oligonucleo	C 901	17	1.9	516	11	G62638	G62638 human STS S
C 829	17	1.9		36	AR034034	AR034034 Sequence	C 902	17	1.9	523	6	BD148253	BD148253 Primer fo
C 830	17	1.9		36	AR124043	AR124043 Sequence	C 903	17	1.9	523	6	AX868191	AX868191 Sequence
C 831	17	1.9		36	AR408693	AR408693 Sequence	C 904	17	1.9	533	8	AF313360	AF313360 Candida c
C 832	17	1.9		60	CO562360	CO562360 Sequence	C 905	17	1.9	553	6	AX461528	AX461528 Sequence
C 833	17	1.9		141	AX505661	AX505661 Sequence	C 906	17	1.9	573	8	AY183060	AY183060 Trifolium
C 834	17	1.9		141	AF280927S2	AF280928 Pongo pyg	C 907	17	1.9	580	11	G75858	G75858 S209P6227RH
C 835	17	1.9		158	BD054154	BD054154 Sequence	C 908	17	1.9	591	6	CQ732011	CQ732011 Sequence
C 836	17	1.9		158	AX918621	AX918621 Sequence	C 909	17	1.9	592	6	BT007453	BT007453 Homo sapi
C 837	17	1.9		166	AX315382	AX315382 Sequence	C 910	17	1.9	601	6	CQ746695	CQ746695 Sequence
C 838	17	1.9		177	BY161418	BY161418 RPRMMSQ0	C 911	17	1.9	606	6	CO525940	CO525940 Sequence
C 839	17	1.9		184	HS13985R	Z59734 H. sapiens C	C 912	17	1.9	621	11	BY036956	BY036956 S212P6037
C 840	17	1.9		187	BT002541	BT002541 Arabidops	C 913	17	1.9	628	3	AY571572	AY571572 Eimeria n
C 841	17	1.9		197	HS197H1R	Z55123 H. sapiens C	C 914	17	1.9	630	6	AR477514	AR477514 Sequence
C 842	17	1.9		219	CRU61371	U61371 Chlamydomon	C 915	17	1.9	658	11	BY028512	BY028512 S212P6867
C 843	17	1.9		227	AF205885	AF205885 West Nile	C 916	17	1.9	661	6	CQ719087	CQ719087 Sequence
C 844	17	1.9		241	CO440061	CO440061 Sequence	C 917	17	1.9	669	6	BD147173	BD147173 Primer fo
C 845	17	1.9		257	AF153281	AF153281 Pollachi	C 918	17	1.9	669	6	AX867111	AX867111 Sequence
C 846	17	1.9		257	AF153292	AF153292 Merlucciu	C 919	17	1.9	683	9	AX834802	AJ334802 Homo sapi
C 847	17	1.9		257	AF153296	AF153296 Zeus fabe	C 920	17	1.9	690	9	HS433257	AJ333257 Homo sapi
C 848	17	1.9		257	AF153297	AF153297 Zenopsis	C 921	17	1.9	705	5	CR391725	CR391725 Gallus ga
C 849	17	1.9		257	CO459882	CO459882 Sequence	C 922	17	1.9	709	5	HS4328492	AJ328492 Homo sapi
C 850	17	1.9		280	AR246122	AR246122 Sequence	C 923	17	1.9	710	5	HS4335380	AJ35380 Homo sapi
C 851	17	1.9		300	CQ707412	CQ707412 Sequence	C 924	17	1.9	715	5	BX950674	BX950674 Gallus ga
C 852	17	1.9		303	AF372854	AF372854 Streptomy	C 925	17	1.9	724	8	BN13	X5732 B. napus m/c
C 853	17	1.9		314	RATCABP	X00994 Rat intesti	C 926	17	1.9	727	6	BD021672	BD021672 Novel gen
C 854	17	1.9		341	AB057547	AB057547 Borrelia	C 927	17	1.9	727	6	BD101610	BD101610 Novel gen
C 855	17	1.9		341	AB105118	AB105118 Borrelia	C 928	17	1.9	728	8	HS4328516	AJ328516 Homo sapi
C 856	17	1.9		341	AB105126	AB105126 Borrelia	C 929	17	1.9	738	8	BN13MBNA	BN13MBNA
C 857	17	1.9		341	AB105132	AB105132 Borrelia	C 930	17	1.9	738	8	AK070795	AK070795 Oryza sat
C 858	17	1.9		341	AB105131	AB105131 Borrelia	C 931	17	1.9	746	6	HS4342308	AJ342308 Homo sapi
C 859	17	1.9		341	AB105132	AB105132 Borrelia	C 932	17	1.9	753	8	DP0131962	AJ131962 Dorticis p
C 860	17	1.9		341	AB105133	AB105133 Borrelia	C 933	17	1.9	772	10	NMSEPRPG	X78543 M. musculus
C 861	17	1.9		341	AB105169	AB105169 Borrelia	C 934	17	1.9	774	6	CQ735938	CQ735938 Sequence
C 862	17	1.9		341	AB105170	AB105170 Borrelia	C 935	17	1.9	780	6	CO586452	CO586452 Sequence
C 863	17	1.9		341	AB113313	AB113313 Borrelia	C 936	17	1.9	783	6	CQ738100	CQ738100 Sequence
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C 868	17	1.9		347	CO079431	CO079431 Sequence	C 941	17	1.9	825	9	BC002599	BC002599 Homo sapi
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C 870	17	1.9		347	CO150048	CO150048 Sequence	C 943	17	1.9	858	6	AX654293	AX654293 Sequence
C 871	17	1.9		347	CO184599	CO184599 Sequence	C 944	17	1.9	876	10	AF439403	AF439403 Rattus no
C 872	17	1.9		347	CO233350	CO233350 Sequence	C 945	17	1.9	896	11	AY027570	AY027570 Rhodococ
C 873	17	1.9		347	CO271254	CO271254 Sequence	C 946	17	1.9	900	11	G65805	G65805 XG3496 KMOX
C 874	17	1.9		347	CO308667	CO308667 Sequence	C 947	17	1.9	909	9	HS4340553	AJ340553 Homo sapi
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C 883	17	1.9		430	AY165554	AY165554 Drosophila	C 956	17	1.9	957	9	AF100341	AF100341 Homo sapi
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C 895	17	1.9		465	CO332672	CO332672 Sequence	C 968	17	1.9	1045	6	AR343032	AR343032 Sequence

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993	17	1.9	1190	5	CR254332	Danio rer
994	17	1.9	1198	8	AK108640	Gallus ga
995	17	1.9	1200	6	AR140552	Oryza sat
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997	17	1.9	1200	6	BD093441	Sequence
998	17	1.9	1211	3	BD093441	PADD-like
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1000	17	1.9	1235	10	AK059873	Oryza sat
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					AFJ78713	Mus muscu

## ALIGNMENTS

RESULT	1
LOCUS	BD093311
DEFINITION	BD093311
ACCESSION	BD093311
VERSION	BD093311.1 GI:22638899
KEYWORDS	WO 0104300-A/1.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 909) Ota,T., Iseogai,T., Nishikawa,T., Kawai,Y., Miyoshi,S. and Sato,S. Apoptosis Relating Factor Patent: WO 0104300-A 1 18-JAN-2001;
AUTHORS	HEIIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOgai,TETSUO NISHIKAWA, TITLE YURI KAWAI,SOUSUKE MIYOSHI,SUSUMU SATO
JOURNAL	OS Homo sapiens (human) PN WO 0104300-A/1
COMMENT	PD 18-JAN-2001 PF 06-JUL-2000 WO 2000JP004516 PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/159586 PI. TOSHIO OTA,TAKAO ISOgai,TETSUO NISHIKAWA,YURI KAWAI,SOUSUKE PI MIYOSHI, PI SUSUMU SATO
	PC C12N15/12,C07K16/18,C12N5/10,C12N1/21,C12N1/19,C12N1/15,C12P21/ PC 02',C07K16/18,C12P21/08,G01N33/53,G01N33/577
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QY 241	AGCAACCTGGCGCTCTGGGGGCACTCTCGGCGGGGTGTGGCCCCGACACCTGTGGCGG	300		
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QY 301	CACCTGAGCGCGCAACGGCGCGCGGACAGTGTCTCCAGAAAGCTATATGACATGACACTCC	360		
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QY 361	AGCTCTTCAAAAGAGGACAGAGGGTATGTCGCGGTCCCGTGGGACATGACAGTCTGCA	420		
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QY 481	CGGGGCGGCGCCACAGTGTGTGTCCAGACGGCGGCGGAGAGGGGCCCAACCCGAC	540		
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Db 601	CGGGTTTCAGACAGATATTCGAGAGCATGGGCCAAGCTTTGAGACAGGGCGTGGCATCCGG	660		
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Db 781	GCCATTGGGGGCACTATCTAGTGGGGCCCTGCGCAGAGGCCCTGGGGCGGTTCCTG	840		
QY 841	ACTAGAGCCCTGCGAGAGGCTGTGGGCCGGGAGGCTGTTCCGCTGCTGATGATGAT	900		
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## RESULT 2





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RESULT 5  
LOCUS AF443591 981 bp mRNA linear PRI 25-FEB-2002  
DEFINITION Homo sapiens death effector domain-containing DNA-binding protein 2  
(DEDD2) mRNA, complete cds.  
ACCESSION AF443591  
VERSION AF443591.1 GI:17933266  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 981)  
Roth,W., Stemmer-Liwenen,F., Pawlowski,K., Godzik,A. and Reed,J.C.  
TITLE Identification and characterization of DEDD2, a death effector  
domain-containing protein  
JOURNAL J. Biol. Chem. 277 (9), 7501-7508 (2002)  
MEDLINE 21850646  
PUBMED 11741985  
REFERENCE 2 (bases 1 to 981)  
Roth,W. and Reed,J.C.  
AUTHORS Direct Submission  
TITLE Submitted (05-NOV-2001) Burnham Institute, 10901 N. Torrey Pines  
JOURNAL Rd, La Jolla, CA 92037, USA  
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## ORIGIN

Query Match 94.4%; Score 858; DB 9; Length 981;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 4 from Patent WO0192527.
ACCESSION AX322754
VERSION AX322754.1 GI:18093742
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Tang, Y.T., Azimzai, Y., Yue, H., Burford, N., Ding, L., Elliott, V.S.,
Paterson, C. and Baughn, M.R.
TITLE Regulators of apoptosis
JOURNAL Patent: WO 0192527-A 06-DEC-2001;
Incyte Genomics, Inc. (US)
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Query Match 94.4%; Score 858; DB 6; Length 1230;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGCGCTATCCGGGTGACCCCGGCGGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 60
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RESULT 7
LOCUS AX431308 1924 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 17 from Patent WO240680.
ACCESSION AX431308
VERSION AX431308.1 GI:21656177
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S. H., Reed, J. C.,
Roch, W. and Steenker-Hjelen, F.
TITLE Novel death domain proteins
JOURNAL Patent: WO 0240680-A 17 23-MAY-2002;
BURNHAM INST (US)
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Query Match 94.4%; Score 858; DB 6; Length 1924;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 61 TAGCGGATGCTGCTGCTTACCGTATGTTGAGGTGTGTGGCGGGCACTGACCGAGTGC 120
Db 151 TAGCGGATGCTGCTGCTTACCGTATGTTGAGGTGTGTGGCGGGCACTGACCGAGTGC 210
QY 121 GAGCTGAGGCTCTGCGCTTCTGCTGATGAGGCTCTGCGCGCGCGGAGGCTTACCC 180
Db 211 GAGCTGAGGCTCTGCGCTTCTGCTGATGAGGCTCTGCGCGCGCGGAGGCTTACCC 270
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Oy 181 CGGGCCCCAGCGGCTAGAGCTCTGTGTGAGCTGAGAGCGCGCGGCGAGTGCAGCGCAG 240
Db 271 CGGGCCCCAGCGGCTAGAGCTCTGTGTGAGCTGAGAGCGCGCGGCGAGTGCAGCGCAG 330
Oy 241 AGCAACCTGCGGCTCTGTGTGAGCTCTGTGTGAGCTGAGAGCGCGCGGCGAGTGCAGCGC 300
Db 331 AGCAACCTGCGGCTCTGTGTGAGCTCTGTGTGAGCTGAGAGCGCGCGGCGAGTGCAGCGC 390
Oy 301 CACCTGCGGCGGCTCTGTGTGAGCTCTGTGTGAGCTGAGAGCGCGCGGCGAGTGCAGCGC 360
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Oy 841 GCTTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 930 GCTTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
Oy 900 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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RESULT 8
LOCUS BC027930
DEFINITION Homo sapiens death effector domain containing 2, mRNA (cDNA clone
ACCESSION BC027930
VERSION BC027930.1
KEYWORDS GC,
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Shih, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaeetz, T.E., Brownstein, M.J., Udell, T.B., Toshitaki, S.,

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## REMARK

## COMMENT

JOURNAL  
PUBMED  
TITLE  
AUTHORS  
JOURNAL

## TITLE

## JOURNAL

## PUBMED

## TITLE

## AUTHORS

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## TITLE

## FEATURES

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## /db\_xref="taxon:9606"

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## /tissue\_type="Brain, adult, 6 pooled whole brains"

## /clone\_lib="N1H MGC\_114"

## /lab\_host="DH10B"

## /note="vector: pCMV-SPORT6"

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## /gene="DEDD2"

## /note="synonym: FLAME-3"

## /db\_xref="LOCUSID:162989"

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## /codon\_start=1

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## /db\_xref="LOCUSID:162989"

## /translation="MAISGSPAPCPMCEDECDYGYMLSLRMPFVVGGLTECELEI

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## GRPFGGARRRRRGAAPAPPOOSSEPARSSSEKVTCDIRLVRVRAVECHGPALEGGVA



## ORIGIN

SRPRLAROLDVFGQATAVILASRDLSGVICIKFSELSYLDAPFWGDIYSLNLOALR  
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Query Match 83.2%; Score 756; DB 9; Length 1951;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 906; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 121 GAGCTGAGAGCTCTGCGCTTTCTGCTGATGAGGCTCTGCGCGCGCGGAGGCTTAAGC 180
DB 169 GAGCTGAGAGCTCTGCGCTTTCTGCTGATGAGGCTCTGCGCGCGCGGAGGCTTAAGC 248
QY 181 CGGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGCGGAGGCTGCGCGAG 240
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QY 361 AGCTTTTGAAGAGAGACAGAGGGTATGCTGCGCGCTGCGCGAGTCAAGCAAGTTCTGCA 420
DB 429 AGCTTTTGAAGAGAGACAGAGGGTATGCTGCGCGCTGCGCGAGTCAAGCAAGTTCTGCA 488
QY 421 AATTCTGACGAGGCTCACTGGGAGACAGGCTTCCCGCCCAACCAACCGGAGGCGGAGT 480
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DB 609 CAGCAGTCAAGAGCCCGGCAACCTTCTCTGAAAGCAAAAGTGAAGCTGTGACATCCGAGCTC 668
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DB 669 CGGGTTCGAGAGAGTACTGCGAGATGAGGCGAGCTTGGAGCAAGGGGCTGAGCAATCCCGG 728
QY 661 CGGGCCCCGAGCGCTGCGCGGAGCTGAGCGTGTGGGAGGCGGCACTGAGTGTGCGC 720
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QY 901 GAGGCTGAC 909
DB 969 GAGGCTGAC 977
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## RESULT 9

AF457575

## LOCUS

AF457575 981 bp mRNA linear PRI 10-APR-2002

## DEFINITION

(FLAME-3) mRNA, complete cds.

## ACCESSION

AF457575

## VERSION

AF457575.1 GI:20126793

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens (human)

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## AUTHORS

Zhan, Y., Hegde, R., Srinivasula, S.M., Fernandes-Alnemri, T. and Alnemri, E.S.

## TITLE

Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the TRIF1C102 subunit of human transcription factor TRIC

## JOURNAL

Cell Death Differ. 9 (4), 439-447 (2002)

## MEDLINE

21961615

## PUBMED

11965497

## REFERENCE

2 (bases 1 to 981)

## AUTHORS

Alnemri, E.S.

## TITLE

Direct Submission

## JOURNAL

Submitted (11-DEC-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA

## FEATURES

location/Qualifiers

## source

1..981

## organism

"Homo sapiens"

## mol\_type

"mRNA"

## db\_xref

"taxon:9606"

## chromosome

"19"

## map

"19q13.2"

## gene

"FLAME-3"

## CDS

1..981

## protein\_id

"AA10835.1"

## translation

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Query Match 66.3%; Score 603; DB 9; Length 981;

Best Local Similarity 99.3%; Pred. No. 66-275;

Matches 903; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db	361	AGCTCTTCAAAAGAGGACAGAGGATAGCTGACCGGTGCGCGGTGCGGAGTCAAGAGATTTGCA	420
Qy	421	AATTCTCAGCAGGAGTCACTGGGAGACAGAGCTTCCGCCCAACCAAGCGGACGGCGAGT	480
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Qy	481	CGGCGCCCGGCGCAAGTGTGTGTGCCAGACGGCGCGCGGAGAGGCGGCCCAAGCGGACCCAG	540
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DEFINITION	Human sapiens death effector domain-containing DNA-binding 2		
ACCESSION	AY125488		
VERSION	AY125488.1	GI:22475163	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2012)		
AUTHORS	Lee,J.C., Schickling,O., Stegh,A.H., Oshima,R.G., Dinsdale,D., Cohen,G.M. and Peter,M.E.		
TITLE	DEDD regulates degradation of intermediate filaments during apoptosis		
JOURNAL	J. Cell Biol. 158 (6), 1051-1066 (2002)		
MEDLINE	22220288		
PUBMED	1235123		
REFERENCE	2 (bases 1 to 2012)		
AUTHORS	Peter,M.E.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-JUN-2002) Ben May Cancer Institute, University of Chicago, 924 E. 57th Street, R112, Chicago, IL 60637, USA		
FEATURES	Location/Qualifiers		

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Qy	688 GACGTGTTTGGGCGAGGCCACCGCAGTGTGTGCTCAAGGACCTGGGCTCTGTGGTTGT	747
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RESULT 11		
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ACCESSION	BC013372	
VERSION	BC013372.2	
KEYWORDS	GI:33872465	
SOURCE	MGC.	
ORGANISM	Homo sapiens (human)	
REFERENCE	1 (bases 1 to 2005)	
AUTHORS	Klauster R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,	

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hasleh, F., Diatchenko, L., Martusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheer, T.E., Brownstein, M.J., Uadiri, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Iguellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wollam, D.K., Hale, S., Garcia, A.M., Gay, L.J., Hally, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherbakov, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalek, U., Smalinski, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
2 (bases 1 to 2005)  
Strausberg, R.  
Direct Submission  
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:15426522.  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systembiology.org>  
contact: [amadan@systembiology.org](mailto:amadan@systembiology.org)  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
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Location/Qualifiers  
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ORIGIN  
Query Match 42.1%; Score 383; DB 9; Length 2005;  
Best Local Similarity 99.8%; Pred. No. 1,6e-170;  
Matches 433; Conservative 0; Mismatches 1; Gaps 0;

QY 1 ATGGGCGTATCCGGTGCACCCCGCCGCTGCTGGAGAGAGATGAGTGCCTTGACTAC 60  
DB 75 ATGGGCGTATCCGGTGCACCCCGCCGCTGCTGGAGAGAGATGAGTGCCTTGACTAC 134  
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DB 135 TACGGAGTCTGTGCTTACACCGTATGTTGCAAGTGTGTGGCGGGCAACTGACCGAGTGC 194  
QY 121 GAGCTGAGCTCTGAGCTTCTGTGTGATGATGAGGCTCTTGCGCGCGCGAGAGGCTTACG 180  
DB 195 GAGCTGAGCTCTGAGCTTCTGTGTGATGATGAGGCTCTTGCGCGCGCGAGAGGCTTACG 254  
QY 181 CGGGCCGCGACGCGCTTACAGCTCTGCTGAGTGCAGCGCGCGCGCACTGCGCGAG 240  
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QY 241 AGCAACTGCGCGCTGCTGAGGCGCACTCTGCGCGCTGCTGCGCGCGCACTGCTGCGG 300  
DB 315 AGCAACTGCGCGCTGCTGAGGCGCACTCTGCGCGCTGCTGCGCGCGCACTGCTGCGG 374  
QY 301 CACCTGCGCGCGCAAGCGCGCGCGCGCACTGCTGCTGAGTGCAGTGCAGTGCAGTGC 360  
DB 375 CACCTGCGCGCGCAAGCGCGCGCGCGCACTGCTGCTGAGTGCAGTGCAGTGCAGTGC 434  
QY 361 AGCTTCTTCAAGAGAGAGAGAGAGTGTGCTGCGCGCGCGCGCACTGAGTGCAGTGC 420  
DB 435 AGCTTCTTCAAGAGAGAGAGAGTGTGCTGCGCGCGCGCGCACTGAGTGCAGTGCAGTGC 494  
QY 421 AATTCTAGCGAGG 434  
DB 495 AATTCTAGCGAGG 508

RESULT 12  
BD149917  
LOCUS 626 bp DNA linear PAT 17-JAN-2003  
DEFINITION  
ACCESSION BD149917  
VERSION BD149917.1 GI:27855675  
KEYWORDS JP 2002191363-A/4760.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Oca, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Iehii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.  
TITLE Primer for synthesizing full-length cDNA and use thereof  
JOURNAL Patent: JP 2002191363-A/4760 09-JUL-2002;  
HEPIX RESEARCH INSTITUTE  
OS Homo sapiens (human)  
PN JP 2002191363-A/4760  
PD 09-JUL-2002  
PF 28-JUL-2000 JP 2000280990  
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,  
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
PI KEIICHI NAGAI, TETSUJI OHSUKI  
PC  
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10,  
PC C12P21/02, C1201/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
Primer for synthesizing full-length cDNA and use thereof FH Key  
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source FT source 1..626  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match	36.7%	Score 334;	DB 6;	Length 626;
Best Local Similarity	99.7%;	Pred. No. 3.3e-147;		
Matches 384;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	1	ATGGGCGCTATCCGGGTCGACCCGGGCCCCGATCTGGAGAGAGAGATGAGTGGCTTGGACTTAC	60
Db	88	ATGGGCGCTATCCGGGTCGACCCGGGCCCCGATCTGGAGAGAGAGATGAGTGGCTTGGACTTAC	147
QY	61	TACGGGATGCTGTGCGTTCACCGTAATGTCAGAGTGATGGGCGGGCACTGACCGAGTGC	120
Db	148	TACGGGATGCTGTGCGTTCACCGTAATGTCAGAGTGATGGGCGGGCACTGACCGAGTGC	207
QY	121	GAGCTGAGAGCTCTGGGCTTTCTGCTGATGAGGCTCTTGCGCGCGCCGAGGCTTAAACC	180
Db	208	GAGCTGAGAGCTCTGGGCTTTCTGCTGATGAGGCTCTTGCGCGCGCCGAGGCTTAAACC	267
QY	181	CGGGCCGCGACAGGCGGCTGAGGCTCTGCGTGGAGGCTGAGAGCGCGGGGCGAGTGGCGGAG	240
Db	268	CGGGCCGCGACAGGCGGCTGAGGCTCTGCGTGGAGGCTGAGAGCGCGGGGCGAGTGGCGGAG	327
QY	241	AGCAACTGCGGCTGTGCTGGGCAACTCTGTCGCGCTGGCCGCGCACAGCACTGTGTCGG	300
Db	328	AGCAACTGCGGCTGTGCTGGGCAACTCTGTCGCGCTGGCCGCGCACAGCACTGTGTCGG	387
QY	301	CACCTGGCGCGCAGCGGCGCCGGCCGACGTGTTCCAGAACGCTTAAGCTATGGCAACTTCC	360
Db	388	CACCTGGCGCGCAGCGGCGCCGGCCGACGTGTTCCAGAACGCTTAAGCTATGGCAACTTCC	447
QY	361	AGCTCTTCAAAAGAGGACAGAGGGTA	385
Db	448	AGCTCTTCAAAAGAGGACAGAGGGTA	472

RESULT 13			
AX869855			
LOCUS	AX869855	626 bp	DNA
DEFINITION	Sequence 4760 from Patent EP1074617.		linear PAT 17-DEC-2003

VERSION	AX869855.1	GI:40024718
KEYWORDS		
SOURCE	Homo sapiens (human)	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## AUTHORS

Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.

**TITLE** Primers for synthesizing full-length cDNA and their use  
**JOURNAL** Patent: EP 1074617-A 4760 07-FEB-2001;

Research Association for Biotechnology (JP)

Location/Qualifiers

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source
1. . 626
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="Taxon:9606"

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**ORIGIN**

Query Match	36.7%	Score 334	DB 6	Length 626
Best Local Similarity	99.7%	Pred. No. 3.3e-147		
Matches 384, Conservative	0	Mismatches 1	Indels 0	Gaps 0

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Oy	61	TACGGGAGTCTGCCTTCAACCGATATGTCAGAGCTGTGGGGGGGACAATGACCCGATGC	120
Db	148	TACGGGATGCTGTCCGTTTCAACCGATATGTCAGAGCTGTGGGGGGGACAATGACCCGATGC	207
Oy	121	GAGCTGAGACTCTTGACCTTTCTGCTGATAGAGGCTCTGTGGCGCGCCGAGGACTTTAGCC	180
Db	208	GAGCTGAGAGCTCTTGACCTTTCTGCTGATAGAGGCTCTGTGGCGCGCCGAGGACTTTAGCC	267

QY	181	CGGGCCCGCAGCGGCGCTAGAGCTCTGTGGAGCTGGAGCGCGCGGCGCACTGGCGGCGAG	240
Db	268	CGGGCCCGCAGCGGCGCTAGAGCTCTGTGGAGCTGGAGCGCGCGGCGCACTGGCGAGCGAG	327
QY	241	AGCAACCTGCGGCTGTCTGGGGCAACTCTCTGGCGTGCTGGCCCGGCAAGCACTGTGGCGG	300
Db	328	AGCAACCTGCGGCGTGTGGGGCAACTCTCTGGCGTGCTGGCCCGGCAAGCACTGTGGCGG	387
QY	301	CACCTGGCGGCGCAAGCGGCGCTCGGCGCACTGTCTCCAGAAAGCTATAGCTATGGCACTTCC	360
Db	388	CACCTGGCGGCGCAAGCGGCGCTCGGCGCACTGTCTCCAGAAAGCTATAGCTATGGCACTTCC	447
QY	361	AGCTCTTCAAGAGAGCAAGAGGCTA	385
Db	448	AGCTCTTCAAGAGAGCAAGAGGCTA	472

RESULT 14	
AK130203	
LOCUS	1659 bp
AK130203	mRNA linear
DEFINITION	Homo sapiens cDNA FLJ26693 f18, clone MEG07953.
	PRI 10-SEP-2003

VERSION	AKI30203.1	GI:34526957	insert sequence)
KEYWORDS	oligo capping; fls (full		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE AUTHORS

Fukuzumi, Y., Fujimori, Y., Komiya, M., Suzuki, Y., Hata, H.,

TITLE  
NEDO human cDNA sequencing project

JOURNAL REFERENCE AUTHORS	unpublished
2 (bases 1 to 1659)	
Sugano, S. and Suzuki, Y.	

JOURNAL

**COMMENT**

NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo; Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

### FEATURES

#### Location/Qualifiers

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oxidant"

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## ORIGIN

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Matches 323	0	Mismatches	0	Gaps	0

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Oy	CTGCGAGCATGGGCGACGCTTTGAGACAGG	648
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Db	CTGCGAGCATGGGCGACGCTTTGAGACAGG	487
Oy	CGTGGCATCCCGCGGGCCCGAGCGCTGGCGGAGCTGAGCGTGTTTGGGCAAGCCAC	707

Db 487 CTTGCGATCCCGCGCCAGCCGTCGCGGCGAGCTGAGAGTGTGGCGAGCCAC 546  
QY 708 CCGAGTCTGCGCTCAAGGAGCCTGGGCTCTGTGTTTGTGACATCAAGTTCTAGAGT 767  
Db 547 CCGAGTCTGCGCTCAAGGAGCCTGGGCTCTGTGTTTGTGACATCAAGTTCTAGAGT 606  
QY 768 CTCCTATCTGAGCGCTTCTGGGGCGACTACTAGTGGCGCCCTGCTGAGAGCCCTGG 827  
Db 607 CTCCTATCTGAGCGCTTCTGGGGCGACTACTAGTGGCGCCCTGCTGAGAGCCCTGG 666  
QY 828 GGGCGGTTCTCTGAGAGCCCTGCGAGAGGCTGTGGGCGCGGAGGCTTCCGCTGT 887  
Db 667 GGGCGGTTCTCTGAGAGCCCTGCGAGAGGCTGTGGGCGCGGAGGCTTCCGCTGT 726  
QY 888 GGTCAGTGTGATGAGGCTGAC 909  
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RESULT 15  
AC010247/c 95663 bp DNA linear PRI 13-JUL-2002  
LOCUS AC010247  
DEFINITION Home sapiens chromosome 19 clone CTC-378H2, complete sequence.  
ACCESSION AC010247  
VERSION AC010247.9 GI:21743752  
KEYWORDS HTG.  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 95663)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submission  
Unpublished  
2 (bases 1 to 95663)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 95663)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submission  
Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
4 (bases 1 to 95663)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Direct Submission  
Submitted (13-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On Jul 13, 2002 this sequence version replaced gi:21637454.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.1.  
NOTE: Small insert shatter library only 85964-86181. 226bp single  
subclone 9479-9697.

## FEATURES

source

1. 95663  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.5e-141;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 90984 GACATCCGCTCCGGGTTGAGCAGAGTACTGCGAGCATGGGCCGACCTTGAGAGAGGC 90925  
QY 649 GTGGCATCCGAGCGGCCCGCCAGAGCGCTGGCGCGGAGCTGAGAGTGTGGCCAGGCCACC 708  
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QY 709 GCAAGTCCGCTCAAGGAGACTGGGCTGTGGTTGTGACATCAAGTTCTAGAGCTC 768  
Db 90864 GCAAGTCCGCTCAAGGAGACTGGGCTGTGGTTGTGACATCAAGTTCTAGAGCTC 90805  
QY 769 TCTTATCTGAGAGCGCTTCTGGGGCGACTACTGAGTGGCGCCCTGCTGAGAGCCCTGGCG 828  
Db 90804 TCTTATCTGAGAGCGCTTCTGGGGCGACTACTGAGTGGCGCCCTGCTGAGAGCCCTGGCG 90745  
QY 829 GACGTTTCTGACTGAGGCGCTTGGGAGAGGCTGTGGCGGAGGCTGTTCCGCTGTG 888  
Db 90744 GACGTTTCTGACTGAGGCGCTTGGGAGAGGCTGTGGCGGAGGCTGTTCCGCTGTG 90685  
QY 889 GTCAGTGTGATGAGGCTGAC 909  
Db 90684 GTCAGTGTGATGAGGCTGAC 90664

Search completed: February 12, 2005, 14:43:14  
Job time : 3018 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:59:32 ; Search time 2934 Seconds  
(without alignment)  
15012.199 Million cell updates/sec

Title: US-10-030-271-1  
Perfect score: 909  
Sequence: 1 atggcgatcgcgcggtcgac.....tcagtgtgcatgagctgac 909

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pal: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_scs: \*  
12: gb\_ey: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	909	100.0	909	6	BD093311 Apoptosis
2	909	100.0	1883	6	BD093312 Apoptosis
3	909	100.0	1883	9	AK075328 Homo sapi
4	907.4	99.8	981	6	CQ119642 Sequence
5	907.4	99.8	981	9	AF443591 Homo sapi
6	907.4	99.8	1230	6	AX322754 Sequence
7	907.4	99.8	1924	6	AX431308 Sequence
8	904.2	99.5	1951	6	BC027930 Homo sapi
9	899.4	98.9	981	9	AF457575 Homo sapi
10	895.8	95.2	2012	9	AY125468 Homo sapi
11	845.4	93.0	2005	9	BC013372 Homo sapi
12	825.8	90.8	1084	6	AX364851 Sequence
13	825.8	90.8	1106	6	AX364852 Sequence
14	701	77.1	993	10	AF457576 Mus muscu
15	701	77.1	993	10	AF543541 Mus muscu
16	541	59.5	1067	6	AR339362 Sequence
17	528	58.1	626	6	BD149917 Primer fo
18	528	58.1	626	6	AX869855 Sequence
19	474.8	52.2	1659	9	AK130203 Homo sapi

20	346.2	38.1	603	6	AX136449 Sequence
21	346.2	38.1	603	6	BD123689 Secretory
22	326.6	35.9	11084	9	AC006486 Homo sapi
23	325.6	35.8	1540	10	BC037043 Mus muscu
24	321	35.3	95663	9	AC010247 Homo sapi
25	301.4	33.2	303	6	AX431298 Sequence
26	280	30.8	226909	2	AC079490 Mus muscu
27	279.4	30.7	190669	2	AC120393 Sequence
28	250.2	27.5	167108	2	AC068283 Homo sapi
29	193.8	21.3	957	9	HS010973 Homo sapi
30	193.8	21.3	1139	6	BD227199 Protein f
31	193.8	21.3	1139	6	AX008886 Sequence
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33	193.8	21.3	1830	6	BD157757 Primer fo
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36	193.8	21.3	2261	6	BD156359 Primer fo
37	193.8	21.3	2261	6	AX397469 Sequence
38	193.8	21.3	2261	6	AX876867 Sequence
39	193.8	21.3	2261	9	AK001497 Homo sapi
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42	192.2	21.1	957	9	AF100341 Homo sapi
43	192.2	21.1	957	9	CR356556 Homo sapi
44	192.2	21.1	1045	6	AR140521 Sequence
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## ALIGNMENTS

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LOCUS	BD093311				
DEFINITION	Apoptosis Relating Factor.				
ACCESSION	BD093311.1				
VERSION	BD093311.1 GI:22638899				
KEYWORDS	WO 0104300-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Ota,T., Isegaki,T., Nishikawa,T., Kawai,Y., Miyoshi,S. and Sato,S.				
TITLE	Apoptosis Relating Factor				
JOURNAL	Patent: WO 0104300-A 1 18-JAN-2001; HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI,SOUSUKE MIYOSHI,SUSUMU SATO				
COMMENT	OS Homo sapiens (human) PN WO 0104300-A/1 PD 18-JAN-2001 PF 06-JUL-2000 WO 2000JP004516 PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/155586 PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,SOUSUKE MIYOSHI, PI SUSUMU SATO				
FEATURES	source				
FEATURES	source				
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Matches 909; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				

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OY 301 CACCTGCGCGGAGAGCGGCGCGGAGGCTCTGAGAGCGCTATAGCTATGAGCACTCC 360
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DEFINITION Apoptosis Relating Factor.
ACCESSION BD093312
VERSION BD093312.1 GI:22638900
KEYWORDS MO 0104300-A/2.
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Otsu, T., Isogai, T., Nishikawa, T., Kawai, Y., Miyoshi, S. and Sato, S.
TITLE Apoptosis Relating Factor
AUTHORS Patent: WO 0104300-A 2 18-JAN-2001;
JOURNAL HELIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
YURI KAWAI, SOTSUKE MIYOSHI, SUSUMU SATO
COMMENT OS Homo sapiens (human)
PN WO 0104300-A/2
PD 18-JAN-2001
PF 06-JUL-2000 WO 2000JP004516
PR 08-JUL-1999 JP 99P 194179, 18-OCT-1999 US 60/159586 PI
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, SOTSUKE MIYOSHI,
SUSUMU SATO
PI SUSUMU SATO
PC C12N15/12, C07K14/47, C12N5/10, C12N1/21, C12N1/19, C12N1/15, C12P21/
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FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 9,7e-135;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 184 TACGGGATGCTTCCCTTCAACCGTATGTTCCAGGTGTGGGGGGGCACTGACCCAGTGC 243
OY 121 GAGCTGAGAGCTCTGAGCTTCTTCTGCTGATGAGGCTCTGAGCGCGCGGAGGCTTAC 180
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DB 304 CGGGCCCGGAGGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 363
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DB 424 CACCTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 483
OY 361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 420
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OY 421 AATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 480
DB 544 AATTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 603
OY 481 CGGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 540
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Qy 901 GAGGCTGAC 909  
Db 1024 GAGGCTGAC 1032

RESULT 3  
AK075328 1883 bp mRNA linear PRI 03-SEP-2002  
LOCUS AK075328 Homo sapiens cDNA PSEC0004 f1s, clone NT2RM100058, weakly similar  
DEFINITION to Homo sapiens death effector domain-containing testicular  
molecule mRNA.  
ACCESSION AK075328  
VERSION AK075328.1 GI:22761346  
KEYWORDS oligo capping; f1s (full insert sequence).  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Sakai, H., Hayashi, K.,  
Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T.  
TITLE HRI human cDNA sequencing project  
JOURNAL Unpublished  
AUTHORS Isogai, T. and Yamamoto, J.  
TITLE Direct Submission  
JOURNAL Submitted (20KAR-2002) Takao Isogai, Helix Research Institute,  
Genomic Laboratory, 1532-3 Yana, Kiseazuru, Chiba 282-0812, Japan  
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

COMMENT  
HRI human cDNA sequencing project; cDNA 5' - & 3' - end one pass  
sequencing, clone selection and full insert sequencing; Helix  
Research Institute (supported by Japan Key Technology Center etc.);  
cDNA library construction; Institute of Medical Science, University  
of Tokyo, Laboratory of Genome Structure, Human Genome Center.  
Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 909; DB 9; Length 1883;  
Best Local Similarity 100.0%; Pred. No. 9, 7e-135;  
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 184 TACGGGATGCTGTGCTTACCGTATGTTCAAGTGTGGCGGCACTGACCGAGTGC 243  
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Db 664 CAGCAGTCAAGAGCCCGCAGACCTTCTGTAAGGCAAGTACCTGTGACATCCGGCTC 723  
Qy 601 CGGGTTGAGCAGAGTACTGCGAGCATGGGCAAGCTTGGAGAGGGCGTGGCATCCCG 660  
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Qy 661 CGGCCCCAGGCGCTGGCGCGGCAAGTGGACGTGTTGGGCAAGGCAACCGAGTGTCTGCG 720  
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Qy 781 GCTTCTGGGGGCGACTACCTGAGTGGCGCCCTGTGAGGCGCTGGGGGGCGTTCCTG 840  
Db 904 GCTTCTGGGGGCGACTACCTGAGTGGCGCCCTGTGAGGCGCTGGGGGGCGTTCCTG 963  
Qy 841 ACTGAGGCGCTGCGAGAGCTGTGGCGCGGAGGCTGTTGCTGTGTGATGTGAT 900  
Db 964 ACTGAGGCGCTGCGAGAGCTGTGGCGCGGAGGCTGTTGCTGTGTGATGTGAT 1023

QY	901	GAGCGTGAC	909	
Db	1024	GAGCGTGAC	1032	
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DEFINITION	Sequence 5576 from Patent WO02068579.			
ACCESSION	COJ19642			
VERSION	COJ19642.1			
KEYWORDS	GI:42280499			
SOURCE				
ORGANISM	Homo sapiens (human)			
REFERENCE				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof			
JOURNAL	Patent: WO 02068579-A 5576, 06-SEP-2002; (P)			
FEATURES	PE Corporation (NY) (US)			
source	Location/Qualifiers			
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Query Match	99.8%; Score 907.4; DB 6; Length 981;			
Best Local Similarity	99.9%; Pred. No. 2.1e-134;			
Matches	908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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QY	121	GAGCTGAGAGCTCTGCGCTTTCTGTGTGATAGAGCTCTTGCGCGCGCTGAGAGCTTACCC	180	
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QY	181	CGGCGCCGACGCGGCTTGAAGCTCTGCTGGAGCTGAGCCCGCGGCGAGTGCAGCGAG	240	
Db	181	CGGCGCCGACGCGGCTTGAAGCTCTGCTGGAGCTGAGCCCGCGGCGAGTGCAGCGAG	240	
QY	241	AGCAACCTGCGGCTGTGGGGCACTCTGCGCGGTGCTGAGCCCGCAAGACTGTGCGG	300	
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Db	301	CACCTTGGCGGCAAGCGGCGCTGAGCTCTGCTGAGCTGAGCCCGCGGCGAGTGCAG	360	
QY	361	AGCTCTTCAAGAGAGAGAGGTAGCTGCGCGGTGCGGCGAGTCAAGGAGTTTTCGA	420	
Db	361	AGCTCTTCAAGAGAGAGAGGTAGCTGCGCGGTGCGGCGAGTCAAGGAGTTTTCGA	420	
QY	421	AATTCTGACGAGGTGAGTGGAGACAGGCTCCCGCCCAACCAAGCGGCGAGCGAGT	480	
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QY	481	CGGGCGCGGCGCAATGTGTGTGCCAGACGCGCGGAGAGGGGGCCCGCGCACCCAG	540	
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QY	541	CAGCAGTCAGAGCCCGGCGAGCTTCCCTGTAAGCAAGTGAATCTGAGATCCGAGTC	600	
Db	541	CAGCAGTCAGAGCCCGGCGAGCTTCCCTGTAAGCAAGTGAATCTGAGATCCGAGTC	600	

Qy	601	CGGGTTTGACAGAGTACTCGAGCATGGGCGAGCTTGGAGAGAGGCGTGGCATCCGG	660
Db	601	CGGGTTGACAGAGTACTCGAGCATGGGCGAGCTTGGAGAGAGGCGTGGCATCCGG	660
Qy	661	CGGCCCCAGGCGCTGCGCGGCACTGGACGTGTTTGGGCAAGCCGACCGAGTGTCCGC	720
Db	661	CGGCCCCAGGCGCTGCGCGGCGAGCTGGAGCGTGTGGGCAAGCCGACCGAGTGTCCGC	720
Qy	721	TCAAGGAGACCTGGGCTGTGGTTTGGACATCAAGTCTCAGAGCTCTCTTATCTGGAC	780
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Qy	781	GCTTCTGGGCGCACTACTGATGAGCGCCCTGTCGAGGCGCTGCGGCGCGTTCCTG	840
Db	781	GCTTCTGGGCGCACTACTGATGAGCGCCCTGTCGAGGCGCTGCGGCGCGTTCCTG	840
Qy	841	ACTGAGGCGCTGCGAGAGCGTGTGGCGCGGAGGCTGTTCGCTGTGTCAGTGTGGAT	900
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Qy	901	GAGGCTGAC 909	
Db	901	GAGGCTGAC 909	
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DEFINITION	Homo sapiens death effector domain-containing DNA-binding protein 2		
ACCESSION	AF443591		
VERSION	AF443591		
KEYWORDS	AF443591.1 GI:17933266		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 981)		
JOURNAL	Roth, W., Stenmer-Jensen, F., Pawlowski, K., Godzik, A. and Reed, J.C.		
MEDLINE	Identification and characterization of DEDD2, a death effector		
PUBMED	domain-containing protein		
REFERENCE	J. Biol. Chem. 277 (9), 7501-7508 (2002)		
AUTHORS	2 (bases 1 to 981)		
TITLE	Roth, W. and Reed, J.C.		
JOURNAL	Direct Submission		
MEDLINE	Submitted (05-NOV-2001) - Burnham Institute, 10901 N. Torrey Pines		
PUBMED	Rd, La Jolla, CA 92037, USA		
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PUBMED	1. 981		
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AUTHORS	1. 981		
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MEDLINE	/product="death effector domain-containing DNA-binding		
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REFERENCE	SRPPLAROLDVFGQATVLRERDLSGVVCDIKFSELSTYLDLFMGDYGALQLRL		
AUTHORS	GVFLTEALNEAVREAVRLVSVDEADYAGRRRLLMEEGRRPTENS"		
ORIGIN			
Query Match	99.8%;	Score 907.4;	DB 9; Length 981;

Best Local Similarity 99.9%; Pred. No. 2.1e-134;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS AX322754 Sequence 4 from Patent WO192527.  
DEFINITION  
ACCESSION AX322754

VERSION AX322754.1 GI:18093742  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Tang, Y.T., Azimzal, Y., Yue, H., Burford, N., Ding, L., Elliott, V.S.,  
Patterson, C. and Baughn, M.R.  
TITLE Regulation of apoptosis  
JOURNAL ~~Patent~~ NO 0192527-A ~~906-DEC-2001~~  
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ORIGIN  
Query Match 99.8%; Score 907.4; DB 6; Length 1230;  
Best Local Similarity 99.9%; Pred. No. 2e-134;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1027 GAGGCTGAC 1035

RESULT 7  
LOCUS AX431308 1924 bp DNA linear PAT 28-JUN-2002  
DEFINITION Sequence 17 from Patent WO0240880.  
ACCESSION AX431308  
VERSION AX431308.1 GI:21656177  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1  
AUTHORS Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,  
Roth, W. and Stenner-Liewen, F.  
TITLE Novel death domain proteins  
JOURNAL Patent: WO 0240880-A 17 23-MAY-2002;  
BURNHAM INST (US)  
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Query Match 99.8%; Score 907.4; DB 6; Length 1924;  
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Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Homo sapiens death effector domain containing 2, mRNA (cDNA clone  
MGC:35529 IMAGE:5199772), complete cds.  
ACCESSION BC027930  
VERSION BC027930.1 GI:20379818  
KEYWORDS MGC.  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 1951)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haile, F.,  
Diachenko, L., Marinsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schaeetz, T.E., Brownstein, M.J., Ueda, T.B., Yoshiyuki, S.,  
Carninci, P., Prange, C., Raja, S.S., Loguigliano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

TITLE  
JOURNAL  
PUBMED  
REFERENCES  
AUTHORS  
JOURNAL  
TITLE

REMARK  
COMMENT

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M., Butlerfield, Y.S., Krzyzinski, M.I., Skalska, U., Smalins, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
2 (baeas 1 to 1951)  
Strausberg, R.  
Direct Submission  
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Larc, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stratiropoulos, S., Thomas, P.J., Touchman, J.W., Tsougenis, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>  
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923049.  
Location/Qualifiers

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ORIGIN  
Query Match 99.5%; Score 904.2; DB 9; Length 1951;  
Best Local Similarity 99.7%; Pred. No. 5.6e-134;

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DEFINITION Homo sapiens death effector domain-containing protein FLAME-3  
(FLAME-3) mRNA, complete cds.  
ACCESSION AF457575

VERSION AF457575.1 GI:20126793  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 981)  
AUTHORS Zhan, Y., Hegde, R., Srinivasula, S.M., Fernandes-Alnemri, T. and Alnemri, E.S.  
TITLE Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the Tffl1c102 subunit of human transcription factor IITC  
JOURNAL Cell Death Differ. 9 (4), 439-447 (2002)  
MEDLINE 21961615  
PUBMED 11965497  
REFERENCE 2 (bases 1 to 981)  
AUTHORS Alnemri, E.S.  
TITLE Direct Submission  
JOURNAL Submitted (11-DEC-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA

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Query Match 98.9%; Score 899.4; DB 9; Length 981;  
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DEFINITION Homo sapiens death effector domain-containing DNA-binding 2  
ACCESSION AY125488  
VERSION AY125488.1 GI:22475163

## KEYWORDS

## SOURCE

ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2012)  
AUTHORS Lee, J.C., Schickling, O., Stegh, A.H., Oshima, R.G., Dinsdale, D., Cohen, G.M., and Peter, M.E.  
TITLE DEDD regulates degradation of intermediate filaments during apoptosis  
JOURNAL J. Cell Biol. 158 (6), 1051-1066 (2002)

JOURNAL MEDLINE 22220288  
PUBMED 12235123  
REFERENCE 2 (bases 1 to 2012)  
AUTHORS Peter, M.E.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUN-2002) Ben May Cancer Institute, University of Chicago, 924 E. 57th Street, R112, Chicago, IL 60637, USA

## FEATURES

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DEFINITION	BC013372 2005 bp mRNA linear PRI 24-FEB-2004	
ACCESSION	MGC:16414 IMAGE:3941907, complete cds.	
VERSION	BC013372 GI:33872465	
KEYWORDS	MGC.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 2005)	
	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gumarate, P.H., Richard, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huliyil, S.N., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalim, D.B., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2005)	
AUTHORS	Straussberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: <a href="http://mgc.ncl.nih.gov">http://mgc.ncl.nih.gov</a>	
COMMENT	On Aug 19, 2003 this sequence version replaced gi:15426522.	
	Contact: MGC help desk	
	Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a>	
	Tissue Procurement: DCTD/DRP	
	CDNA Library Preparation: Rubin Laboratory	
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Institute for Systems Biology	
	<a href="http://www.systemsbiology.org">http://www.systemsbiology.org</a>	
	contact: <a href="mailto:amadnan@systemsbiology.org">amadnan@systemsbiology.org</a>	
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>

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REFERENCE					
AUTHORS	1 Mintz, L., Freilich, S. and Bernstein, J.				
TITLE	Novel nucleic acid and amino acid sequences				
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RESULT 14	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AF457576	993 bp	Mus musculus death effector domain-containing protein FLAME-3 (Flame-3) mRNA, complete cds.	AF457576	GI:20126795		Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 993)	Zhan, Y., Hegde, R., Srinivasula, S.M., Fernandes-Alnemri, T. and Alnemri, E.S.	Death effector domain-containing proteins DEDD and FLAME-3 form	

nuclear complexes with the TP11C102 subunit of human transcription factor IIC  
Cell Death Differ. 9 (4), 439-447 (2002)  
JOURNAL  
MEDLINE  
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PUBMED  
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REFERENCE  
2 (bases 1 to 993)  
Alnemri, E.S.  
Title  
Direct Submission  
Submitted (11-DEC-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA  
JOURNAL

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## ORIGIN

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ACCESSION AF543541  
VERSION AF543541.1 GI:23452816

KEYWORDS  
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ORGANISM  
Mus musculus  
(house mouse)

REFERENCE  
AUTHORS  
TITLE  
DEDD2 is a DED-containing protein targeted to the nucleolus  
Unpublished

2 (bases 1 to 993)  
Alcivar, A., Hu, S., and Yang, X.  
Direct Submission  
Submitted (06-SEP-2002) Abramson Family Cancer Research Institute,  
Univ of Pennsylvania, 421 Curie Blvd. 635 BRB1/III, Philadelphia,  
PA 19104-6160, USA

JOURNAL  
TITLE  
AUTHORS  
REFERENCE  
Unpublished

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Alcivar, A., Hu, S., and Yang, X.  
Direct Submission  
Submitted (06-SEP-2002) Abramson Family Cancer Research Institute,  
Univ of Pennsylvania, 421 Curie Blvd. 635 BRB1/III, Philadelphia,  
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## ORIGIN

Query Match 77.1%; Score 701; DB 10; Length 993;  
Best Local Similarity 86.8%; Pred. No. 1,1e-101;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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32: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1550	100.0	303	26	US-10-030-271-2
2	1550	100.0	326	26	US-10-030-271-4
3	1543	99.5	318	26	US-10-001-254-18
4	1543	99.5	318	37	US-60-301-889-18
5	1543	99.5	326	27	US-10-170-205E-10544
6	1543	99.5	326	27	US-10-170-205E-11301
7	1543	99.5	326	28	US-10-226-539-1
8	1543	99.5	326	37	US-60-452-680-19741
9	1543	99.5	326	37	US-60-452-680-19745
10	1543	99.5	366	1	PCT-US00-265248-4616
11	1543	99.5	366	27	US-10-106-628-4626
12	1413	91.2	304	20	US-09-669-445-11
13	1413	91.2	304	26	US-10-013-477-11
14	1413	91.2	304	27	US-10-100-683-7694
15	1413	91.2	304	36	US-11-001-793-7694
16	1404	90.6	319	1	PCT-US00-05918-758
17	1404	90.6	319	24	US-09-925-302-758
18	1366	88.1	266	21	US-09-715-893-18
19	987	63.7	242	1	PCT-US00-35017A-1220
20	987	63.7	242	28	US-10-236-115-1220
21	985	63.5	234	37	US-60-452-680-19742
22	950.5	61.3	277	18	US-09-488-725A-2950
23	950.5	61.3	277	28	US-10-258-898A-2950
24	950.5	61.3	277	28	US-10-286-897-2950
25	854	55.1	217	18	US-09-488-725A-6522
26	854	55.1	217	28	US-10-258-898A-6522
27	854	55.1	217	28	US-10-286-897-6522
28	703	45.4	220	22	US-09-758-446-1208
29	703	45.4	220	28	US-10-212-759-1208
30	622.5	40.2	318	35	US-09-629-669A-14195
31	622.5	40.2	318	35	US-10-917-503-14195
32	614.5	39.6	318	24	US-09-935-223-4
33	614.5	39.6	318	27	US-10-170-205E-12295
34	614.5	39.6	318	27	US-10-170-205E-12596
35	614.5	39.6	318	35	US-10-990-328-11652
36	614.5	39.6	318	35	US-10-990-328-11653
37	614.5	39.6	318	35	US-10-990-328-11654
38	614.5	39.6	318	37	US-60-443-566-3778
39	614.5	39.6	318	37	US-60-443-566-3778
40	614.5	39.6	318	37	US-60-452-680-19405
41	614.5	39.6	318	37	US-60-452-680-19405
42	614.5	39.6	318	37	US-60-453-050-11584
43	614.5	39.6	318	37	US-60-453-050-11584
44	614.5	39.6	318	37	US-60-453-135-11584
45	614.5	39.6	318	37	US-60-453-135-11585

## ALIGNMENTS

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RESULT 1
US-10-030-271-2
; Sequence 2, Application US/10030271
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HIO, YURI
; APPLICANT: MIYOSHI, SOUSUKE
; APPLICANT: SATOH, SUSUMU
; TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR
; FILE REFERENCE: 217860USOPT
; CURRENT APPLICATION NUMBER: US/10/030, 271
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: JP 11-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: US 60/159, 586
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 13
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SOFTWARE: Patentin version 3.1  
SEQ ID NO 2  
LENGTH: 303  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-030-271-2

Query Match 100.0%; Score 1550; DB 26; Length 303;  
Best Local Similarity 100.0%; Pred. No. 7e-128;  
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAAGIA 60  
DB 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAAGIA 60  
QY 61 RARSGLELLELERRGCGESNRLGQLRLVLAHDLPHLARRRRPPSPERSYSGTS 120  
DB 61 RARSGLELLELERRGCGESNRLGQLRLVLAHDLPHLARRRRPPSPERSYSGTS 120  
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRQRSGRPSGGARRRRRGAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRQRSGRPSGGARRRRRGAPAPQ 180  
QY 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALGEGVARRPPQALARQLDVFGQATVLR 240  
DB 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALGEGVARRPPQALARQLDVFGQATVLR 240  
QY 241 SRDLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300  
DB 241 SRDLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 2  
US-10-030-271-4

*extended and combined*

Sequence 4, Application US/10030271  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TOSHIO  
APPLICANT: NISHIKAWA, TETSUO  
APPLICANT: HIO, YORI  
APPLICANT: MIYOSHI, SOUSUKE  
TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR  
FILE REFERENCE: 21780USOPT  
CURRENT FILING DATE: US/10/030,271  
PRIOR FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: JP 11-194179  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: US 60/159,586  
PRIOR FILING DATE: 1999-10-18  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 326  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-030-271-4

Query Match 100.0%; Score 1550; DB 26; Length 326;  
Best Local Similarity 100.0%; Pred. No. 7e-128;  
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAAGIA 60  
DB 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAAGIA 60  
QY 61 RARSGLELLELERRGCGESNRLGQLRLVLAHDLPHLARRRRPPSPERSYSGTS 120  
DB 61 RARSGLELLELERRGCGESNRLGQLRLVLAHDLPHLARRRRPPSPERSYSGTS 120

QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRQRSGRPSGGARRRRRGAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRQRSGRPSGGARRRRRGAPAPQ 180  
QY 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALGEGVARRPPQALARQLDVFGQATVLR 240  
DB 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALGEGVARRPPQALARQLDVFGQATVLR 240  
QY 241 SRDLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300  
DB 241 SRDLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 3  
US-10-001-254-18

Sequence 18, Application, US/10001254  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Fiorentino, Loredana  
APPLICANT: Lee, Sung Hyung  
APPLICANT: Roth, Wilfred  
TITLE OF INVENTION: Novel Death Domain Proteins  
FILE REFERENCE: P-LJ 5037  
CURRENT FILING DATE: US/10/001,254  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/301,889  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/715,893  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-001-254-18

Query Match 99.5%; Score 1543; DB 26; Length 318;  
Best Local Similarity 99.7%; Pred. No. 3.1e-127;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAAGIA 60  
DB 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAAGIA 60  
QY 61 RARSGLELLELERRGCGESNRLGQLRLVLAHDLPHLARRRRPPSPERSYSGTS 120  
DB 61 RARSGLELLELERRGCGESNRLGQLRLVLAHDLPHLARRRRPPSPERSYSGTS 120  
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRQRSGRPSGGARRRRRGAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRQRSGRPSGGARRRRRGAPAPQ 180  
QY 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALGEGVARRPPQALARQLDVFGQATVLR 240  
DB 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALGEGVARRPPQALARQLDVFGQATVLR 240  
QY 241 SRDLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300  
DB 241 SRDLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300  
QY 301 EAD 303  
DB 301 EAD 303



RESULT 4  
US-60-301-889-18  
; Sequence 18, Application US/60301889  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawlowski, Krzysztof  
; APPLICANT: Fiorentino, Loredana  
; APPLICANT: Lee, Sung Hyung  
; APPLICANT: Roth, Wilfred  
; APPLICANT: Steiner-Liewen, Frank  
; TITLE OF INVENTION: Novel Death Domain Proteins  
; FILE REFERENCE: P-LJ 4718  
; CURRENT APPLICATION NUMBER: US/60/301,889  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-301-889-18

Query Match 99.5%; Score 1543; DB 37; Length 318;  
Best Local Similarity 99.7%; Pred. No. 3.1e-127;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPPCWEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60  
DB 1 MALSGTAPPCWEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60  
QY 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120  
DB 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120  
QY 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKQRRSRGPGGARRRRRGAAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKQRRSRGPGGARRRRRGAAPAPQ 180  
QY 181 QOSEPARPSSGKYTCIDRLRVRAVYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
DB 181 QOSEPARPSSGKYTCIDRLRVRAVYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
QY 241 SRDLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300  
DB 241 SRDLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 5  
US-10-170-205B-10544  
; Sequence 10544, Application US/10170205B  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark  
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN  
; FILE REFERENCE: CL001381  
; CURRENT APPLICATION NUMBER: US/10/170,205B  
; CURRENT FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 40312  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10544  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-205B-10544

Query Match 99.5%; Score 1543; DB 27; Length 326;  
Best Local Similarity 99.7%; Pred. No. 3.2e-127;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MALSGTAPPCWEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60  
DB 1 MALSGTAPPCWEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60  
QY 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120  
DB 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120  
QY 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKQRRSRGPGGARRRRRGAAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKQRRSRGPGGARRRRRGAAPAPQ 180  
QY 181 QOSEPARPSSGKYTCIDRLRVRAVYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
DB 181 QOSEPARPSSGKYTCIDRLRVRAVYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
QY 241 SRDLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300  
DB 241 SRDLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 6  
US-10-170-205B-11301  
; Sequence 11301, Application US/10170205B  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark  
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN  
; FILE REFERENCE: CL001381  
; CURRENT APPLICATION NUMBER: US/10/170,205B  
; CURRENT FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 40312  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11301  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-205B-11301

Query Match 99.5%; Score 1543; DB 27; Length 326;  
Best Local Similarity 99.7%; Pred. No. 3.2e-127;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPPCWEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60  
DB 1 MALSGTAPPCWEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60  
QY 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120  
DB 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120  
QY 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKQRRSRGPGGARRRRRGAAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKQRRSRGPGGARRRRRGAAPAPQ 180  
QY 181 QOSEPARPSSGKYTCIDRLRVRAVYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
DB 181 QOSEPARPSSGKYTCIDRLRVRAVYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
QY 241 SRDLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300  
DB 241 SRDLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300  
QY 301 EAD 303  
DB 301 EAD 303

patch

```
RESULT 7
US-10-296-539-1
; Sequence 1, Application US/10296539
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: REGULATORS OF APOPTOSIS
; FILE REFERENCE: PI-0307 PCT
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/10/296,539
; PRIOR FILING DATE: 2000-06-01; 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO: 3102521CD1
US-10-296-539-1
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Query Match      99.5%; Score 1543; DB 28; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MALSGSTPAPCWEDECDIDYGMLSLHRMFEVVGQLTCELELLAFLIDBAPGAAGLA 60
DB 1 MALSGSTPAPCWEDECDIDYGMLSLHRMFEVVGQLTCELELLAFLIDBAPGAAGLA 60
QY 61 RARSGLELLELERRGCGESNLRLLGQLRLVLAHDLPHLARKRRPVSPERYSGTS 120
DB 61 RARSGLELLELERRGCGESNLRLLGQLRLVLAHDLPHLARKRRPVSPERYSGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRVRAEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRVRAEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSTYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVLLVSVD 300
DB 241 SRDLGSVVCIDIKFSELSTYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVLLVSVD 300
QY 301 EAD 303
DB 301 EAD 303
US-60-452-680-19741
; Sequence 19741, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 19741
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-19741
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Query Match      99.5%; Score 1543; DB 37; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MALSGSTPAPCWEDECDIDYGMLSLHRMFEVVGQLTCELELLAFLIDBAPGAAGLA 60
DB 1 MALSGSTPAPCWEDECDIDYGMLSLHRMFEVVGQLTCELELLAFLIDBAPGAAGLA 60
QY 61 RARSGLELLELERRGCGESNLRLLGQLRLVLAHDLPHLARKRRPVSPERYSGTS 120
DB 61 RARSGLELLELERRGCGESNLRLLGQLRLVLAHDLPHLARKRRPVSPERYSGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRVRAEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRVRAEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSTYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVLLVSVD 300
DB 241 SRDLGSVVCIDIKFSELSTYLDAPFMDYLSGALLQALRGVFLTEALREAVGREAVLLVSVD 300
QY 301 EAD 303
DB 301 EAD 303
```

```
RESULT 9
US-60-452-680-19745
; Sequence 19745, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19745
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-19745
```

```
Query Match      99.5%; Score 1543; DB 37; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 MALSGSTPAPCWEDECDIDYGMLSLHRMFEVVGQLTCELELLAFLIDBAPGAAGLA 60
DB 1 MALSGSTPAPCWEDECDIDYGMLSLHRMFEVVGQLTCELELLAFLIDBAPGAAGLA 60
QY 61 RARSGLELLELERRGCGESNLRLLGQLRLVLAHDLPHLARKRRPVSPERYSGTS 120
DB 61 RARSGLELLELERRGCGESNLRLLGQLRLVLAHDLPHLARKRRPVSPERYSGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRVRAEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRVRAEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
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Qy	241	SRDLGSVVCDDIKFSELSYLDAFMGDPYLSGALLQALRGVFTLTALREAVGRVRLVSYD	300
Dy	241 <td>SRDLGSVVCDDIKFSELSYLDAFMGDPYLSGALLQALRGVFTLTALREAVGRVRLVSYD <td>300</td> </td>	SRDLGSVVCDDIKFSELSYLDAFMGDPYLSGALLQALRGVFTLTALREAVGRVRLVSYD <td>300</td>	300
Qy	301	EAD 303	
Dy	301	EAD 303	

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RESULT 10
PCT-US00-26524B-4616
; Sequence 4616, Application PC/TUS0026524B
. GENERAL INFORMATION.

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Query Match	99.5%	Score 1543	DB 1	Length 366
Best Local Similarity	99.7%	Pred. No. 3.8e-127		
Matches 302, Conservative	0	Mismatches 1	Indels 0	Gaps 0

RESULT 11  
US-10-106-698-4626  
: Sequence 4626, Application US/10106698  
: GENERAL INFORMATION:

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? PRIOR APPLICATION NUMBER: US 60/163,280
? PRIOR FILING DATE: 1999-11-03
? NUMBER OF SEQ ID NOS: 8554
? SOFTWARE: PatentIn Ver. 3.0
? SEQ ID NO 4626
? LENGTH: 366
? TYPE: FRT
? ORGANISM: Homo sapiens
? US-10-106-698-4626

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Query Match	99.5%	Score 1543	DB 27	Length 366
Best Local Similarity	99.7%	Pred. No. 3.8e-127		
Matches 302; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

RESULT 12  
 US-09-669-445-11  
 : Sequence 11, Application US/09669445  
 : GENERAL INFORMATION:  
 : APPLICANT: Ni et al.  
 : TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies  
 : FILE REFERENCE: PTO02PI  
 : CURRENT APPLICATION NUMBER: US/09/669,445  
 : PRIOR FILING DATE: 2000-09-25  
 : PRIOR APPLICATION NUMBER: PCT/US00/06642  
 : PRIOR FILING DATE: 2000-03-15  
 : PRIOR APPLICATION NUMBER: 60/126,018  
 : PRIOR FILING DATE: 1999-03-24  
 : PRIOR APPLICATION NUMBER: 60/139,638  
 : PRIOR FILING DATE: 1999-06-17  
 : PRIOR APPLICATION NUMBER: 60/149,449  
 : PRIOR FILING DATE: 1999-08-18  
 : NUMBER OF SEQ ID NOS: 27  
 : SOFTWARE: Patentln Ver. 2.0  
 : SEQ ID NO 11  
 : LENGTH: 304  
 : TYPE: prt  
 : ORGANISM: Homo sapiens  
 : US-09-669-445-11

Query Match	91.2%	Score 1413	DB 20	Length 304
Best Local Similarity	99.6%	Pred. No. 9.1e-116		
Matches 280; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

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Db      241 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 281

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RESULT 13
US-10-013-477-11
; Sequence 11, Application US/10013477
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P1002P1
; CURRENT APPLICATION NUMBER: US/10/013,477
; PRIOR FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/669,445
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US00/06642
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/126,018
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/139,638
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/149,449
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-477-11

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Query Match      91.2%; Score 1413; DB 26; Length 304;
Best Local Similarity 99.6%; Pred. No. 9,1e-116;
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Db      181 RAEYCEHGPALAEQGVASRRPQALARQLDVFGQATVILSRDLGSVCDIKFSELSYLDLF 240
Qy      263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
Db      241 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 281

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RESULT 14
US-10-100-683-7694
; Sequence 7694, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.

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; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5900
; CURRENT APPLICATION NUMBER: US/10/100,683
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,539
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7694
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-683-7694

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Query Match      91.2%; Score 1413; DB 27; Length 304;
Best Local Similarity 99.6%; Pred. No. 9,1e-116;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      23 MLSHRMFEVVGQUTCELELILAFLLDEAPGAGGLARARSGLELLELERRGCGGSEN 82
Db      1 MLSHRMFEVVGQUTCELELILAFLLDEAPGAGGLARARSGLELLELERRGCGGSEN 60
Qy      83 LRLGQLRLVLRARDLPLHLARKRRPVSPEYSGTSSSKRTGSCRRRRQSSSSANS 142
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Qy      143 OQGOWETSPPTKQRRSRGRRSGGARRRRRGAPAPPOQOSEPARPSSEGVTCDIRLRV 202
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Qy      263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
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RESULT 15
US-11-001-793-7694
; Sequence 7694, Application US/11001793
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5900
; CURRENT APPLICATION NUMBER: US/11/001,793
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/100,683
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11

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; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7694
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-001-793-7694

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Query Match      91.2%; Score 1413; DB 36; Length 304;
Best Local Similarity 99.6%; Pred. No. 9.1e-116;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Db 901 GAGGCTGAC 909

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## RESULT 2

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; Sequence 3, Application US/10030271
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HIO, YURI
; APPLICANT: MIYOSHI, SOUSUKE
; APPLICANT: SATOH, SUSUMU
; TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR
; FILE REFERENCE: 217860USOECT
; CURRENT APPLICATION NUMBER: US/10/030,271
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: JP 11-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: US 60/159,586
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(1101)
; OTHER INFORMATION:
US-10-030-271-3

```

Don

Compared APO 1 to 3

```

Query Match 100.0%; Score 909; DB 46; Length 1883;
Beet Local Similarity 100.0%; Pred. No. 4e-150;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGCTATCCGGGTGAGACCCCGGCGCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 60
Db 124 ATGGCGCTATCCGGGTGAGACCCCGGCGCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 183
Qy 61 TAGCGGATGCTGTGCTTCAACCGTATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC 120
Db 184 TAGCGGATGCTGTGCTTCAACCGTATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC 243
Qy 121 GAGCTGAGACTCTGGCTTTGCTGCTGANTGAGGCTCTGGGCGCGCGGAGGCTTAGGC 180
Db 244 GAGCTGAGACTCTGGCTTTGCTGCTGANTGAGGCTCTGGGCGCGCGGAGGCTTAGGC 303
Qy 181 CGGGCCCGGAGCGGCTTAGAGCTCTGTGTGAGCTGAGAGCGCGCGGAGAGTGCAGCGAG 240

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Db 304 CGGGCCCCAGGCGCTGAGAGCTCTGTGTGAGCTGAGAGCGCGCGGCGAGTGCAGCGAG 363
Qy 241 AGCAACTGCGGCTGTGTGGGCAACTCTGTGGCGGCTGTGGAGCGCGGCGAGCTGTGCGG 300
Db 364 AGCAACTGCGGCTGTGTGGGCAACTCTGTGGCGGCTGTGGAGCGCGGCGAGCTGTGCGG 423
Qy 301 CACTGTGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAACCTATAGCTATGAGCACTTC 360
Db 424 CACTGTGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAACCTATAGCTATGAGCACTTC 483
Qy 361 AGCTTTCAAGAGAGACAGAGGTTAGTGTGCGGTGCGCTGTGAGTCAAGCACTTCTGCA 420
Db 484 AGCTTTCAAGAGAGACAGAGGTTAGTGTGCGGTGCGCTGTGAGTCAAGCACTTCTGCA 543
Qy 421 AATTCTCAGCAGGCTCAGTGGAGACAGGCTCCCCCAACCAACGAGGCGGAGT 480
Db 544 AATTCTCAGCAGGCTCAGTGGAGACAGGCTCCCCCAACCAACGAGGCGGAGT 603
Qy 481 CGGGGCGGCGCAGTGTGTGTGTCAGACGCGCGGCGAGAGGCGGCGGCGGCGGCGGAGT 540
Db 604 CGGGGCGGCGCAGTGTGTGTGTCAGACGCGCGGCGAGAGGCGGCGGCGGCGGCGGAGT 663
Qy 541 CAGCAGTCAAGAGCCCGCAGACCTTCTGTGAGGCGAAAGTGAAGCTGTGATCCGAGTTC 600
Db 664 CAGCAGTCAAGAGCCCGCAGACCTTCTGTGAGGCGAAAGTGAAGCTGTGATCCGAGTTC 723
Qy 601 CGGGTTCCAGCAGAGTAATCTGAGCATGAGGCGCAGCCTTGAGACAGGCGCTGGCATCCGG 660
Db 724 CGGGTTCCAGCAGAGTAATCTGAGCATGAGGCGCAGCCTTGAGACAGGCGCTGGCATCCGG 783
Qy 661 CGGGCCCCAGGCGCTGCGCGCGCAGCTGAGAGTGTGTTGGCGAGCCACCGCAGTGTCTGGC 720
Db 784 CGGGCCCCAGGCGCTGCGCGCGCAGCTGAGAGTGTGTTGGCGAGCCACCGCAGTGTCTGGC 843
Qy 721 TCAGGAGGACCTGGGCTGTGTGTGTGTGATCAATCAAGTTCTGAGAGTCTCCATCTGAGC 780
Db 844 TCAGGAGGACCTGGGCTGTGTGTGTGTGATCAATCAAGTTCTGAGAGTCTCCATCTGAGC 903
Qy 781 GCGCTTCTGGGCGCAGTAACCTGAGTGGCGCCTGTCTGACAGGCGCTGGCGGCTGTCTCTG 840
Db 904 GCGCTTCTGGGCGCAGTAACCTGAGTGGCGCCTGTCTGACAGGCGCTGGCGGCTGTCTCTG 963
Qy 841 ACTGAGGCGCTTCTGAGAGGCTGTGGGCGCGAGGCTGTTCGCTGTGCTGATGTGAT 900
Db 964 ACTGAGGCGCTTCTGAGAGGCTGTGGGCGCGAGGCTGTTCGCTGTGCTGATGTGAT 1023
Qy 901 GAGGCTGAC 909
Db 1024 GAGGCTGAC 1032

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## RESULT 3

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US-10-296-539-4
; Sequence 4, Application US/10296539
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. TOM
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: ELIOTT, Vicki S.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: REGULATORS OF APOPTOSIS
; FILE REFERENCE: PI-0307 PCT
; CURRENT APPLICATION NUMBER: US/10/296,539
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
; PRIOR FILING DATE: 2000-06-24; 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program

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; SEQ ID NO 4
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3102521CB1
US-10-236-539-4

```

```

Query Match      99.8%; Score 907.4; DB 51; Length 1230;
Best Local Similarity 99.9%; Pred. No. 7,8e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 ATGGCGCTATCCGGGTGCAACCCCGCCCTGCTGGAGAGAGATGCTGACTTAC 60
DB 127 ATGGCGCTATCCGGGTGCAACCCCGCCCTGCTGGAGAGAGATGCTGACTTAC 186
QY 61 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGGCACTGACCGAGTGC 120
DB 187 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGGCACTGACCGAGTGC 246
QY 121 GAGCTGAGACTCTGCGCTTTCTGCTGATGAGGCTCTCTGCGCGCCGAGGCTTAAGC 180
DB 247 GAGCTGAGACTCTGCGCTTTCTGCTGATGAGGCTCTCTGCGCGCCGAGGCTTAAGC 306
QY 181 CGGGCCCGAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 240
DB 307 CGGGCCCGAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 366
QY 241 AGCAACCTGCGGCTGCTGGGCACTCTGCGCGCTGCTGGCGCGCGCAACCTGCTGCG 300
DB 367 AGCAACCTGCGGCTGCTGGGCACTCTGCGCGCTGCTGGCGCGCGCAACCTGCTGCG 426
QY 301 CACCTGCGCGCAAGCGCGCGCGCACTGCTGCAAGACGCTATAGTATGCACTCC 360
DB 427 CACCTGCGCGCAAGCGCGCGCGCACTGCTGCAAGACGCTATAGTATGCACTCC 486
QY 361 AGCTTTTAAAGAGACAGAGGTAAGTGTGCTGCGCTGCGGCACTGCAAGCTTCTGCA 420
DB 487 AGCTTTTAAAGAGACAGAGGTAAGTGTGCTGCGCTGCGGCACTGCAAGCTTCTGCA 546
QY 421 AATTCTGAGAGGCTCAGTGGGAGACAGGCTCCCCCAACCAAGCGGCAAGCGGAGT 480
DB 547 AATTCTGAGAGGCTCAGTGGGAGACAGGCTCCCCCAACCAAGCGGAGGCGGAGT 606
QY 481 CGGGGCGCGCCAGTGTGTGTCAGACGCGCGCGAGAGGGGCCCAAGCCGCAAGCCAG 540
DB 607 CGGGGCGCGCCAGTGTGTGTCAGACGCGCGCGAGAGGGGCCCAAGCCGCAAGCCAG 666
QY 541 CAGCACTCAAGACCCCGCAACCTTCTCTGAAAGCAAGTGAAGCTTGTGACATCCGCTC 600
DB 667 CAGCACTCAAGACCCCGCAACCTTCTCTGAAAGCAAGTGAAGCTTGTGACATCCGCTC 726
QY 601 CGGGTTCAGAGAGTACTGAGAGATGGGCAAGCTTGAAGAGGGGTGGCAATCCCGG 660
DB 727 CGGGTTCAGAGAGTACTGAGAGATGGGCAAGCTTGAAGAGGGGTGGCAATCCCGG 786
QY 661 CGGGCCCGAGCGCTGCGCGCGAGCTGATGTTGGGCAAGCCAGCAAGTGTGCGC 720
DB 787 CGGGCCCGAGCGCTGCGCGCGAGCTGATGTTGGGCAAGCCAGCAAGTGTGCGC 846
QY 721 TCAAGGAGACTGCTGTGTGTTGTGACATCAAGTTCTCAAGCTTCTCTATCTGAGC 780
DB 847 TCAAGGAGACTGCTGTGTGTTGTGACATCAAGTTCTCTATCTGAGC 906
QY 781 GCCTTCGGGGGCACTACTAGTGGGCGCTGCTGAGGCGCTGCGGGGGGTGTTCTCG 840
DB 907 GCCTTCGGGGGCACTACTAGTGGGCGCTGCTGAGGCGCTGCGGGGGGTGTTCTCG 966
QY 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTCGCTGCTGCTGAGTGTGAT 900
DB 967 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTCGCTGCTGCTGAGTGTGAT 1026

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QY 901 GAGGCTGAC 909
DB 1027 GAGGCTGAC 1035

```

## RESULT 4

US-10-001-254-17

Sequence 17, Application US/10001254

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Godzik, Adam

APPLICANT: Pawlowski, Krzysztof

APPLICANT: Fiorentino, Loredana

APPLICANT: Lee, Sug Hyung

APPLICANT: Roth, Wilfred

APPLICANT: Stenmer-Liwen, Frank

TITLE OF INVENTION: Novel Death Domain Proteins

FILE REFERENCE: P-IJ 5037

CURRENT APPLICATION NUMBER: US/10/001,254

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/301,889

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: 09/715,893

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 1924

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: CDS

LOCATION: (91)...(1044)

NAME/KEY: misc feature

LOCATION: (1)...(1900)

OTHER INFORMATION: n = A,T,C or G

US-10-001-254-17

```

Query Match      99.8%; Score 907.4; DB 46; Length 1924;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 ATGGCGCTATCCGGGTGCAACCCCGCCCTGCTGGAGAGAGATGCTGACTTAC 60
DB 91 ATGGCGCTATCCGGGTGCAACCCCGCCCTGCTGGAGAGAGATGCTGACTTAC 150
QY 61 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGCAACTGACCGAGTGC 120
DB 151 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGCAACTGACCGAGTGC 210
QY 121 GAGCTGAGACTCTGCGCTTTCTGCTGATGAGGCTCTGCGCGCGCGCAAGCTTAAGC 180
DB 211 GAGCTGAGACTCTGCGCTTTCTGCTGATGAGGCTCTGCGCGCGCGCAAGCTTAAGC 270
QY 181 CGGGCCCGAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGCGCAAGCTTGTGCGC 240
DB 271 CGGGCCCGAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGCGCAAGCTTGTGCGC 330
QY 241 AGCAACCTGCGGCTGCTGGGCAACTCTGCGCGTGGCGCGCGCAAGCTTGTGCGC 300
DB 331 AGCAACCTGCGGCTGCTGGGCAACTCTGCGCGTGGCGCGCGCAAGCTTGTGCGC 390
QY 301 CACCTGCGCGCAAGCGGCGCGCAAGTGTCTCAAGACGCTATAGTATGAGCACTCC 360
DB 391 CACCTGCGCGCAAGCGGCGCGCAAGTGTCTCAAGACGCTATAGTATGAGCACTCC 450
QY 361 AGCTTTTAAAGAGACAGAGGTAAGTGTGCTGCGGCTGCGGCAAGCAAGTGTGCA 420
DB 451 AGCTTTTAAAGAGACAGAGGTAAGTGTGCTGCGGCTGCGGCAAGCAAGTGTGCA 510
QY 421 AATTCTGAGAGGCTCAGTGGGAGACAGGCTCCCCCAACCAAGCGGCAAGCGGAGT 480
DB 511 AATTCTGAGAGGCTCAGTGGGAGACAGGCTCCCCCAACCAAGCGGCAAGCGGAGT 570

```



ORGANISM: HUMAN  
US-10-170-235-12745

Query Match 99.8%; Score 907.4; DB 49; Length 1959;  
Best Local Similarity 99.9%; Pred. No. 7,6e-150;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ATGGGCTATCCGGCTGACCCCGCCGCTGCTGGAGAGATGAGTGGCTGACTAC 60
DB 138 ATGGGCTATCCGGCTGACCCCGCCGCTGCTGGAGAGATGAGTGGCTGACTAC 197
QY 61 TACGGAGATGCTGCTGACCGTATGTTGAGGTGTGGGGGCACTGACCGAGTGC 120
DB 198 TACGGAGATGCTGCTGACCGTATGTTGAGGTGTGGGGGCACTGACCGAGTGC 257
QY 121 GAGCTGAGACTCTGAGCTTTCTGCTGATGAGGCTCTGGCGCCGCGAGAGCTTAAGCC 180
DB 258 GAGCTGAGACTCTGAGCTTTCTGCTGATGAGGCTCTGGCGCCGCGAGAGCTTAAGCC 317
QY 181 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 240
DB 318 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 377
QY 241 AGCAACTGCGGCTGCTGGGAGCACTCCGCGCGGCTGCGCCGCGCAGACCTGCTGCG 300
DB 378 AGCAACTGCGGCTGCTGGGAGCACTCCGCGCGGCTGCGCCGCGCAGACCTGCTGCG 437
QY 301 CACCTGCGCGCAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGCTATAGCACTCC 360
DB 438 CACCTGCGCGCAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGCTATAGCACTCC 497
QY 361 AGCTTTTAAAGAGACAGAGGTAGCTGCGCGCTGCGCGCTGCGGCACTGAGCACTTCCCA 420
DB 498 AGCTTTTAAAGAGACAGAGGTAGCTGCGCGCTGCGCGCTGCGGCACTGAGCACTTCCCA 557
QY 421 AATTCTCAGCAGAGGTCACTGAGGAGACAGAGTCCCCCAACCAACGCGGAGCGAGT 480
DB 558 AATTCTCAGCAGAGGTCACTGAGGAGACAGAGTCCCCCAACCAACGCGGAGCGAGT 617
QY 481 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 540
DB 618 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 677
QY 541 CAGCAGTGAAGAGCCCGCAGACCTTCTCTGAAGCAAGTGAAGCTTGTGACATCCGCTC 600
DB 678 CAGCAGTGAAGAGCCCGCAGACCTTCTCTGAAGCAAGTGAAGCTTGTGACATCCGCTC 737
QY 601 CGGGTTGAGAGAGTACTGAGAGCATGAGGCAAGCTTGAAGAGAGGAGTATCCCGG 660
DB 738 CGGGTTGAGAGAGTACTGAGAGCATGAGGCAAGCTTGAAGAGAGGAGTATCCCGG 797
QY 661 CGGGCCCGCAGCGGCTTAGAGCTGTTTGGGAGGCGCAGCGGCACTGGCTGCGC 720
DB 798 CGGGCCCGCAGCGGCTTAGAGCTGTTTGGGAGGCGCAGCGGCACTGGCTGCGC 857
QY 721 TCAAGGAGACCTGGGCTCTGTGTGTTGTGACATCAAGTTCTCAAGCTCTCTATCTGAC 780
DB 858 TCAAGGAGACCTGGGCTCTGTGTGTTGTGACATCAAGTTCTCTATCTGAC 917
QY 781 GCTTCTGGGGGAGACTGAGTGGCGCCCTGCTGAGGCGCCGCGGGGAGGTTCTCG 840
DB 918 GCTTCTGGGGGAGACTGAGTGGCGCCCTGCTGAGGCGCCGCGGGGAGGTTCTCG 977
QY 841 ACTGAGGCGCTGAGAGAGCTGTGGGCGGAGGCTGTTGCTGCTGTGCTGAGTGTGAT 900
DB 978 ACTGAGGCGCTGAGAGAGCTGTGGGCGGAGGCTGTTGCTGCTGTGCTGAGTGTGAT 1037
QY 901 GAGGCTGAC 909
DB 1038 GAGGCTGAC 1046
```

RESULT 7

US-10-170-235-11944  
Sequence 11944, Application US/10170235  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig  
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN  
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF  
FILE REFERENCE: CLO01380  
CURRENT APPLICATION NUMBER: US/10/170,235  
CURRENT FILING DATE: 2003-03-17  
NUMBER OF SEQ ID NOS: 42514  
SEQ ID NO 11944  
LENGTH: 2011  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-170-235-11944

Query Match 99.8%; Score 907.4; DB 49; Length 2011;  
Best Local Similarity 99.9%; Pred. No. 7,6e-150;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ATGGGCTATCCGGCTGACCCCGCCGCTGCTGGAGAGATGAGTGGCTGACTAC 60
DB 189 ATGGGCTATCCGGCTGACCCCGCCGCTGCTGGAGAGATGAGTGGCTGACTAC 248
QY 61 TACGGAGATGCTGCTGACCGTATGTTGAGGTGTGGGGGCACTGACCGAGTGC 120
DB 249 TACGGAGATGCTGCTGACCGTATGTTGAGGTGTGGGGGCACTGACCGAGTGC 308
QY 121 GAGCTGAGACTCTGAGCTTTCTGCTGATGAGGCTCTGGCGCCGCGAGAGCTTAAGCC 180
DB 309 GAGCTGAGACTCTGAGCTTTCTGCTGATGAGGCTCTGGCGCCGCGAGAGCTTAAGCC 368
QY 181 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 240
DB 369 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 428
QY 241 AGCAACTGCGGCTGCTGGGAGCACTCCGCGCGCTGCTGCGCCGCGCAGACCTGCTGCG 300
DB 429 AGCAACTGCGGCTGCTGGGAGCACTCCGCGCGCTGCTGCGCCGCGCAGACCTGCTGCG 488
QY 301 CACCTGCGCGCAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGCTATAGCACTCC 360
DB 489 CACCTGCGCGCAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGCTATAGCACTCC 548
QY 481 CGGGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGCGGCACTGGCGGAG 540
DB 609 AATTCTCAGCAGAGGTCACTGAGGAGACAGAGTCCCCCAACCAAGCGGAGCGGAGT 668
QY 661 CGGGCCCGCAGCGGCTTAGAGCTGTTTGGGAGGCGCAGCGGCACTGGCTGCGC 720
DB 729 CAGCAGTGAAGAGCCCGCAGACCTTCTCTGAAGCAAGTGAAGCTTGTGACATCCGCTC 788
QY 781 GCTTCTGGGGGAGACTGAGTGGCGCCCTGCTGAGGCGCCGCGGGGAGGTTCTCG 840
DB 918 GCTTCTGGGGGAGACTGAGTGGCGCCCTGCTGAGGCGCCGCGGGGAGGTTCTCG 977
QY 841 ACTGAGGCGCTGAGAGAGCTGTGGGCGGAGGCTGTTGCTGCTGTGCTGAGTGTGAT 900
DB 909 TCAAGGAGACCTGGGCTCTGTGTGTTGTGACATCAAGTTCTCAAGCTCTCTATCTGAC 968
QY 721 TCAAGGAGACCTGGGCTCTGTGTGTTGTGACATCAAGTTCTCAAGCTCTCTATCTGAC 780
DB 909 TCAAGGAGACCTGGGCTCTGTGTGTTGTGACATCAAGTTCTCAAGCTCTCTATCTGAC 968
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Db 969 GCGCTTCGGGGAGACCTGAGTGGCGCCCTGCTGACAGGCCCTGGGGCGCTGTCCG 1028
Qy 841 ACTGAGGCCCTGCGAGAGGCTGTGGGCGGGAGGCGCTTCCGCTGCTGCTGAGTGGAT 900
Db 1029 ACTGAGGCCCTTCCGAGAGGCTGTGGGCGGGAGGCTGTTCGCTGCTGCTGAGTGGAT 1088
Qy 901 GAGGCTGAC 909
Db 1089 GAGGCTGAC 1097

RESULT 8
PCT-US00-26524B-339
; Sequence 339, Application PC/TUS0026524B
; GENERAL INFORMATION:
; APPLICANT: Birse et. al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26524B
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-26524B-339

Query Match 99.8%; Score 907.4; DB 1; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGTATCCGGGTCGAGCCCGGCGCCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 60
Db 121 ATGGGCGTATCCGGGTCGAGCCCGGCGCCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 180
Qy 61 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGTGGCGGCACTGACCGAGTGC 120
Db 181 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGTGGCGGCACTGACCGAGTGC 240
Qy 121 GAGCTGAGACTCTGSCCTTTTCTGCTGAGTGAAGCTCTTGGCGCCCGCGAGGCTTAGCC 180
Db 241 GAGCTGAGACTCTTGGCTTTTCTGCTGAGTGAAGCTCTTGGCGCCCGCGAGGCTTAGCC 300
Qy 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGAGCGCGCGGAGAGTGGCGAG 240
Db 301 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGAGCGCGCGGAGAGTGGCGAG 360
Qy 241 AGCAACCTGCGGCTGTGGGGCAACTCTGCGCGTGTGGCGCCCGCGACGACTGCTGCCG 300
Db 361 AGCAACCTGCGGCTGTGGGGCAACTCTGCGCGTGTGGCGCCCGCGACGACTGCTGCCG 420
Qy 361 ACCTCTTCAAGAGAGCAGAGGAGTACCTCCGTCGCGCTGCGGAGCTCAAGCAAGTTCTGA 420
Db 481 ACCTCTTCAAGAGAGCAGAGGAGTACCTCCGTCGCGCTGCGGAGCTCAAGCAAGTTCTGA 540
Qy 421 CACTGTGGCGGCAAGGCGGCGCGGCAAGTGTCTCCAGAAAGCTATGCTATGGCACTTCC 480
Db 541 CACTGTGGCGGCAAGGCGGCGCGGCAAGTGTCTCCAGAAAGCTATGCTATGGCACTTCC 600
Qy 541 AATTCTCAGCAGAGGTAGTGGAGACAGGCTCCCGCCCAACCAAGGCGAGCGCGAGT 600
Db 601 AATTCTCAGCAGAGGTAGTGGAGACAGGCTCCCGCCCAACCAAGGCGAGCGCGAGT 660
Qy 601 CGGGCCCGGCGGCTGAGTGTGTGCAAGCGCGCGGAGAGAGGCGCCCGACCGCACCCGAG 660
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Qy 541 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAAGCTGTGAATCCGAGCTC 600
Db 661 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAAGCTGTGAATCCGAGCTC 720
Qy 601 CGGGTTCCAGAGAGTACTTCCGAGAGATGGGCGCAGCTTGGAGCAGAGGGGTGGATCCGG 660
Db 721 CGGGTTCCAGAGAGTACTTCCGAGAGATGGGCGCAGCTTGGAGCAGAGGGGTGGATCCGG 780
Qy 661 CGGGCCCGGCGGCTGGCGCGGAGCTGAGAGCTGTGGGAGCAGCGCAGAGTGTGGC 720
Db 781 CGGGCCCGGCGGCTGGCGCGGAGCTGAGAGCTGTGGGAGCAGCGCAGAGTGTGGC 840
Qy 721 TCAGAGGACTGTGGCTGTGTGTTGTGACATCAAGTTCTGAGACTCTCTATCTGAGC 780
Db 841 TCAGAGGACTGTGGCTGTGTGTTGTGACATCAAGTTCTGAGACTCTCTATCTGAGC 900
Qy 781 GCGTTCTGGGGGAGTACTTGAAGTGGCGCCCTGCTGAGAGCCCTGCGGGGCGTGTCCG 840
Db 901 GCGTTCTGGGGGAGTACTTGAAGTGGCGCCCTGCTGAGAGCCCTGCGGGGCGTGTCCG 960
Qy 841 ACTGAGGCCCTTCCGAGAGGCTGTGGGCGGGAGGCTGTTCGCTGCTGCTGAGTGGAT 900
Db 961 ACTGAGGCCCTTCCGAGAGGCTGTGGGCGGGAGGCTGTTCGCTGCTGCTGAGTGGAT 1020
Qy 901 GAGGCTGAC 909
Db 1021 GAGGCTGAC 1029
```

```
RESULT 9
US-09-669-445-2
; Sequence 2, Application US/09669445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P0002P1
; CURRENT APPLICATION NUMBER: US/09/669,445
; CURRENT FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US00/06642
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/126,018
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/139,638
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/149,449
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-669-445-2

Query Match 99.8%; Score 907.4; DB 30; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGTATCCGGGTCGAGCCCGGCGCCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 60
Db 121 ATGGGCGTATCCGGGTCGAGCCCGGCGCCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 180
Qy 61 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGTGGCGGCACTGACCGAGTGC 120
Db 181 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGTGGCGGCACTGACCGAGTGC 240
Qy 121 GAGCTGAGACTCTGSCCTTTTCTGCTGAGTGAAGCTCTTGGCGCCCGCGAGGCTTAGCC 180
Db 241 GAGCTGAGACTCTGSCCTTTTCTGCTGAGTGAAGCTCTTGGCGCCCGCGAGGCTTAGCC 300
Qy 241 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGAGCGCGGAGAGTGGCGAG 240
Db 301 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGAGCGCGGAGAGTGGCGAG 360
```







```
RESULT 11
US-10-100-683-2084
; Sequence 2084, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2084
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-683-2084

Query Match 99.8%; Score 907.4; DB 48; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATCCGGGTCGACCCCGGCGCGTGTGGGAGAGAGATGAGTCCGTGACTAC 60
DB 121 ATGGGCGCTATCCGGGTCGACCCCGGCGCGTGTGGGAGAGAGATGAGTCCGTGACTAC 180
QY 61 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 181 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 240
QY 121 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTTCTGGCGCCCGGAGGCTTACGC 180
DB 241 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTTCTGGCGCCCGGAGGCTTACGC 300
QY 181 CGGGCCCGGAGCGGCGCTTACGAGCTCTGCTGAGCTGAGGCGCGGCGGAGTCCGAG 240
DB 301 CGGGCCCGGAGCGGCGCTTACGAGCTCTGCTGAGCTGAGGCGCGGCGGAGTCCGAG 360
QY 241 AGCAACCTGTGGCTGTGGGCAACTCTGCGGTGCTGGCCCGGCACTGAGTCCGCG 300
DB 361 AGCAACCTGTGGCTGTGGGCAACTCTGCGGTGCTGGCCCGGCACTGAGTCCGCG 420
QY 301 CACCTGGCGGCAAGGGCGCGCGGCGGCAAGTCTTCCGAAAGCTATGACTATGGCACTTC 360
DB 421 CACCTGGCGGCAAGGGCGCGCGGCGGCAAGTCTTCCGAAAGCTATGACTATGGCACTTC 480
QY 361 AGCTCTTCAAAGAGAGAGAGGAGTGTGCTGCGCGTGGAGAGTCAAGCACTTCTGCA 420
DB 481 AGCTCTTCAAAGAGAGAGAGGAGTGTGCTGCGCGTGGAGAGTCAAGCACTTCTGCA 540
QY 421 AATTCTCAGCAGGAGTGTGAGAGACAGGCTTCCCGCAACCAAGCGGCGGCGAGT 480
DB 541 AATTCTCAGCAGGAGTGTGAGAGACAGGCTTCCCGCAACCAAGCGGCGGCGAGT 600
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QY 481 CGGGCCCGGAGAGAGTGTGCTGAGAGCGGCGGAGAGAGGAGGCGCCAGCGCACTCCGAG 540
DB 601 CGGGCCCGGAGAGAGTGTGCTGAGAGCGGCGGAGAGAGGAGGCGCCAGCGCACTCCGAG 660
QY 541 CAGCAGTCAAGAGCCCGCAAGACTTCTCTTGAAGCAAGTGAAGTGTGACATCCGAGTCC 600
DB 661 CAGCAGTCAAGAGCCCGCAAGACTTCTCTTGAAGCAAGTGAAGTGTGACATCCGAGTCC 720
QY 601 CGGGTTCCAGAGAGTATGAGAGATGAGAGGCGGCTTGAAGCAAGGAGGAGTCCGAG 660
DB 721 CGGGTTCCAGAGAGTATGAGAGATGAGAGGCGGCTTGAAGCAAGGAGGAGTCCGAG 780
QY 661 CGGGCCCGGAGAGAGTGTGAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 781 CGGGCCCGGAGAGAGTGTGAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 721 TCAAGGAGACTGGGCTGTGTGTTGTGATCAAGTCTCAGAGCTTCTATCTGAGC 780
DB 841 TCAAGGAGACTGGGCTGTGTGTTGTGATCAAGTCTCAGAGCTTCTATCTGAGC 900
QY 781 GCTTCTGGGAGGAGTACTTGTGAGTGGCGGCTTGTGAGAGGAGGAGGAGGAGGAGGAG 840
DB 901 GCTTCTGGGAGGAGTACTTGTGAGTGGCGGCTTGTGAGAGGAGGAGGAGGAGGAGGAG 960
QY 841 ACTGAGGCGCTGAGAGAGGCTGTGGGCGGAGAGGCTTGTGAGTGTGAGTGTGAGTGT 900
DB 961 ACTGAGGCGCTGAGAGAGGCTGTGGGCGGAGAGGCTTGTGAGTGTGAGTGTGAGTGT 1020
QY 901 GAGGCTGAC 909
DB 1021 GAGGCTGAC 1029
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RESULT 12
US-10-106-698-349
; Sequence 349, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT FILING DATE: 2002-03-27
; CURRENT APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 349
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-349
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Query Match 99.8%; Score 907.4; DB 48; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCGCTATCCGGGTCGACCCCGGCGCGTGTGGGAGAGAGATGAGTCCGTGACTAC 60
DB 121 ATGGGCGCTATCCGGGTCGACCCCGGCGCGTGTGGGAGAGAGATGAGTCCGTGACTAC 180
QY 61 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 181 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 240
QY 121 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTTCTGGCGCCCGGAGGCTTACGC 180
DB 241 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTTCTGGCGCCCGGAGGCTTACGC 300
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QY 181 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCCGCGGAGAGTCCGCGAG 240  
Db 301 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCCGCGGAGAGTCCGCGAG 360  
QY 241 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 300  
Db 361 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 420  
QY 301 CACCTGCGCGGAGCGGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGG 360  
Db 421 CACCTGCGCGGAGCGGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGG 480  
QY 361 AGCTCTTCAAG 420  
Db 481 AGCTCTTCAAG 540  
QY 421 AATTCTCAGCAG 480  
Db 541 AATTCTCAGCAG 600  
QY 481 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 540  
Db 601 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 660  
QY 541 CAGCAGTCAAG 600  
Db 661 CAGCAGTCAAG 720  
QY 601 CCGGTTTCAGCAG 660  
Db 721 CCGGTTTCAGCAG 780  
QY 661 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 781 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 721 TCAAGGAG 780  
Db 841 TCAAGGAG 900  
QY 781 GCTTTCTGAGGAG 840  
Db 901 GCTTTCTGAGGAG 960  
QY 841 ACTGAGGCGGCTGCGGAG 900  
Db 961 ACTGAGGCGGCTGCGGAG 1020  
QY 901 GAGGCTGAC 909  
Db 1021 GAGGCTGAC 1029

RESULT 13  
US-11-001-793-2084  
; Sequence 2084, Application US/11001793  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, et al.  
; TITLE OF INVENTION: Human Secreted Proteins  
; FILE REFERENCE: PS900  
; CURRENT APPLICATION NUMBER: US/11/001,793  
; PENDING FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: US/10/100,683  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: US 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: US 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: US 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: US 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/043,580

QY 181 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCCGCGGAGAGTCCGCGAG 240  
Db 301 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCCGCGGAGAGTCCGCGAG 360  
QY 241 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 300  
Db 361 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 420  
QY 301 CACCTGCGCGGAGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGGAG 360  
Db 421 CACCTGCGCGGAGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGGAG 480  
QY 361 AGCTCTTCAAG 420  
Db 481 AGCTCTTCAAG 540  
QY 421 AATTCTCAGCAG 480  
Db 541 AATTCTCAGCAG 600  
QY 481 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 540  
Db 601 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 660  
QY 541 CAGCAGTCAAG 600  
Db 661 CAGCAGTCAAG 720  
QY 601 CCGGTTTCAGCAG 660  
Db 721 CCGGTTTCAGCAG 780  
QY 661 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 781 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 721 TCAAGGAG 780  
Db 841 TCAAGGAG 900

QY 181 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCCGCGGAGAGTCCGCGAG 240  
Db 301 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCCGCGGAGAGTCCGCGAG 360  
QY 241 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 300  
Db 361 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 420  
QY 301 CACCTGCGCGGAGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGGAG 360  
Db 421 CACCTGCGCGGAGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGGAG 480  
QY 361 AGCTCTTCAAG 420  
Db 481 AGCTCTTCAAG 540  
QY 421 AATTCTCAGCAG 480  
Db 541 AATTCTCAGCAG 600  
QY 481 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 540  
Db 601 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 660  
QY 541 CAGCAGTCAAG 600  
Db 661 CAGCAGTCAAG 720  
QY 601 CCGGTTTCAGCAG 660  
Db 721 CCGGTTTCAGCAG 780  
QY 661 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 781 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 721 TCAAGGAG 780  
Db 841 TCAAGGAG 900

Query Match 99.8%; Score 907.4; DB 68; Length 2045;  
Best Local Similarity 99.9%; Pred. No. 7,6e-150;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCCGCGGAGAGTCCGCGAG 240  
Db 301 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCCGCGGAGAGTCCGCGAG 360  
QY 241 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 300  
Db 361 AGCAACTCTGCGCTGCTGCGGCACTCTGCGGCTGCGGCGCGGAGCGGCTGCGGCGG 420  
QY 301 CACCTGCGCGGAGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGGAG 360  
Db 421 CACCTGCGCGGAGCGGCGGCGGAGTCTGCGGAGCGGCTGCGGAGCGGCTGCGGAG 480  
QY 361 AGCTCTTCAAG 420  
Db 481 AGCTCTTCAAG 540  
QY 421 AATTCTCAGCAG 480  
Db 541 AATTCTCAGCAG 600  
QY 481 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 540  
Db 601 CCGGCGCGGCGGCGGAGTGTGCTGCGGAGCGGCGGAGAGAGAGAGAGAGAGAGAG 660  
QY 541 CAGCAGTCAAG 600  
Db 661 CAGCAGTCAAG 720  
QY 601 CCGGTTTCAGCAG 660  
Db 721 CCGGTTTCAGCAG 780  
QY 661 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
Db 781 CCGGCCCCGAGCGGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840  
QY 721 TCAAGGAG 780  
Db 841 TCAAGGAG 900

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QY 781 GCCTTCGAGGCGCACTACCTGAGTGGGCGCCCTGCTGCAAGGCCCTGCGGGGCGTGTTCCTG 840
DB 901 GCGTTTCGAGGCGCACTACCTGAGTGGGCGCCCTGCTGCAAGGCCCTGCGGGGCGTGTTCCTG 960
QY 841 ACTGAGGCCCTGCGAGAGGCTGTGTGGCCCGGAGGAGCTGTTCGCTGTGTGTCACTGTGAT 900
DB 961 ACTGAGGCCCTGCGAGAGGCTGTGTGGCCCGGAGGAGCTGTTCGCTGTGTGTCACTGTGAT 1020
QY 901 GAGGCTGAC 909
DB 1021 GAGGCTGAC 1029

RESULT 14
US-09-652-355-10438
; Sequence 10438, Application US/09652355
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew M.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1192-001
; CURRENT APPLICATION NUMBER: US/09/652,355
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,136
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 11227
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10438
; LENGTH: 2460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2460)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-355-10438

* Query Match 99.8%; Score 907.4; DB 29; Length 2460;
Best Local Similarity 99.9%; Pred. No. 7.5e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTGACACCCCGGCGCTGCTGGAGAGAGATGCTGAGACTAC 60
DB 165 ATGGCGCTATCCGGGTGACACCCCGGCGCTGCTGGAGAGAGATGCTGAGACTAC 224
QY 61 TACGGATGCTGTGCTTCACTGATGTTGAGTGTGGCGGGCAACTGACCGAGTGC 120
DB 225 TACGGATGCTGTGCTTCACTGATGTTGAGTGTGGCGGGCAACTGACCGAGTGC 284
QY 121 GAGCTGAGCTCTGCGCTTTCGCTGAGATGAGGCTCTGGGCGCCCGGAGGCTTAGCC 180
DB 285 GAGCTGAGCTCTGCGCTTTCGCTGAGATGAGGCTCTGGGCGCCCGGAGGCTTAGCC 344
QY 181 CGGCGCCGAGCGGCTGAGAGCTCTGCTGAGAGCTGAGCGCGGGGAGTGGCGAG 240
DB 345 CGGCGCCGAGCGGCTGAGAGCTCTGCTGAGAGCTGAGCGCGGGGAGTGGCGAG 404
QY 241 AGCAACTGCGGCTGCTGGGGCACTCTGCGGCTGCGCCGCAAGCTGCTGCGC 300
DB 405 AGCAACTGCGGCTGCTGGGGCACTCTGCGGCTGCGCCGCAAGCTGCTGCGC 464
QY 301 CACCTGCGCGGAGAGGCGCGCGGCAAGTCTCCGAAGGCTATGCTTAGCTACCTCC 360
DB 465 CACCTGCGCGGAGAGGCGCGCGGCAAGTCTCCGAAGGCTATGCTTAGCTACCTCC 524
QY 361 AGCTTTCAAGAGGAGCAGAGGCTAGCTGCGCTGCGCTGCGAGTCAAGCACTTCTGCA 420
DB 525 AGCTTTCAAGAGGAGCAGAGGCTAGCTGCGCTGCGCTGCGAGTCAAGCACTTCTGCA 584
QY 421 AATTTTCAGAGGAGTCAATGAGAGCAAGGCTCCCCCAACCAAGCGGCGAGCGAGT 480
DB 585 AATTTTCAGAGGAGTCAATGAGAGCAAGGCTCCCCCAACCAAGCGGCGAGCGAGT 644
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QY 481 CGGCGCCGCGCCAGTGTGTGTGCAAGCGCGGAGAGAGGAGGAGCCCGACCGCCAG 540
DB 645 CGGCGCCGCGCCAGTGTGTGTGCAAGCGCGGAGAGAGGAGGAGCCCGACCGCCAG 704
QY 541 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAAGGCAAGTCACTGTGACATCCGCTC 600
DB 705 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAAGGCAAGTCACTGTGACATCCGCTC 764
QY 601 CGGTTTCAGAGCAGATGATCTGCGAGCATGGGCGCAGGCTTGGAGCAGGGCGTGGCATCCCG 660
DB 765 CGGTTTCAGAGCAGATGATCTGCGAGCATGGGCGCAGGCTTGGAGCAGGGCGTGGCATCCCG 824
QY 661 CGGCGCCAGGCGCTGGCGCGGAGCTGAGCAGTGTGGGCAAGGCGCAGGAGTGGCGCG 720
DB 825 CGGCGCCAGGCGCTGGCGGAGCTGAGCAGTGTGGGCAAGGCGCAGGAGTGGCGCG 884
QY 721 TCAAGGACCTGAGCTGTGTGTGTGATCAATCAAGTTCTCAGAGCTCTCTATCTGAG 780
DB 885 TCAAGGACCTGAGCTGTGTGTGTGATCAATCAAGTTCTCAGAGCTCTCTATCTGAG 944
QY 781 GCCTTCGAGGCGCACTACCTGAGTGGCGCCCTGCTGCAAGCCCTGCGGGCGTGTTCCTG 840
DB 945 GCCTTCGAGGCGCACTACCTGAGTGGCGCCCTGCTGCAAGCCCTGCGGGCGTGTTCCTG 1004
QY 841 ACTGAGGCCCTGCGAGAGGCTGTGGGCGGGAGGCTGTGCGCTGCTGATGATGAT 900
DB 1005 ACTGAGGCCCTGCGAGAGGCTGTGGGCGGGAGGCTGTGCGCTGCTGATGATGAT 1064
QY 901 GAGGCTGAC 909
DB 1065 GAGGCTGAC 1073

RESULT 15
US-09-652-814-9661
; Sequence 9661, Application US/09652814
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1191-001
; CURRENT APPLICATION NUMBER: US/09/652,814
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,109
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10797
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9661
; LENGTH: 2460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2460)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-814-9661

* Query Match 99.8%; Score 907.4; DB 29; Length 2460;
Best Local Similarity 99.9%; Pred. No. 7.5e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTGACACCCCGGCGCTGCTGGAGAGAGATGCTGAGACTAC 60
DB 165 ATGGCGCTATCCGGGTGACACCCCGGCGCTGCTGGAGAGAGATGCTGAGACTAC 224
QY 61 TACGGATGCTGTGCTTCACTGATGTTGAGTGTGGCGGGCAACTGACCGAGTGC 120
DB 225 TACGGATGCTGTGCTTCACTGATGTTGAGTGTGGCGGGCAACTGACCGAGTGC 284
QY 121 GAGCTGAGCTCTGCGCTTTCGCTGATGAGGCTCTGCGCGCGCGAGGCTTAGCC 180
DB 285 GAGCTGAGCTCTGCGCTTTCGCTGATGAGGCTCTGCGCGCGCGAGGCTTAGCC 344
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QY 181 CCGGCCCGCAGCGGCTTAGAGCTCTGTGAGCTGAGCGCGCGGCGAGTGGCGAG 240  
 DB 345 CCGGCCCGCAGCGGCTTAGAGCTCTGTGAGCTGAGCGCGCGGCGAGTGGCGAG 404  
 QY 241 AGCAACCTGCGGCTGTGGGGCAACTCTGCGGCTGTGGCGCGCGGCGAGTGGCGAG 300  
 DB 405 AGCAACCTGCGGCTGTGGGGCAACTCTGCGGCTGTGGCGCGCGGCGAGTGGCGAG 464  
 QY 301 CACTGGCGCGCAGCGCGCGCGCGCGAGTGTCTCCAGAAAGCTATAGCTATGAGCACTCC 360  
 DB 465 CACTGGCGCGCAGCGCGCGCGCGCGAGTGTCTCCAGAAAGCTATAGCTATGAGCACTCC 524  
 QY 361 AGCTCTTCAAAAGAGACAGAGGGTACTGCTCCGCTGCGCGAGTCAAAGCAAGTCTGCA 420  
 DB 525 AGCTCTTCAAAAGAGACAGAGGGTACTGCTCCGCTGCGCGAGTCAAAGCAAGTCTGCA 584  
 QY 421 AATTCTCAGCAGGCTCAGTGGGAGACAGGCTCCCGCCCAACCAAGCGCGAGCGCGAGT 480  
 DB 585 AATTCTCAGCAGGCTCAGTGGGAGACAGGCTCCCGCCCAACCAAGCGCGAGCGCGAGT 644  
 QY 481 CCGGCCCGGCGCGAGTGTGTGTCAGACCGCGCGGAGAGGGGCGCCAGCGCGACCCAG 540  
 DB 645 CCGGCCCGGCGCGAGTGTGTGTCAGACCGCGCGGAGAGGGGCGCCAGCGCGACCCAG 704  
 QY 541 CAGCAGTCAAGAGCCCGCCAGACCTTCTTGAAGGCAAGTGA CTTGTGACATCCGAGTC 600  
 DB 705 CAGCAGTCAAGAGCCCGCCAGACCTTCTTGAAGGCAAGTGA CTTGTGACATCCGAGTC 764  
 QY 601 CCGGTTTCGAGCAGAGTACTGCGAGTGGGCCAGGCTTGGAGCAGGGCGTGGCATCCCGG 660  
 DB 765 CCGGTTTCGAGCAGAGTACTGCGAGTGGGCCAGGCTTGGAGCAGGGCGTGGCATCCCGG 824  
 QY 661 CCGGCCCGCAGGCGCTGCGCGCGCGAGCTGACGTTGTTGGGCAAGCCAGTGTGCGC 720  
 DB 825 CCGGCCCGCAGGCGCTGCGCGCGCGAGCTGACGTTGTTGGGCAAGCCAGTGTGCGC 884  
 QY 721 TCAAGGACCTGCGGCTGTGTGTGTGATCATCAAGTTCTCAGAGCTCTCTATCTGAGC 780  
 DB 885 TCAAGGACCTGCGGCTGTGTGTGTGATCATCAAGTTCTCAGAGCTCTCTATCTGAGC 944  
 QY 781 GCCTTCTGCGGCGCATCTACTGAGTGGCGCGCTGCTGCAAGGCCCTGCGGGGCGTGTCCG 840  
 DB 945 GCCTTCTGCGGCGCATCTACTGAGTGGCGCGCTGCTGCAAGGCCCTGCGGGGCGTGTCCG 1004  
 QY 841 ACTGAGGCCCTGCGAGAGGCTGTGAGCCCGGAGGCTGTTGCGCTGCTGATCAGTGTGAT 900  
 DB 1005 ACTGAGGCCCTGCGAGAGGCTGTGAGCCCGGAGGCTGTTGCGCTGCTGATCAGTGTGAT 1064  
 QY 901 GAGGCTGAC 909  
 DB 1065 GAGGCTGAC 1073

Search completed: February 12, 2005, 13:34:23  
 Job time : 2970 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:30:05 ; Search time 56 Seconds  
(without alignments)  
1767.946 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 1550  
Sequence: 1 MALSGSTAPPCWEDECDLY.....LREAVGRVRLVSVDEAD 303

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubppa/US09C\_PUBCOMB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	99.5	318	14	US-10-001-254-18
2	1543	99.5	326	14	US-10-296-539-1
3	1543	99.5	366	14	US-10-106-698-4626
4	1413	91.2	304	14	US-10-013-477-11
5	1404	90.6	319	9	US-09-925-302-758
6	1404	90.6	319	10	US-09-925-302-758
7	987	63.7	242	15	US-10-296-115-1220
8	614.5	39.6	318	9	US-09-935-223-4
9	614.5	39.6	318	9	US-09-733-167-1
10	608.5	39.3	318	9	US-09-935-223-6
11	608.5	39.3	318	9	US-09-733-167-3
12	545.5	35.2	217	9	US-09-799-777-26
13	514	33.2	101	14	US-10-001-254-8

14	422	27.2	210	9	US-09-733-167-6	Sequence 6, Appl1
15	265.5	17.1	146	14	US-10-001-254-38	Sequence 38, Appl1
16	227	14.6	99	14	US-10-001-254-36	Sequence 36, Appl1
17	225.5	14.5	114	9	US-09-733-167-5	Sequence 5, Appl1
18	224	14.5	99	14	US-10-001-254-37	Sequence 37, Appl1
19	136	8.8	340	15	US-10-352-839-3	Sequence 3, Appl1
20	135.5	8.7	163	16	US-10-437-963-106027	Sequence 106027, A
21	132	8.5	384	15	US-10-425-114-42732	Sequence 42732, A
22	120	7.7	182	16	US-10-437-963-116637	Sequence 116637, A
23	120	7.7	399	15	US-10-425-114-64272	Sequence 64272, A
24	119.5	7.7	19723	15	US-10-084-846A-5	Sequence 5, Appl1
25	119	7.7	547	16	US-10-437-963-184154	Sequence 184154, A
26	118.5	7.6	459	16	US-10-437-963-186228	Sequence 186228, A
27	118	7.6	281	15	US-10-425-114-72807	Sequence 72807, A
28	117	7.5	247	16	US-10-437-963-164918	Sequence 164918, A
29	116.5	7.5	218	16	US-10-437-963-117915	Sequence 117915, A
30	116.5	7.5	649	16	US-10-437-963-117651	Sequence 117651, A
31	115	7.4	82	16	US-10-437-963-110001	Sequence 110001, A
32	114.5	7.4	126	16	US-10-767-701-33992	Sequence 33992, A
33	114.5	7.4	134	16	US-10-767-701-42899	Sequence 42899, A
34	114.5	7.4	741	16	US-10-437-963-193189	Sequence 193189, A
35	114.5	7.4	19608	15	US-10-084-846A-8	Sequence 8, Appl1
36	114	7.4	134	16	US-10-437-963-185509	Sequence 185509, A
37	113.5	7.3	291	16	US-10-437-963-195777	Sequence 195777, A
38	113.5	7.3	599	15	US-10-094-749-1828	Sequence 1828, Ap
39	113.5	7.3	758	15	US-10-108-260A-2612	Sequence 2612, Ap
40	113	7.3	155	16	US-10-437-963-103601	Sequence 103601, A
41	112.5	7.3	240	16	US-10-437-963-190104	Sequence 190104, A
42	112.5	7.3	19652	15	US-10-084-846A-7	Sequence 7, Appl1
43	111	7.2	178	16	US-10-437-963-203446	Sequence 203446, A
44	111	7.2	347	15	US-10-425-114-51867	Sequence 51867, A
45	110	7.1	539	15	US-10-425-114-39176	Sequence 39176, A

#### ALIGNMENTS

RESULT 1  
US-10-001-254-18  
Sequence 18, Application US/10001254  
Publicatation No. US20030049702A1  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Fiorentino, Loredana  
APPLICANT: Lee, Sung Hyung  
APPLICANT: Roth, Wilfried  
APPLICANT: Steiner-Llewen, Frank  
TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins  
FILE REFERENCE: P-IL 5037  
CURRENT APPLICATION NUMBER: US/10/001,254  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/301,889  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 09/715,893  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-001-254-18  
Query Match 99.5% Score 1543; DB 14; Length 318;  
Best Local Similarity 99.7% Pred. No. 9.7e-12;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTAPPCWEDECDLYGKLSHMFVVGQQLTECELELLAFLLDRAFGAGGLA 60  
DB 1 MALSGSTAPPCWEDECDLYGKLSHMFVVGQQLTECELELLAFLLDRAFGAGGLA 60

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QY 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKQRGRSRGPGGARRRRRGAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKQRGRSRGPGGARRRRRGAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
DB 241 SRDLGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300

RESULT 2
US-10-296-539-1
; Sequence 1, Application US/10296539
; Publication No. US20030165933A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. TOM
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: REGULATORS OF APOPTOSIS
; FILE REFERENCE: PI-0307 PCT
; CURRENT APPLICATION NUMBER: US/10/296,539
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
; PRIOR FILING DATE: 2000-06-01; 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165933A1 3102521CD1
US-10-296-539-1

Query Match 99.5%; Score 1543; DB 14; Length 326;
Best Local Similarity 99.7%; Pred. No. 1e-126;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 241 SRDLGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 3
US-10-106-698-4626
; Sequence 4626, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4626
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4626

Query Match 99.5%; Score 1543; DB 14; Length 366;
Best Local Similarity 99.7%; Pred. No. 1.1e-126;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MALSGSTPAPCWEDECDLDYGMLSLRMFVVGQLTCELELLAFLLDEAPGAGGLA 60
DB 41 MALSGSTPAPCWEDECDLDYGMLSLRMFVVGQLTCELELLAFLLDEAPGAGGLA 100
QY 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 101 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 160
QY 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKQRGRSRGPGGARRRRRGAPAPQ 180
DB 161 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKQRGRSRGPGGARRRRRGAPAPQ 220
QY 181 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
DB 221 QOSEPARPSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 280
QY 241 SRDLGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
DB 281 SRDLGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 340
QY 301 EAD 303
DB 341 EAD 343

RESULT 4
US-10-013-477-11
; Sequence 11, Application US/10013477
; Publication No. US20030049732A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO0291
; CURRENT APPLICATION NUMBER: US/10/013,477
; PRIOR FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/669,445
; PRIOR FILING DATE: 2000-09-25
```

PRIOR APPLICATION NUMBER: PCT/US00/06642  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/126,018  
PRIOR FILING DATE: 1999-03-24  
PRIOR APPLICATION NUMBER: 60/139,638  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/149,449  
PRIOR FILING DATE: 1999-08-18  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 11  
LENGTH: 304  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-013-477-11

Query Match 91.2%; Score 1413; DB 14; Length 304;  
Best Local Similarity 99.6%; Pred. No. 2.2e-115;  
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 MLSHRMFEVVGQULTECELELLAFLIDBAPGAAGLAARSGLELLELERRGQCGESN 82  
DB 1 MLSHRMFEVVGQULTECELELLAFLIDBAPGAAGLAARSGLELLELERRGQCGESN 60  
QY 83 LRLGQLRLVLAHDLPLHARKRRRPPVSPERYSTSSSKRTGSCRRRQSSSSANS 142  
DB 61 LRLGQLRLVLAHDLPLHARKRRRPPVSPERYSTSSSKRTGSCRRRQSSSSANS 120  
QY 143 OOGWETGSPPTKRRSRGRSPGARRRRGAPAPPOOSPARSSGKTCIDRLAV 202  
DB 121 OOGWETGSPPTKRRSRGRSPGARRRRGAPAPPOOSPARSSGKTCIDRLAV 180  
QY 203 RAEYCEHGPALBEGVARRRPOALARQLDVFGQATAVLARSDIGSVVCDIKFSELSTLDAF 262  
DB 181 RAEYCEHGPALBEGVARRRPOALARQLDVFGQATAVLARSDIGSVVCDIKFSELSTLDAF 240  
QY 263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303  
DB 241 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 281

RESULT 5  
US-09-925-302-758  
Sequence 758, Application US/09925302  
Patent No. US20020044941A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 758  
LENGTH: 319  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-302-758

Query Match 90.6%; Score 1404; DB 9; Length 319;  
Best Local Similarity 99.6%; Pred. No. 1.4e-114;  
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQULTECELELLAFLIDBAPGAAGLA 60  
DB 41 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQULTECELELLAFLIDBAPGAAGLA 100  
QY 61 PARSGLELLELERRGQCGESNLRLLGQLRLVLAHDLPLHARKRRRPPVSPERYSTGS 120

DB 101 PARSGLELLELERRGQCGESNLRLLGQLRLVLAHDLPLHARKRRRPPVSPERYSTGS 160  
QY 121 SSSKRTGSCRRRROSSSSANSOOGWETGSPPTKRRSRGRPGGARRRRRGAAPAPQ 180  
DB 161 SSSKRTGSCRRRROSSSSANSOOGWETGSPPTKRRSRGRPGGARRRRRGAAPAPQ 220  
QY 181 OOSEPARPSSGKTCIDRLRVAEYCEHGPALBEGVARRRPOALARQLDVFGQATAVLR 240  
DB 221 OOSEPARPSSGKTCIDRLRVAEYCEHGPALBEGVARRRPOALARQLDVFGQATAVLR 280  
QY 241 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 273  
DB 281 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 313

RESULT 6  
US-09-925-302-758  
Sequence 758, Application US/09925302  
Publication No. US20030064072A9  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 758  
LENGTH: 319  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-302-758

Query Match 90.6%; Score 1404; DB 10; Length 319;  
Best Local Similarity 99.6%; Pred. No. 1.4e-114;  
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQULTECELELLAFLIDBAPGAAGLA 60  
DB 41 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQULTECELELLAFLIDBAPGAAGLA 100  
QY 61 PARSGLELLELERRGQCGESNLRLLGQLRLVLAHDLPLHARKRRRPPVSPERYSTGS 120  
DB 101 PARSGLELLELERRGQCGESNLRLLGQLRLVLAHDLPLHARKRRRPPVSPERYSTGS 160  
QY 121 SSSKRTGSCRRRROSSSSANSOOGWETGSPPTKRRSRGRPGGARRRRRGAAPAPQ 180  
DB 161 SSSKRTGSCRRRROSSSSANSOOGWETGSPPTKRRSRGRPGGARRRRRGAAPAPQ 220  
QY 181 OOSEPARPSSGKTCIDRLRVAEYCEHGPALBEGVARRRPOALARQLDVFGQATAVLR 240  
DB 221 OOSEPARPSSGKTCIDRLRVAEYCEHGPALBEGVARRRPOALARQLDVFGQATAVLR 280  
QY 241 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 273  
DB 281 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 313

RESULT 7  
US-10-296-115-1220  
Sequence 1220, Application US/10296115  
Publication No. US20040053248A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides  
FILE REFERENCE: 784PCT  
CURRENT APPLICATION NUMBER: US/10/296,115  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: US09/488,725



PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 NUMBER OF SEQ ID NOS: 1478  
 SEQ ID NO 1220  
 LENGTH: 242  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-296-115-1220

Query Match 63.7%; Score 987; DB 15; Length 242;  
 Best Local Similarity 97.0%; Pred. No. 3.3e-78;  
 Matches 196; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 104 KRRRP--VSPERRSYGSSSSSKRTGSCRRRRROSSSSANQOQWETGSPPTKRQRSR 161  
 DB 18 RSHPTPEVSPEYSGYSSSSSKRTGSCRRRRROSSSSANQOQWETGSPPTKRQRSR 77  
 QY 162 GRPSGARRRRGAPAAPQOQSEPARSPSEKVTCDILRVRAECYCEHPALGQVASSR 221  
 DB 78 GRPSGARRRRGAPAAPQOQSEPARSPSEKVTCDILRVRAECYCEHPALGQVASSR 137  
 QY 222 PQLARQDLVFGQATAVLRSDLSGVCDIKFSELSYLDATFWGDYLSGALLQALRGVELT 281  
 DB 138 PQLARQDLVFGQATAVLRSDLSGVCDIKFSELSYLDATFWGDYLSGALLQALRGVELT 197  
 QY 282 EALREAVGREAVRLVSYDEAD 303  
 DB 198 EALREAVGREAVRLVSYDEAD 219

## RESULT 8

US-09-935-223-4  
 Sequence 4, Application US/09935223  
 Publication No. US20020086983A1  
 GENERAL INFORMATION:

APPLICANT: Alnemuri, Emad S.  
 TITLE OF INVENTION: Fadd-like Anti-Apoptotic Molecules, Methods Of Using The Same, At  
 FILE REFERENCE: T02499  
 CURRENT APPLICATION NUMBER: US/09/935,223  
 PRIOR FILING DATE: 2001-08-22  
 PRIOR APPLICATION NUMBER: 09/723,450  
 PRIOR FILING DATE: 2000-11-28  
 PRIOR APPLICATION NUMBER: 09/276,993  
 PRIOR FILING DATE: 1999-03-26  
 PRIOR APPLICATION NUMBER: 08/859,167  
 PRIOR FILING DATE: 1997-05-20  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 4  
 LENGTH: 318  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Novel Sequence  
 US-09-935-223-4

Query Match 39.6%; Score 614.5; DB 9; Length 318;  
 Best Local Similarity 44.9%; Pred. No. 1.9e-45;  
 Matches 135; Conservative 54; Mismatches 91; Indels 21; Gaps 6;

QY 12 WEDECLDYGMLSLHMEFVVGQLTCELELLAFL-LDEAPGAAGLARASGELLE 70  
 DB 12 WPEHGEQEHGLYSLHMFIDVTHLTRDVVLSFLFVDVIDHERGL--IRNGRDFLL 69  
 QY 71 ELERRGQGESNLRILGQLRVLARHDLPHLARKRRPVSP---ERYSYGTS---SSSK 124  
 DB 70 ALERQGRCDSENFQVQLRIITRHDLPIYTLKRRRAVCPDLDVTKLETSIRYVTPR 129  
 QY 125 RTEGSCRRRRROSSSSANQOQ--WETGSPPTKRQRSGRPSGARRRRRGAPAAPQOQ 182  
 DB 130 ALSDEPRPPQSKVTPPHYVVCPTSGPQWCSKRPARGATLGSQRKR----- 180

QY 183 SEPARSPSEKVTCDILRVRAECYCEHPALGQVASSRPPQALARQDLVFGQATAVLRSR 242  
 DB 181 -KSVTPPKRKQTCIDILRVRAECYCEHPALGQVASSRPPQALARQDLVFGQATAVLRSR 239  
 QY 243 DLGSLVDIKFSELSYLDATFWGDYLSGALLQALRGVELTLEALREAVGREAVRLVSYDEA 302  
 DB 240 DLGSLVDIKFSELSYLDATFWGDYLSGALLQALRGVELTLEALREAVGREAVRLVSYDEA 299  
 QY 303 D 303  
 DB 300 D 300

## RESULT 9

US-09-733-167-1  
 Sequence 1, Application US/09733167  
 Patent No. US20020099009A1  
 GENERAL INFORMATION:

APPLICANT: Krammer, Peter  
 TITLE OF INVENTION: Protein for Regulation of Apoptosis  
 FILE REFERENCE: 4121-120  
 CURRENT APPLICATION NUMBER: US/09/733,167  
 PRIOR FILING DATE: 2000-12-08  
 PRIOR APPLICATION NUMBER: PCT/DE99/01712  
 PRIOR FILING DATE: 1999-06-08  
 PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3  
 PRIOR FILING DATE: 1998-06-08  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 318  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-733-167-1

Query Match 39.6%; Score 614.5; DB 9; Length 318;  
 Best Local Similarity 44.9%; Pred. No. 1.9e-45;  
 Matches 135; Conservative 54; Mismatches 91; Indels 21; Gaps 6;

QY 12 WEDECLDYGMLSLHMEFVVGQLTCELELLAFL-LDEAPGAAGLARASGELLE 70  
 DB 12 WPEHGEQEHGLYSLHMFIDVTHLTRDVVLSFLFVDVIDHERGL--IRNGRDFLL 69  
 QY 71 ELERRGQGESNLRILGQLRVLARHDLPHLARKRRPVSP---ERYSYGTS---SSSK 124  
 DB 70 ALERQGRCDSENFQVQLRIITRHDLPIYTLKRRRAVCPDLDVTKLETSIRYVTPR 129  
 QY 125 RTEGSCRRRRROSSSSANQOQ--WETGSPPTKRQRSGRPSGARRRRRGAPAAPQOQ 182  
 DB 130 ALSDEPRPPQSKVTPPHYVVCPTSGPQWCSKRPARGATLGSQRKR----- 180  
 QY 183 SEPARSPSEKVTCDILRVRAECYCEHPALGQVASSRPPQALARQDLVFGQATAVLRSR 242  
 DB 181 -KSVTPPKRKQTCIDILRVRAECYCEHPALGQVASSRPPQALARQDLVFGQATAVLRSR 239  
 QY 243 DLGSLVDIKFSELSYLDATFWGDYLSGALLQALRGVELTLEALREAVGREAVRLVSYDEA 302  
 DB 240 DLGSLVDIKFSELSYLDATFWGDYLSGALLQALRGVELTLEALREAVGREAVRLVSYDEA 299  
 QY 303 D 303  
 DB 300 D 300

## RESULT 10

US-09-935-223-6  
 Sequence 6, Application US/09935223  
 Publication No. US20020086983A1  
 GENERAL INFORMATION:

APPLICANT: Alnemuri, Emad S.  
 TITLE OF INVENTION: Fadd-like Anti-Apoptotic Molecules, Methods Of Using The Same, At

TITLE OF INVENTION: Compositions For And Methods Of Making The Same  
FILE REFERENCE: TJUJ499  
CURRENT APPLICATION NUMBER: US/09/935,223  
CURRENT FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 09/723,450  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/276,993  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 08/859,167  
PRIOR FILING DATE: 1997-05-20  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Novel Sequence  
US-09-935-223-6

Query Match 39.3%; Score 608.5; DB 9; Length 318;  
Best Local Similarity 43.5%; Pred. No. 6, 4e-45;  
Matches 131; Conservative 56; Mismatches 93; Indels 21; Gaps 5;

QY 12 WEDECLDYGMLSLHMEVVGQLTECELELAF-LDEAPGAAGIARASGLELL 70  
DB 12 WPEERGOEHGLYSLHMFVDIVGTHLTHRDVLSFLPVDVIDDHERGL--IRNGDFLL 69  
QY 71 ELERGGCGESNLRLGLQLRLVLAHDDLPHLARKRRRVSP---ERYSGTSSSKRTE 127  
DB 70 ALERGGRCDESINFRQVLQRLITTHDDLPTVTLKRRVAVCDVDKYLEETSIKYVTPR 129  
QY 128 GSCRRRRQSSSSSQCGMETGSPPTK-----RGRSRGRRSGGARRRRGAPAPQOQ 182  
DB 130 ALSDEPRPPQSKTVPPHYVCCPTSGSQMCKSRPARGRTTLLSQRRR----- 180  
QY 183 SEPAPSSGKVTCDIRLRVRAEYCEHGPALBQGVASRRPQALARQLDFGQATVLSR 242  
DB 181 -KSVTPDPKQKQTCIRLRVRAEYCOHETALQGNVFSNKQDPLEKQFERFNQANTILKSR 239  
QY 243 DLGSVVCIDIKFSELSYDAFMGDYLSGALLQALRGVPLTEALREAVGREAVRLVSVDEA 302  
DB 240 DLGSIIICDIKFSSELYLDAFMFDYINGSLLEALKGVFTIDSLKQAVGHEAIVKLNVVDEE 299  
QY 303 D 303  
DB 300 D 300

RESULT 11  
US-09-733-167-3  
Sequence 3, Application US/09733167  
Patent No. US20020099009A1  
GENERAL INFORMATION:  
APPLICANT: Peter, Marcus  
APPLICANT: Krammer, Peter  
TITLE OF INVENTION: Protein for Regulation of Apoptosis  
FILE REFERENCE: 4121-120  
CURRENT APPLICATION NUMBER: US/09/733,167  
CURRENT FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: PCT/DS99/01712  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-733-167-3

Query Match 39.3%; Score 608.5; DB 9; Length 318;

Best Local Similarity 43.5%; Pred. No. 6, 4e-45;  
Matches 131; Conservative 56; Mismatches 93; Indels 21; Gaps 5;

QY 12 WEDECLDYGMLSLHMEVVGQLTECELELAF-LDEAPGAAGIARASGLELL 70  
DB 12 WPEERGOEHGLYSLHMFVDIVGTHLTHRDVLSFLPVDVIDDHERGL--IRNGDFLL 69  
QY 71 ELERGGCGESNLRLGLQLRLVLAHDDLPHLARKRRRVSP---ERYSGTSSSKRTE 127  
DB 70 ALERGGRCDESINFRQVLQRLITTHDDLPTVTLKRRVAVCDVDKYLEETSIKYVTPR 129  
QY 128 GSCRRRRQSSSSSQCGMETGSPPTK-----RGRSRGRRSGGARRRRGAPAPQOQ 182  
DB 130 ALSDEPRPPQSKTVPPHYVCCPTSGSQMCKSRPARGRTTLLSQRRR----- 180  
QY 183 SEPAPSSGKVTCDIRLRVRAEYCEHGPALBQGVASRRPQALARQLDFGQATVLSR 242  
DB 181 -KSVTPDPKQKQTCIRLRVRAEYCOHETALQGNVFSNKQDPLEKQFERFNQANTILKSR 239  
QY 243 DLGSVVCIDIKFSELSYDAFMGDYLSGALLQALRGVPLTEALREAVGREAVRLVSVDEA 302  
DB 240 DLGSIIICDIKFSSELYLDAFMFDYINGSLLEALKGVFTIDSLKQAVGHEAIVKLNVVDEE 299  
QY 303 D 303  
DB 300 D 300

RESULT 12  
US-09-799-777-26  
Sequence 26, Application US/09799777  
Patent No. US20020091244A1  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
Hillman, Jennifer L.  
Corley, Neil C.  
Guegler, Karl J.  
Baugh, Mariah  
Sather, Susan  
Shah, Purvi  
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS  
NUMBER OF SEQUENCES: 154  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/799,777  
FILING DATE: 06-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/002,485  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BILLINGS, LUCY J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0459 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: UTRSNOT06  
CLONE: 1638407  
SEQUENCE DESCRIPTION: SEQ ID NO: 26  
US-09-799-777-26

Query Match 35.2%; Score 545.5; DB 9; Length 217;  
Best Local Similarity 79.5%; Pred. No. 1.3e-39;  
Matches 116; Conservative 1; Mismatches 20; Indels 9; Gaps 2;

QY 164 PSGGARRRRGAPAPQOQSEPARPSSEKVTCT-----DILRVRAVEYCEHGPALRGV 217  
DB 52 PDGGSEGPQ---PFPSSSQSPDPPLAKAGDTVMGKQAKORDIRLVRALVEYCEHGPALRGV 108  
QY 218 ASRRPQALRQLDVFGQATAVLRSDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRG 277  
DB 109 ASRRPQALRQLDVFGQATAVLRSDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRG 168  
QY 278 VFTLEAREAVGRVAVRLVSVDEAD 303  
DB 169 VFTLEAREAVGRVAVRLVSVDEAD 194

## RESULT 13

US-10-001-254-8  
Sequence 8, Application US/10001254  
Publication No. US20030049702A1  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Fiorentino, Loredana  
APPLICANT: Lee, Sug Hyung  
APPLICANT: Roch, Wilfred  
APPLICANT: Steiner-Jewen, Frank  
TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins  
FILE REFERENCE: P-LJ 5037  
CURRENT FILING DATE: 2001-11-15  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 60/301,889  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapien  
US-10-001-254-8

Query Match 33.2%; Score 514; DB 14; Length 101;  
Best Local Similarity 99.0%; Pred. No. 3e-37;  
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 WEDECLDYGMGLSHRMFEVVGQLTCELELLAFILDEAGAGGAGARASGLLELLE 71  
DB 1 WEDECLDYGMGLSHRMFEVVGQLTCELELLAFILDEAGAGGAGARASGLLELLE 60  
QY 72 LERRGCGESNRLIGOLLRLVLRHDLPLHARKRRRPVP 112  
DB 61 LERRGCGESNRLIGOLLRLVLRHDLPLHARKRRRPVP 101

## RESULT 14

US-09-733-167-6  
Sequence 6, Application US/09733167  
Publication No. US20020099009A1  
GENERAL INFORMATION:  
APPLICANT: Peter, Marcus  
APPLICANT: Kramer, Peter  
TITLE OF INVENTION: Protein for Regulation of Apoptosis

FILE REFERENCE: 4121-120  
CURRENT APPLICATION NUMBER: US/09/733,167  
CURRENT FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: PCT/DE99/01712  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3  
PRIOR FILING DATE: 1998-06-08  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 210  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising amino acids 109-318 of the naturally occurring human DEDD.  
US-09-733-167-6

Query Match 27.2%; Score 422; DB 9; Length 210;  
Best Local Similarity 52.3%; Pred. No. 8.2e-29;  
Matches 81; Conservative 30; Mismatches 34; Indels 10; Gaps 1;

QY 149 TGSPTTKQRKRSRGPSGARRRRGAPAPQOQSEPARPSSEKVTCDIRLVRAYCE 208  
DB 48 TSGPQMSKRPARRATVSGQRK-----KSVTPKQKQCTDIRLVRAYCQ 97  
QY 209 HGPALGQVASRRPQALRQLDVFGQATAVLRSDIGSVVCDIKFSELSYLDAPWGDYLS 268  
DB 98 HETLQGNVSNKQDPLERQERENQANTIKSRDLSIICDIFSELSYLDAPWGDYIN 157  
QY 269 GALLQALRGVFTLEAREAVGRVAVRLVSVDEAD 303  
DB 158 GLLLEALKGVTITSLKQAVGHEALKLVNVEED 192

## RESULT 15

US-10-001-254-38  
Sequence 38, Application US/10001254  
Publication No. US20030049702A1  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Fiorentino, Loredana  
APPLICANT: Lee, Sug Hyung  
APPLICANT: Roch, Wilfred  
APPLICANT: Steiner-Jewen, Frank  
TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins  
FILE REFERENCE: P-LJ 5037  
CURRENT FILING DATE: 2001-11-15  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: 60/301,889  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 146  
TYPE: PRT  
ORGANISM: Danio rerio  
US-10-001-254-38

Query Match 17.1%; Score 265.5; DB 14; Length 146;  
Best Local Similarity 43.5%; Pred. No. 2.7e-15;  
Matches 64; Conservative 13; Mismatches 23; Indels 47; Gaps 4;

QY 12 WEDECLDYGMGLSHRMFEVVGQLTCELELLAFILDEA-----P 53  
DB 1 WEDECLDYGMGLSHRMFEVVGQLTCELELLAFILDEA-----P 59  
QY 54 GAAG-----GLARASGLLELLEERRGCGESNRL 85

Db 60 GPDGSPQANTPCFRLIKSWORMQPOKEGCSIASRHRPKSGVELLELERRGYLSDANLRP 119

Qy 86 LGQLRVLARHDLPHLARRRRPVSP 112

Db 120 LQQLRLITRHDVLPFVSQKGRTVSP 146

Search completed: February 12, 2005, 16:35:32  
Job time : 57 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:30:35 ; Search time 74 Seconds  
(without alignments)  
1583.627 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 303  
Sequence: 1 MALSGSTPAPCWEDECLDY.....LREAVGREAVLLVSDPAD 303

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

1: Geneseq\_16Dec04:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2002s:\*  
7: geneseqp2003as:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303	100.0	303	4 AAB60386	Aab60386 Human apo
2	303	100.0	326	4 AAB60387	Aab60387 Human apo
3	224	73.9	304	4 AAB15551	Aab15551 Apoptosis
4	224	73.9	318	5 AAE24860	Aae24860 Human DED
5	224	73.9	318	5 AAE38903	Aae38903 Human DED
6	224	73.9	326	5 ABB07263	Abb07263 Human apo
7	224	73.9	326	7 ADC79260	Adc79260 Human DED
8	224	73.9	366	4 AAG73852	Aag73852 Human col
9	194	64.0	319	3 AAB58420	Aab58420 Lung canc
10	134	44.2	242	4 AAM25705	Aam25705 Human pro
11	117	38.6	361	5 ABB06038	Abb06038 Human NS
12	117	38.6	368	5 ABB06039	Abb06039 Human NS
13	67	22.1	101	5 AAE24855	Aae24855 Human DED
14	67	22.1	101	5 AAE38898	Aae38898 Human DED
15	66	21.8	217	4 AAM41591	Aam41591 Human pol
16	66	21.8	277	4 AAM39805	Aam39805 Human pol
17	13	4.3	318	2 AAM90108	Aam90108 Human FLA
18	13	4.3	318	2 AAM90109	Aam90109 Mouse FLA
19	13	4.3	318	3 AAY51023	Aay51023 Murine DE
20	13	4.3	318	3 AAY51022	Aay51022 Murine DE
21	13	4.3	318	4 AAB93016	Aab93016 Human pro
22	13	4.3	318	4 AAB94040	Aab94040 Human pro
23	13	4.3	318	5 AAE26087	Aae26087 Human FLA
24	13	4.3	318	5 AAE26088	Aae26088 Mouse FLA
25	9	3.0	91	7 ABO81797	Ab081797 Pseudomon

26	9	3.0	336	4 AAB79137	Aab79137 Coryneb
27	9	3.0	336	4 AAB79487	Aab79487 Coryneb
28	9	3.0	350	7 ABO70227	Ab070227 Pseudom
29	9	3.0	386	7 ABO76378	Ab076378 Pseudom
30	9	3.0	395	4 AAG32890	Aag32890 C glutami
31	9	3.0	504	7 ABO74628	Ab074628 Pseudom
32	9	3.0	657	7 ABO79255	Ab079255 Pseudom
33	8	2.6	21	4 AAB45725	Aab45725 Human 7TM
34	8	2.6	52	2 AAY20499	Aay20499 Human neu
35	8	2.6	76	3 AAG44964	Aag44964 Zea may
36	8	2.6	96	3 AAG27146	Aag27146 Zea may
37	8	2.6	117	3 AAG44892	Aag44892 Zea may
38	8	2.6	125	5 ABP68597	Abp68597 Human pan
39	8	2.6	129	4 ABB11245	Abb11245 Human GPC
40	8	2.6	129	7 ADI21723	Adi21723 Novel hum
41	8	2.6	133	7 ABO69168	Ab069168 Pseudom
42	8	2.6	135	5 ABP69540	Abp69540 Human pol
43	8	2.6	140	2 AAY76561	Aay76561 Human ova
44	8	2.6	148	8 ADN26230	Adn26230 Bacteri
45	8	2.6	157	8 ABO60515	Ab060515 Human gen
46	8	2.6	179	7 ABO76220	Ab076220 Pseudom
47	8	2.6	192	7 ABO79808	Ab079808 Pseudom
48	8	2.6	197	6 ABU36555	Abu36555 Protein e
49	8	2.6	199	5 AAM51590	Aam51590 Brevibac
50	8	2.6	221	4 AAB45702	Aab45702 Human 7TM
51	8	2.6	221	7 ADC87013	Adc87013 Human GPC
52	8	2.6	223	6 ABU34429	Abu34429 Protein e
53	8	2.6	223	7 ABO76564	Ab076564 Pseudom
54	8	2.6	227	4 AAG90072	Aag90072 C glutami
55	8	2.6	228	8 ADM45834	Adm45834 Coryneb
56	8	2.6	231	7 ADB65411	Adb65411 Human pro
57	8	2.6	235	7 ADG10469	Adg10469 Human STA
58	8	2.6	237	5 AAU73245	Aau73245 Human pla
59	8	2.6	260	7 ADI21280	Adi21280 Novel hum
60	8	2.6	266	7 ABO65089	Ab065089 Pseudom
61	8	2.6	311	7 ADC12756	Adc12756 Human GPC
62	8	2.6	319	2 AAM18658	Aam18658 Fragment
63	8	2.6	323	8 ADN04692	Adn04692 Antipepti
64	8	2.6	338	7 ABO82887	Ab082887 Pseudom
65	8	2.6	341	3 AAY58836	Aay58836 Rice cell
66	8	2.6	352	5 ABB97581	Abb97581 Novel hum
67	8	2.6	360	7 ADB47642	Adb47642 Human GPC
68	8	2.6	361	3 AAB08538	Aab08538 A murine
69	8	2.6	361	3 AAB08539	Aab08539 A murine
70	8	2.6	361	3 AAY44817	Aay44817 Murine 142
71	8	2.6	361	3 AAY44662	Aay44662 Murine 142
72	8	2.6	361	3 AAY44816	Aay44816 Murine 142
73	8	2.6	361	3 AAY44815	Aay44815 Murine 142
74	8	2.6	361	4 AAM51426	Aam51426 Human G-P
75	8	2.6	361	4 AAM04564	Aam04564 Human G-P
76	8	2.6	361	5 ABJ04071	Abj04071 Human G-P
77	8	2.6	361	5 ABG95170	Abg95170 Human GPC
78	8	2.6	361	5 ABG95169	Abg95169 Human GPC
79	8	2.6	361	5 ABG95157	Abg95157 Human GPC
80	8	2.6	361	5 ABB79907	Abb79907 Mouse 142
81	8	2.6	361	5 ABB79906	Abb79906 Human 142
82	8	2.6	361	5 ABB09715	Abb09715 Novel hum
83	8	2.6	361	6 ABB73199	Abb73199 Human ocp
84	8	2.6	361	6 ABB81754	Abb81754 Human G-P
85	8	2.6	361	7 ADF50516	Adf50516 GPCR PCMO
86	8	2.6	361	7 ADF50515	Adf50515 GPCR PCMO
87	8	2.6	361	7 ADF50513	Adf50513 GPCR PCMO
88	8	2.6	361	7 ADF50514	Adf50514 GPCR PCMO
89	8	2.6	361	7 ADO28988	Ado28988 Human nov
90	8	2.6	361	8 ADO28990	Ado28990 Mouse nov
91	8	2.6	361	8 ADR18582	Adr18582 Murine GP
92	8	2.6	361	8 ADR18584	Adr18584 Human GPC
93	8	2.6	361	8 ADR40536	Adr40536 Human G-P
94	8	2.6	362	8 AAY44814	Aay44814 Human 142
95	8	2.6	416	5 ABB55218	Abb55218 Lactococc
96	8	2.6	439	4 ABB24024	Abb24024 Novel hum
97	8	2.6	439	4 ABB21346	Abb21346 Novel hum
98	8	2.6	439	4 ABB21346	Abb21346 Novel hum

Aab79137	Coryneb
Aab79487	Coryneb
Ab070227	Pseudom
Ab076378	Pseudom
Aag32890	C glutami
Ab074628	Pseudom
Ab079255	Pseudom
Aab45725	Human 7TM
Aay20499	Human neu
Aag44964	Zea may
Aag27146	Zea may
Aag44892	Zea may
Abp68597	Human pan
Abb11245	Human GPC
Adi21723	Novel hum
Ab069168	Pseudom
Abp69540	Human pol
Aay76561	Human ova
Adn26230	Bacteri
Ab060515	Human gen
Ab076220	Pseudom
Ab079808	Pseudom
Abu36555	Protein e
Aam51590	Brevibac
Aab45702	Human 7TM
Adc87013	Human GPC
Abu34429	Protein e
Ab076564	Pseudom
Aag90072	C glutami
Adm45834	Coryneb
Adb65411	Human pro
Adg10469	Human STA
Aau73245	Human pla
Adi21280	Novel hum
Ab065089	Pseudom
Adc12756	Human GPC
Aam18658	Fragment
Adn04692	Antipepti
Ab082887	Pseudom
Aay58836	Rice cell
Abb97581	Novel hum
Adb47642	Human GPC
Aab08538	A murine
Aab08539	A murine
Aay44817	Murine 142
Aay44662	Murine 142
Aay44816	Murine 142
Aay44815	Murine 142
Aam51426	Human G-P
Aam04564	Human G-P
Abj04071	Human G-P
Abg95170	Human GPC
Abg95169	Human GPC
Abg95157	Human GPC
Abb79907	Mouse 142
Abb79906	Human 142
Abb09715	Novel hum
Abb73199	Human ocp
Abb81754	Human G-P
Adf50516	GPCR PCMO
Adf50515	GPCR PCMO
Adf50513	GPCR PCMO
Adf50514	GPCR PCMO
Ado28988	Human nov
Ado28990	Mouse nov
Adr18582	Murine GP
Adr18584	Human GPC
Adr40536	Human G-P
Aay44814	Human 142
Abb55218	Lactococc
Abb24024	Novel hum
Abb21346	Novel hum

99	8	2.6	452	7	ABO75449	ABO75449 Pseudomon	172	7	2.3	16	6	ABU09743	Abu09743 N-myristo
100	8	2.6	462	3	AAY92344	Aay92344 Human can	173	7	2.3	16	7	ADBA7663	AdbA7663 Human HGP
101	8	2.6	474	2	AAR14676	Aar14676 Rabbid vi	174	7	2.3	16	8	ADRA40569	AdrA40569 Human HGP
102	8	2.6	493	7	ABO83717	ABO83717 Pseudomon	175	7	2.3	31	2	AAY02997	AAy02997 Fragment
103	8	2.6	520	6	ABU34144	Abu34144 Protein e	176	7	2.3	31	7	ADAO7832	Ada07832 Human sec
104	8	2.6	599	7	ADF70409	Adf70409 Orphan re	177	7	2.3	31	8	ADNA1249	AdnA1249 Novel hum
105	8	2.6	632	7	ADG75710	Adg75710 Human pro	178	7	2.3	40	4	AAO12076	AAo12076 Human pol
106	8	2.6	679	7	ABO76654	ABO76654 Pseudomon	179	7	2.3	41	4	ABG02584	Abg02584 Novel hum
107	8	2.6	679	7	ABO80204	ABO80204 Pseudomon	180	7	2.3	46	3	AAAB34183	AAb34183 Gene 28 h
108	8	2.6	690	7	ABO83604	ABO83604 Pseudomon	181	7	2.3	48	3	AAAB34513	AAb34513 Human sec
109	8	2.6	693	8	ADRO8900	Adr08900 Human pro	182	7	2.3	57	5	ABP33077	ABp33077 Human ORF
110	8	2.6	712	4	ABG00341	Abg00341 Novel hum	183	7	2.3	61	3	AAAG3150	AAg3150 Arabidops
111	8	2.6	736	8	AD115342	Adi15342 Human pro	184	7	2.3	61	4	AAAM2210	AAm2210 Peptide #
112	8	2.6	748	3	AAAG31702	AAg31702 Arabidops	185	7	2.3	61	4	AAAB44515	AAb44515 Peptide #
113	8	2.6	783	3	ABM83777	ABm83777 Human dia	186	7	2.3	61	4	AAAM38563	AAm38563 Peptide #
114	8	2.6	805	4	ABG24026	ABg24026 Novel hum	187	7	2.3	61	4	ABB27344	ABb27344 Protein #
115	8	2.6	810	7	ABO63231	ABm63231 Klebsiell	188	7	2.3	61	4	AAAM78316	AAm78316 Human bon
116	8	2.6	812	8	ABM84231	ABm84231 Human dia	189	7	2.3	61	4	AAAM65701	AAm65701 Human bra
117	8	2.6	828	8	ADN24077	Adn24077 Bacterial	190	7	2.3	61	4	ABG59924	ABg59924 Human liv
118	8	2.6	835	3	AAAG31412	AAg31412 Arabidops	191	7	2.3	61	5	ABG47342	ABg47342 Human pep
119	8	2.6	840	7	ADG75711	Adg75711 Human pro	192	7	2.3	64	4	ABG22428	ABg22428 Novel hum
120	8	2.6	847	6	ADAS5477	Ada55477 Human pro	193	7	2.3	66	4	AAUA1567	AAu41567 Propionib
121	8	2.6	882	7	ADBE78996	Adbe78996 Human pro	194	7	2.3	67	6	ABM38066	ABm38066 Propionib
122	8	2.6	897	8	ABM84232	ABm84232 Human dia	195	7	2.3	67	5	AAO19126	AAo19126 Human cit
123	8	2.6	902	7	ADBE58718	Adbe58718 Human pro	196	7	2.3	68	4	AAU64738	AAu64738 Propionib
124	8	2.6	902	8	ADHO9584	Adh09584 Human hos	197	7	2.3	68	6	ABM61257	ABm61257 Propionib
125	8	2.6	908	8	ABM84230	ABm84230 Human dia	198	7	2.3	72	4	AAUA6000	AAu64000 Propionib
126	8	2.6	909	3	AAAG31701	AAg31701 Arabidops	199	7	2.3	72	6	ABM42519	ABm42519 Propionib
127	8	2.6	914	3	AAAG31700	AAg31700 Arabidops	200	7	2.3	73	8	ABO60213	ABo60213 Human gen
128	8	2.6	929	3	AAAG31411	AAg31411 Arabidops	201	7	2.3	78	4	AAU59388	AAu59388 Propionib
129	8	2.6	937	3	AAAG31410	AAg31410 Arabidops	202	7	2.3	78	6	ABM55907	ABm55907 Propionib
130	8	2.6	937	6	ABP59344	ABp59344 Arabidops	203	7	2.3	79	4	AAUA3607	AAu43608 Propionib
131	8	2.6	945	6	ABU92034	ABu92034 Human pro	204	7	2.3	79	6	ABM40127	ABm40127 Propionib
132	8	2.6	949	8	ADHO9583	Adh09583 Human hos	205	7	2.3	82	5	ABP09067	ABp09067 Human ORF
133	8	2.6	952	3	AAAY70014	AAy70014 Human pro	206	7	2.3	84	3	AAAG26049	AAg26049 Zea may
134	8	2.6	952	8	ADHO9582	Adh09582 Human hos	207	7	2.3	85	4	AAUA48994	AAu48994 Propionib
135	8	2.6	952	8	ADDO9316	Ado09316 Human USP	208	7	2.3	85	4	ABBI5294	ABb15294 Human ner
136	8	2.6	952	8	ADP24284	Adp24284 PRO polyp	209	7	2.3	85	5	ABP64016	ABp64016 Human ORF
137	8	2.6	952	8	ADP97378	Adp97378 Human USP	210	7	2.3	85	6	ABM45513	ABm45513 Propionib
138	8	2.6	963	7	ADU68716	Adj68716 Human hea	211	7	2.3	86	4	AAUA5772	AAu45772 Propionib
139	8	2.6	963	8	ADHO9586	Adh09586 Human hos	212	7	2.3	86	4	ABRO0929	ABr00929 Gene 216
140	8	2.6	963	8	ADHO9587	Adh09587 Human hos	213	7	2.3	86	6	ABMA42291	ABm42291 Propionib
141	8	2.6	963	8	ADL23951	Adl23951 Deubiquit	214	7	2.3	86	6	ABU55857	ABu55857 Human gen
142	8	2.6	989	7	ABO68689	ABo68689 Pseudomon	215	7	2.3	86	6	ADU35946	ADj35946 Human gen
143	8	2.6	1032	4	AAU01206	AAu01206 Human cas	216	7	2.3	86	8	ADL81524	ADl81524 Human gen
144	8	2.6	1032	5	AAU73247	AAu73247 Human pla	217	7	2.3	89	3	AAAG26065	AAg26065 Zea may
145	8	2.6	1032	5	AAAG79554	AAg79554 Human CAR	218	7	2.3	98	3	AAAB43733	AAb43733 Human can
146	8	2.6	1059	6	ABU12111	ABu12111 Human pro	219	7	2.3	99	4	AAU00391	AAu00391 Human sec
147	8	2.6	1066	4	ABG24025	ABg24025 Novel hum	220	7	2.3	99	5	ABP22275	ABp22275 Human ORF
148	8	2.6	1085	4	AAAM38692	AAm38692 Human pol	221	7	2.3	99	8	ADH89008	ADh89008 Human POL
149	8	2.6	1089	2	AAW82396	AAw82396 Human UBP	222	7	2.3	102	4	AAAM94871	AAm94871 Human rep
150	8	2.6	1089	4	AAAM38691	AAm38691 Human pol	223	7	2.3	103	3	AAAG00834	AAg00834 Human sec
151	8	2.6	1089	4	ABG23332	ABg23332 Novel hum	224	7	2.3	104	3	AAAG51165	AAg51165 Arabidops
152	8	2.6	1116	7	ABO75628	ABo75628 Pseudomon	225	7	2.3	110	4	AAUA2088	AAu2088 Propionib
153	8	2.6	1125	4	ABG21348	ABg21348 Novel hum	226	7	2.3	110	6	ABM38607	ABm38607 Propionib
154	8	2.6	1127	7	AAAM40477	AAm40477 Human pol	227	7	2.3	110	6	AAE35272	AAe35272 Human P45
155	8	2.6	1127	7	AAAM40478	AAm40478 Human pol	228	7	2.3	113	2	AAAY36969	AAy36969 Antno ac
156	8	2.6	1127	7	ADAC32650	Adc32650 Human nov	229	7	2.3	113	4	ABG19394	ABg19394 Novel hum
157	8	2.6	1131	4	ABG21347	ABg21347 Novel hum	230	7	2.3	113	6	ABRO0932	ABr00932 Gene 216
158	8	2.6	1142	4	ABG24027	ABg24027 Novel hum	231	7	2.3	113	6	ABU55860	ABu55860 Human gen
159	8	2.6	1274	7	ADU75578	Adu75578 Human ubi	232	7	2.3	113	8	ADJ36949	ADj36949 Human gen
160	8	2.6	1274	7	ADU770043	Adu770043 Human hea	233	7	2.3	113	8	ADL81527	ADl81527 Human gen
161	8	2.6	1292	7	ADCC30915	Adc30915 Human nov	234	7	2.3	115	6	ADAS5708	Ada55708 Human pro
162	8	2.6	1317	5	ABG32160	ABg32160 Novel hum	235	7	2.3	115	7	ADH85583	ADh85583 Enterococ
163	8	2.6	1388	4	ABG21344	ABg21344 Novel hum	236	7	2.3	116	4	AAUS8632	AAu8632 Propionib
164	8	2.6	1604	5	AAU82715	AAu82715 Antno aci	237	7	2.3	116	6	ABME5151	ABme5151 Propionib
165	8	2.6	1700	2	ADCI10002	Adci10002 Human NOV	238	7	2.3	117	5	AD117219	ADi17219 NOVX prot
166	8	2.6	1958	2	AAAB60620	AAa60620 Protein f	239	7	2.3	117	7	ADDA5022	ADd45022 Human pro
167	8	2.6	5217	7	ABU070675	ABu070675 Photoxhab	240	7	2.3	118	7	ADDA5018	ADd45018 Human mac
168	7	2.3	7	6	ABU09729	ABu09729 Novel hum	241	7	2.3	118	5	AAAR83048	AAa83048 Human ORF
169	7	2.3	7	7	ADBA7649	AdbA7649 Human GPC	242	7	2.3	118	5	AD117220	ADi17220 Human NOV
170	7	2.3	7	8	ADRA40555	AdrA40555 Human HGP	243	7	2.3	118	5	AD117228	ADi17228 Human NOV
171	7	2.3	10	4	AAAG93538	AAg93538 Transcript	244	7	2.3	123	2	AAAM23891	AAm23891 Human E1D



245	7	2.3	124	4	AAU44043	Aau44043	Propionib	318	7	2.3	195	2	AAW83898	Aaw83898	Bovine in
246	7	2.3	124	5	AAW50525	Aam50525	Sentinel	319	7	2.3	195	5	ABG32983	Abg32983	Bovine je
247	7	2.3	124	6	ABM40562	Abm40562	Propionib	320	7	2.3	195	7	ABO73033	AbO73033	Pseudomon
248	7	2.3	126	6	AAU51805	Aau51805	Propionib	321	7	2.3	197	7	ADC01496	AdC01496	Enterohae
249	7	2.3	126	6	ABM48324	Abm48324	Propionib	322	7	2.3	197	7	ABO77791	AbO77791	Pseudomon
250	7	2.3	127	6	ABM48324	Abm48324	Propionib	323	7	2.3	197	7	ABO77791	AbO77791	Pseudomon
251	7	2.3	127	7	ABO89337	AbO89337	Novel pro	324	7	2.3	202	4	ABB64930	Abb64930	Drosophi1
252	7	2.3	128	4	AAU58056	Aau58056	Propionib	325	7	2.3	202	4	ABB67278	Abb67278	Drosophi1
253	7	2.3	128	6	ABM54575	Abm54575	Propionib	326	7	2.3	210	7	ABO63406	AbO63406	Klebsiell
254	7	2.3	130	6	AAU31276	Aau31276	Novel hum	327	7	2.3	212	4	AAG73899	Aag73899	Human col
255	7	2.3	131	4	ABO7849	AbO7849	Novel pro	328	7	2.3	212	4	ABO63529	AbO63529	Klebsiell
256	7	2.3	134	4	AAW73965	Aag73965	Human col	329	7	2.3	212	8	ADN13992	AdN13992	Human pro
257	7	2.3	134	7	ABO70316	AbO70316	Pseudomon	330	7	2.3	214	8	ADN19470	AdN19470	Human PRO
258	7	2.3	134	7	ABO77324	AbO77324	Pseudomon	331	7	2.3	214	7	ABO79049	AbO79049	Pseudomon
259	7	2.3	136	7	ABO75786	AbO75786	Pseudomon	332	7	2.3	214	8	ADP43674	AdP43674	Human PMM
260	7	2.3	142	7	ABO71511	AbO71511	Pseudomon	333	7	2.3	215	2	AAE68954	Aae68954	Pseudomon
261	7	2.3	147	3	AAW32633	Aab32633	Eucalyptu	334	7	2.3	217	2	AAE68556	Aae68556	Klebsiell
262	7	2.3	147	8	ADM87674	Adm87674	Human EST	335	7	2.3	220	2	AAW57361	Aaw57361	Translati
263	7	2.3	150	4	AAU18305	Aau18305	Human end	336	7	2.3	220	3	AAW08246	Aaw08246	Arabidops
264	7	2.3	151	4	AAU44529	Aau44529	Propionib	337	7	2.3	224	6	ADA48140	Ada48140	Rice prot
265	7	2.3	151	6	ABM41048	Abm41048	Propionib	338	7	2.3	224	8	ADR96071	Adr96071	Novel S.
266	7	2.3	153	4	AAU17322	Aau17322	Novel sig	339	7	2.3	225	6	ABU02036	AbU02036	S. pneumo
267	7	2.3	153	7	ADB94030	AdB94030	Human nov	340	7	2.3	225	8	ADK46786	AdK46786	Streptoco
268	7	2.3	154	8	ADR10124	Adr10124	Human pro	341	7	2.3	227	8	ADP43673	AdP43673	Human PMM
269	7	2.3	155	3	AAW33880	Aag33880	Zea maye	342	7	2.3	230	3	AAW08245	Aaw08245	Arabidops
270	7	2.3	155	8	ADH22519	Adh22519	Human tra	343	7	2.3	237	5	ABG92821	AbG92821	Protein e
271	7	2.3	159	6	ABM65418	Abm65418	Propionib	344	7	2.3	240	2	AAW05910	Aaw05910	Thermophi
272	7	2.3	160	7	ABO71712	AbO71712	Pseudomon	345	7	2.3	240	7	ABO68955	AbO68955	Pseudomon
273	7	2.3	160	8	AD16359	Ad16359	Human pro	346	7	2.3	241	8	ABM82437	AbM82437	Tumour-as
274	7	2.3	161	7	ABO63735	AbO63735	Klebsiell	347	7	2.3	241	8	ADN21995	AdN21995	Bacterial
275	7	2.3	163	8	ADP81260	AdP81260	Protein o	348	7	2.3	243	2	AAW37299	Aaw37299	Amينو aci
276	7	2.3	165	4	ABR00933	AbR00933	Gene 216	349	7	2.3	243	8	ADN24753	AdN24753	Bacterial
277	7	2.3	165	6	ABU55861	Abu55861	Human gen	350	7	2.3	246	4	AAE00639	Aae00639	Human fib
278	7	2.3	165	8	ADJ36950	Adj36950	Human gen	351	7	2.3	246	4	AAE00640	Aae00640	Human fib
279	7	2.3	165	8	ADL81528	Adl81528	Human gen	352	7	2.3	246	8	ADR86103	AdR86103	Aspergill
280	7	2.3	166	4	AAU16609	Aau16609	Human nov	353	7	2.3	246	8	ADU21739	AdU21739	Bacterial
281	7	2.3	166	4	AAU40009	Aau40009	Propionib	354	7	2.3	247	2	AAW31793	Aaw31793	Human fib
282	7	2.3	166	6	ABM36528	Abm36528	Propionib	355	7	2.3	247	3	AAW42005	Aaw42005	Arabidops
283	7	2.3	166	6	ABU55678	Abu55678	Human nov	356	7	2.3	247	3	AAW52568	Aaw52568	Arabidops
284	7	2.3	166	8	ABM84271	Abm84271	Human dia	357	7	2.3	247	3	AAW44802	Aaw44802	Zea maye
285	7	2.3	170	4	AAU20144	Aau20144	Human DNA	358	7	2.3	248	2	AAW31791	Aaw31791	Human fib
286	7	2.3	170	5	ABG91393	AbG91393	Novel hum	359	7	2.3	248	5	ABW78096	AbW78096	Human aci
287	7	2.3	170	8	ABO58515	AbO58515	Human gen	360	7	2.3	249	7	ABO80226	AbO80226	Pseudomon
288	7	2.3	172	2	AAW09281	Aaw09281	Human mat	361	7	2.3	253	8	AD139286	Ad139286	S. hygro
289	7	2.3	172	2	AAW09280	Aaw09280	Human mat	362	7	2.3	253	8	AD139256	Ad139256	S. epider
290	7	2.3	172	2	AAW9399	Aaw9399	Human tau	363	7	2.3	255	7	AAW82105	Aaw82105	S. epider
291	7	2.3	172	2	AAW31700	Aaw31700	Human int	364	7	2.3	255	7	ABO62558	AbO62558	Klebsiell
292	7	2.3	172	2	AAW44108	Aaw44108	Mature hu	365	7	2.3	256	3	AAW17337	Aaw17337	Arabidops
293	7	2.3	173	2	AAW74460	Aaw74460	Human int	366	7	2.3	259	6	ABW17340	AbW17340	Staphyloc
294	7	2.3	173	2	AAW74461	Aaw74461	Human int	367	7	2.3	259	6	ABW17340	AbW17340	Staphyloc
295	7	2.3	173	2	ADP05649	AdP05649	Bacterial	368	7	2.3	260	3	AAW17816	Aaw17816	Arabidops
296	7	2.3	173	7	ADM04746	AdM04746	Human pro	369	7	2.3	260	4	AAW79851	Aaw79851	Corynebac
297	7	2.3	173	7	ABO75581	AbO75581	Pseudomon	370	7	2.3	260	8	ADN73667	AdN73667	Thale cre
298	7	2.3	177	7	ABO78617	AbO78617	Pseudomon	371	7	2.3	263	3	AAW17815	Aaw17815	Arabidops
299	7	2.3	177	8	ADG22530	AdG22530	Cyanophag	372	7	2.3	264	7	ABO72311	AbO72311	Pseudomon
300	7	2.3	178	3	AAW41424	Aaw41424	Human ORF	373	7	2.3	265	7	ABO80404	AbO80404	Pseudomon
301	7	2.3	178	4	ABR00931	AbR00931	Gene 216	374	7	2.3	265	8	ADN25444	AdN25444	Bacterial
302	7	2.3	178	5	ABP09514	AbP09514	Human ORF	375	7	2.3	266	3	AAW87852	Aaw87852	Human FGF
303	7	2.3	178	6	ABU55859	AbU55859	Human gen	376	7	2.3	266	3	AAW87858	Aaw87858	Human FGF
304	7	2.3	178	8	ADJ36948	Adj36948	Human gen	377	7	2.3	266	6	ABW74160	AbW74160	Human fib
305	7	2.3	178	8	ADL81526	AdL81526	Human gen	378	7	2.3	266	6	ABW3848	AbW3848	Human fib
306	7	2.3	179	7	ABO81658	AbO81658	Human gen	379	7	2.3	266	6	ABG72719	AbG72719	Recombina
307	7	2.3	184	8	ADN17366	AdN17366	Bacterial	380	7	2.3	266	6	ABG72713	AbG72713	Recombina
308	7	2.3	186	7	ABO83504	AbO83504	Pseudomon	381	7	2.3	267	1	AAW82964	Aaw82964	Encoded b
309	7	2.3	188	5	ABW04638	AbW04638	Human tect	382	7	2.3	267	2	AAW48064	Aaw48064	FGF-3 CDN
310	7	2.3	191	3	AAW08247	Aaw08247	Arabidops	383	7	2.3	267	2	AAW22600	Aaw22600	Human fib
311	7	2.3	194	3	AAW51164	Aaw51164	Arabidops	384	7	2.3	267	4	AAW50709	Aaw50709	Human fib
312	7	2.3	194	7	ABO78339	AbO78339	Pseudomon	385	7	2.3	267	4	AAW00645	Aaw00645	Human fib
313	7	2.3	195	1	AAW30076	Aaw30076	Sequence	386	7	2.3	267	4	AAW65651	Aaw65651	Human fib
314	7	2.3	195	2	AAW04541	Aaw04541	Bovine in	387	7	2.3	267	4	AAW50277	Aaw50277	Human FGF
315	7	2.3	195	2	AAW09289	Aaw09289	Human com	388	7	2.3	267	5	AAW18810	Aaw18810	Human FGF
316	7	2.3	195	2	AAW44107	Aaw44107	Human int	389	7	2.3	267	5	ABW9124	AbW9124	Human fib
317	7	2.3	195	2	AAW73227	Aaw73227	Bovine in	390	7	2.3	267	8	ADM94750	AdM94750	Human fib

391	7	2.3	268	2	AAR75703	AAR75703 Human FGF	464	7	2.3	265	8	ADM93510	ADM93510 Human NOV
392	7	2.3	268	2	AAR70813	AAR70813 FGF-5, 3/	465	7	2.3	285	8	ADM93512	ADM93512 Human NOV
393	7	2.3	268	2	AAR80780	AAR80780 Fibrinoblast	466	7	2.3	285	8	ADM93508	ADM93508 Human NOV
394	7	2.3	268	2	AAW75715	AAW75715 Fibrinoblast	467	7	2.3	285	8	ADM93514	ADM93514 Human NOV
395	7	2.3	268	2	AAW53031	AAW53031 Fibrinoblast	468	7	2.3	285	8	ADM93518	ADM93518 Human NOV
396	7	2.3	268	2	AAV08585	AAV08585 Human FGF	469	7	2.3	289	8	ADU67796	ADU67796 T. thermo
397	7	2.3	268	2	AAV31792	AAV31792 Human FGF	470	7	2.3	289	8	ADU66008	ADU66008 T. thermo
398	7	2.3	268	3	AAV32337	AAV32337 Human fib	471	7	2.3	289	8	ADK01086	ADK01086 DNA polym
399	7	2.3	268	3	AAV90414	AAV90414 FGF-5, SE	472	7	2.3	289	8	ADJ79305	ADJ79305 T. thermo
400	7	2.3	268	3	AAH10296	AAH10296 Fibrinoblast	473	7	2.3	289	8	ADJ84745	ADJ84745 T. thermo
401	7	2.3	268	4	AAE01660	AAE01660 FGF5 prot	474	7	2.3	289	8	ADM77533	ADM77533 DNA polym
402	7	2.3	268	4	AAE00636	AAE00636 Human MUS	475	7	2.3	289	8	ADM66200	ADM66200 T. thermo
403	7	2.3	268	4	AAE00642	AAE00642 Human fib	476	7	2.3	289	8	ADU04253	ADU04253 T. thermo
404	7	2.3	268	4	AAE04405	AAE04405 Human fib	477	7	2.3	289	8	ADP82330	ADP82330 DNA polym
405	7	2.3	268	4	AAE050701	AAE050701 Human fib	478	7	2.3	292	3	AAAG40208	AAAG40208 Arabidops
406	7	2.3	268	4	AAH85816	AAH85816 Human fib	479	7	2.3	295	5	ABH855001	ABH855001 Human PRO
407	7	2.3	268	6	ABP54276	ABP54276 Human fib	480	7	2.3	295	5	ABH95607	ABH95607 Human ang
408	7	2.3	268	6	ADA95451	ADA95451 Fibrinoblast	481	7	2.3	295	6	ABU56619	ABU56619 Lung canc
409	7	2.3	268	7	ADC34580	ADC34580 Human fib	482	7	2.3	295	7	ADD10659	ADD10659 Human sec
410	7	2.3	268	7	ADD66124	ADD66124 Fibrinoblast	483	7	2.3	295	7	ADD11619	ADD11619 Human sec
411	7	2.3	268	7	ADH92004	ADH92004 Fibrinoblast	484	7	2.3	295	7	ADD37412	ADD37412 Human sec
412	7	2.3	268	8	ADS20334	ADS20334 Fibrinoblast	485	7	2.3	295	7	ADN38796	ADN38796 Cancer/an
413	7	2.3	268	8	ADT97922	ADT97922 Human ker	486	7	2.3	295	8	ADPA1620	ADPA1620 Human sec
414	7	2.3	269	7	ABO79905	ABO79905 Pseudomon	487	7	2.3	295	8	ADH43803	ADH43803 Human PRO
415	7	2.3	271	6	ADA47978	ADA47978 Rice prot	488	7	2.3	295	8	ADK83148	ADK83148 Human PRO
416	7	2.3	272	8	ADN46632	ADN46632 Thermococ	489	7	2.3	296	6	ABU27185	ABU27185 Protein e
417	7	2.3	273	6	ABUL6404	ABUL6404 Protein e	490	7	2.3	297	7	ABO70186	ABO70186 Pseudomon
418	7	2.3	273	7	ABO67947	ABO67947 Pseudomon	491	7	2.3	298	7	ADC87387	ADC87387 Human GPC
419	7	2.3	273	7	ABO82987	ABO82987 Pseudomon	492	7	2.3	299	8	ADJ76361	ADJ76361 Marker ge
420	7	2.3	276	3	AAU37525	AAU37525 Staphyloc	493	7	2.3	304	4	AAH93719	AAH93719 Human pol
421	7	2.3	278	3	AAAG6910	AAAG6910 Arabidops	494	7	2.3	304	4	AAH72383	AAH72383 Human car
422	7	2.3	278	4	AAE02480	AAE02480 Arabidops	495	7	2.3	304	4	AAH72384	AAH72384 Murine ca
423	7	2.3	278	8	ADJ37069	ADJ37069 Plant yle	496	7	2.3	304	6	ABR58661	ABR58661 Human can
424	7	2.3	278	8	AD143863	AD143863 Plant tra	497	7	2.3	304	8	ADJ75656	ADJ75656 Marker ge
425	7	2.3	278	8	ADDO1839	ADDO1839 Thalecres	498	7	2.3	304	8	ADJ13634	ADJ13634 Human pro
426	7	2.3	279	7	ABO81782	ABO81782 Pseudomon	499	7	2.3	305	4	AAU35194	AAU35194 Arabidops
427	7	2.3	281	7	ADE28785	ADE28785 Human NOV	500	7	2.3	305	6	ABU29145	ABU29145 Protein e
428	7	2.3	281	7	ADE28777	ADE28777 Human NOV	501	7	2.3	306	4	AAU34399	AAU34399 Staphyloc
429	7	2.3	281	7	ADE28793	ADE28793 Human NOV	502	7	2.3	310	4	AAU34380	AAU34380 Staphyloc
430	7	2.3	281	7	ADE28799	ADE28799 Human NOV	503	7	2.3	312	3	AAH13058	AAH13058 Cyclic pl
431	7	2.3	281	7	ADE28797	ADE28797 Human NOV	504	7	2.3	312	3	AAH23255	AAH23255 Streptomy
432	7	2.3	281	7	ADE28789	ADE28789 Human NOV	505	7	2.3	312	7	ADBO8326	ADBO8326 Novel pro
433	7	2.3	281	7	ADE28787	ADE28787 Human NOV	506	7	2.3	313	7	ABO73121	ABO73121 Pseudomon
434	7	2.3	281	7	ADE28795	ADE28795 Human NOV	507	7	2.3	314	7	ABO70090	ABO70090 Pseudomon
435	7	2.3	281	7	ABDE28791	ABDE28791 Human NOV	508	7	2.3	318	6	ABU36529	ABU36529 Protein e
436	7	2.3	281	7	ABO69002	ABO69002 Pseudomon	509	7	2.3	318	6	ABR55201	ABR55201 Amino acyl
437	7	2.3	281	7	ABO76152	ABO76152 Pseudomon	510	7	2.3	319	7	ABO74811	ABO74811 Pseudomon
438	7	2.3	281	8	ADM93532	ADM93532 Human NOV	511	7	2.3	319	4	AAU63124	AAU63124 Propionib
439	7	2.3	281	8	ADM93538	ADM93538 Human NOV	512	7	2.3	319	6	ABH59643	ABH59643 Propionib
440	7	2.3	281	8	ADM93540	ADM93540 Human NOV	513	7	2.3	321	3	AAAG1409	AAAG1409 Arabidops
441	7	2.3	281	8	ADM93542	ADM93542 Human NOV	514	7	2.3	321	7	ADH85922	ADH85922 Enterococ
442	7	2.3	281	8	ADM93544	ADM93544 Human NOV	515	7	2.3	322	4	AAU37394	AAU37394 Staphyloc
443	7	2.3	281	8	ADM93530	ADM93530 Human NOV	516	7	2.3	323	3	AAAG5257	AAAG5257 Arabidops
444	7	2.3	281	8	ADM93534	ADM93534 Human NOV	517	7	2.3	323	3	AAAG42004	AAAG42004 Arabidops
445	7	2.3	281	8	ADM93522	ADM93522 Human NOV	518	7	2.3	323	3	ABO00535	ABO00535 Novel hum
446	7	2.3	281	8	ADM93536	ADM93536 Human NOV	519	7	2.3	323	6	AD143585	AD143585 Plant tira
447	7	2.3	283	4	AAAB68051	AAAB68051 Amino acyl	520	7	2.3	323	8	ADDO03389	ADDO03389 Thalecres
448	7	2.3	283	4	AAAG90222	AAAG90222 C glutami	521	7	2.3	324	6	ABR42537	ABR42537 Chlorobac
449	7	2.3	283	4	AAAG17736	AAAG17736 Arabidops	522	7	2.3	325	4	AAH79411	AAH79411 Corynebac
450	7	2.3	284	6	ABU34729	ABU34729 Protein e	523	7	2.3	325	4	AAAG1986	AAAG1986 C. glutami
451	7	2.3	284	6	ADA48496	ADA48496 Rice prot	524	7	2.3	325	4	ADJ70753	ADJ70753 Human hea
452	7	2.3	284	7	ADU11706	ADU11706 Pseudomon	525	7	2.3	325	7	ABO79420	ABO79420 Pseudomon
453	7	2.3	284	7	ABO78826	ABO78826 Pseudomon	526	7	2.3	330	3	AAAG14408	AAAG14408 Arabidops
454	7	2.3	285	7	ADE28767	ADE28767 Human NOV	527	7	2.3	330	7	ABO69827	ABO69827 Pseudomon
455	7	2.3	285	7	ADE28773	ADE28773 Human NOV	528	7	2.3	330	8	AD161489	AD161489 A. thalia
456	7	2.3	285	7	ADE28769	ADE28769 Human NOV	529	7	2.3	335	7	ADB70078	ADB70078 C. neofo
457	7	2.3	285	7	ADE28765	ADE28765 Human NOV	530	7	2.3	336	3	AAAG5096	AAAG5096 Arabidops
458	7	2.3	285	7	ADE28763	ADE28763 Human NOV	531	7	2.3	336	3	AAAG19302	AAAG19302 Arabidops
459	7	2.3	285	7	ADE28761	ADE28761 Human NOV	532	7	2.3	339	4	AAU16193	AAU16193 Human nov
460	7	2.3	285	7	ADE28771	ADE28771 Human NOV	533	7	2.3	340	6	ABU55262	ABU55262 Human nov
461	7	2.3	285	7	ADJ70889	ADJ70889 Human hea	534	7	2.3	340	2	AAW31544	AAW31544 Human cyt
462	7	2.3	285	8	ADM93516	ADM93516 Human NOV	535	7	2.3	340	2	AAW17081	AAW17081 EPH Famil
463	7	2.3	285	8	ADM93506	ADM93506 Human NOV	536	7	2.3	340	2	AAW33699	AAW33699 AL-2-bhor

537	7	2.3	340	2	AAW10637	AAW10637 NLERK2 1i	610	7	2.3	391	6	ABU23338	ABU23338 Protein e
538	7	2.3	340	2	AAW46615	AAW46615 Human tta	611	7	2.3	393	7	ADP05580	ADP05580 Bacterial
539	7	2.3	340	6	ABU07845	ABU07845 Human eph	612	7	2.3	396	6	ABU39851	ABU39851 Protein e
540	7	2.3	340	8	ADO21436	Adq21436 Human eof	613	7	2.3	396	8	ADI43318	ADI43318 Plant tta
541	7	2.3	345	6	ABP80534	Abp80534 N. gonorr	614	7	2.3	396	8	ADM48230	ADM48230 Polypepti
542	7	2.3	346	7	ABO73355	ABO73355 Pseudomon	615	7	2.3	397	8	ADM30416	ADM30416 Bacterial
543	7	2.3	348	4	AAG82304	AAg82304 S. epider	616	7	2.3	399	7	ABO76293	ABO76293 Pseudomon
544	7	2.3	348	7	ABO76859	ABO76859 Pseudomon	617	7	2.3	399	8	ADJ48713	ADJ48713 O11-aesoc
545	7	2.3	351	4	AAAG81622	AAg81622 S. epider	618	7	2.3	401	3	ABAB21014	ABAB21014 Human nuc
546	7	2.3	355	4	ABBT0336	Abbt0336 Drosophi1	619	7	2.3	402	7	ABOC6449	ABOC6449 Pseudomon
547	7	2.3	356	8	ADP43678	Adp43678 Human FPM	620	7	2.3	402	7	ABO71401	ABO71401 Pseudomon
548	7	2.3	357	8	ADR96379	Adr96379 Novel S.	621	7	2.3	405	8	ADR16080	ADR16080 Human ADA
549	7	2.3	359	3	AAAG19301	AAg19301 Arabidops	622	7	2.3	405	8	ADR30763	ADR30763 Human ADA
550	7	2.3	359	3	AAAG50995	AAg50995 Arabidops	623	7	2.3	413	7	ADG75124	ADG75124 Human her
551	7	2.3	359	8	ADDO2511	Ado02511 Thalecres	624	7	2.3	413	8	ADR16133	ADR16133 Human ADA
552	7	2.3	359	8	ADN73397	Adn73397 Thale cre	625	7	2.3	413	8	ADR16883	ADR16883 Human wil
553	7	2.3	360	8	ADN21970	Adn21970 Bacterial	626	7	2.3	414	2	AAW72139	AAW72139 HSV-2 btr
554	7	2.3	360	8	ADN24728	Adn24728 Bacterial	627	7	2.3	414	2	AAW72159	AAW72159 HSV-2 btr
555	7	2.3	361	8	ADR18589	Adr18589 Rat GPCR	628	7	2.3	416	3	AAAG17735	AAg17735 Arabidops
556	7	2.3	366	2	AAAY38904	AAy38904 Neisseria	629	7	2.3	416	4	AAAG82654	AAg82654 S. epider
557	7	2.3	366	2	AAAY38907	AAy38907 Neisseria	630	7	2.3	416	6	ABU42635	ABU42635 Protein e
558	7	2.3	366	2	AAAY38905	AAy38905 Neisseria	631	7	2.3	416	6	ABU42635	ABU42635 Protein e
559	7	2.3	366	2	ABP77026	Abp77026 N. gonorr	632	7	2.3	417	5	ABP40161	ABP40161 Staphy1oc
560	7	2.3	366	6	ABO00421	ABO00421 Novel hum	633	7	2.3	417	8	ADSO7208	ADSO7208 Staphy1oc
561	7	2.3	367	8	ADS25131	AdS25131 Bacterial	634	7	2.3	419	4	AAU48288	AAU48288 Propionib
562	7	2.3	368	6	ABU19639	Abu19639 Protein e	635	7	2.3	419	6	ABM44507	ABM44507 Protein e
563	7	2.3	368	8	ABO67236	ABO67236 Klebsiell	636	7	2.3	419	6	ABU43572	ABU43572 Protein e
564	7	2.3	368	8	ADJ77832	Adj77832 Rice lipa	637	7	2.3	421	4	AAU37252	AAU37252 Staphy1oc
565	7	2.3	369	7	ADM05113	Adm05113 Human pro	638	7	2.3	421	4	AAU36595	AAU36595 Staphy1oc
566	7	2.3	372	7	ABO78613	ABO78613 Pseudomon	639	7	2.3	421	4	AAU33833	AAU33833 Staphy1oc
567	7	2.3	372	8	ADO02844	ADO02844 Thalecres	640	7	2.3	421	5	ABU78317	ABU78317 Amino aci
568	7	2.3	374	7	ABO73679	ABO73679 Pseudomon	641	7	2.3	421	6	ABU15882	ABU15882 Protein e
569	7	2.3	375	2	AAAY50008	AAy50008 Thermus t	642	7	2.3	421	6	ABM72095	ABM72095 Staphy1oc
570	7	2.3	375	4	AAW48177	AAw48177 Thermus t	643	7	2.3	422	7	ABO70706	ABO70706 Pseudomon
571	7	2.3	375	4	ADH87967	Adh87967 Enterococ	644	7	2.3	422	7	ABO81879	ABO81879 Pseudomon
572	7	2.3	376	2	AAW64377	AAw64377 Mycobacte	645	7	2.3	423	4	AAU33567	AAU33567 Pseudomon
573	7	2.3	376	2	AAW85054	AAw85054 Beta subu	646	7	2.3	423	6	ABU15665	ABU15665 Protein e
574	7	2.3	376	2	AAW81744	AAw81744 M. tuberc	647	7	2.3	426	8	ADP29657	ADP29657 Human sec
575	7	2.3	376	2	AAAY39031	AAy39031 M. tuberc	648	7	2.3	426	8	ADP29657	ADP29657 Human sec
576	7	2.3	376	2	AAAY39174	AAy39174 M. tuberc	649	7	2.3	429	4	AAAG4551	AAg4551 Human sug
577	7	2.3	376	8	ADU67878	Adj67878 T. thermo	650	7	2.3	429	7	ABO74810	ABO74810 Pseudomon
578	7	2.3	376	8	ADJ67877	Adj67877 T. thermo	651	7	2.3	432	6	ADAA33668	ADa33668 Acinetoba
579	7	2.3	376	8	ADJ68089	Adj68089 T. thermo	652	7	2.3	432	8	ADN22868	ADn22868 Bacterial
580	7	2.3	376	8	ADJ68090	Adj68090 T. thermo	653	7	2.3	434	8	ADNS2067	ADs2067 Bacterial
581	7	2.3	376	8	ADK01168	Adk01168 DNA polym	654	7	2.3	437	5	AAAY94930	AAy94930 Human sec
582	7	2.3	376	8	ADK01167	Adk01167 DNA polym	655	7	2.3	437	5	ABP65593	ABp65593 Bifidobac
583	7	2.3	376	8	ADJ79387	Adj79387 T. thermo	656	7	2.3	439	4	ABG12185	ABg12185 Novel hum
584	7	2.3	376	8	ADJ79386	Adj79386 T. thermo	657	7	2.3	439	8	ADH41603	ADh41603 Novel hum
585	7	2.3	376	8	ADJ84827	Adj84827 T. thermo	658	7	2.3	440	7	ABO74167	ABO74167 Pseudomon
586	7	2.3	376	8	ADJ84826	Adj84826 T. thermo	659	7	2.3	440	7	ABO81421	ABO81421 Pseudomon
587	7	2.3	376	8	ADM77614	Adm77614 DNA polym	660	7	2.3	444	7	ADCG4325	ADc94325 E. faeciu
588	7	2.3	376	8	ADM77615	Adm77615 DNA polym	661	7	2.3	446	8	ADOC5661	ADo5661 Novel hum
589	7	2.3	376	8	ADM66282	Adm66282 T. thermo	662	7	2.3	448	6	ABU070545	ABU070545 Human adi
590	7	2.3	376	8	ADM66281	Adm66281 T. thermo	663	7	2.3	448	7	ABO81484	ABO81484 Pseudomon
591	7	2.3	376	8	ADOO4334	ADOO4334 T. thermo	664	7	2.3	450	7	ABO83538	ABO83538 Pseudomon
592	7	2.3	376	8	ADOO4335	ADOO4335 T. thermo	665	7	2.3	454	2	AAW85046	AAW85046 Gamma sub
593	7	2.3	376	8	ADP82411	Adp82411 Thermus t	666	7	2.3	454	2	AAAY50005	AAy50005 Thermus t
594	7	2.3	376	8	ADP82412	Adp82412 DNA polym	667	7	2.3	454	8	ADU67775	ADu67775 T. thermo
595	7	2.3	379	8	ADRI6128	Adri6128 Human ADA	668	7	2.3	454	8	ADU67987	ADu67987 T. thermo
596	7	2.3	379	8	ADRI6129	Adri6129 Human ADA	669	7	2.3	454	8	ADK01065	ADk01065 DNA polym
597	7	2.3	379	8	ADRI6110	Adri6110 Human ADA	670	7	2.3	454	8	ADJ79284	ADj79284 T. thermo
598	7	2.3	379	8	ADRI6108	Adri6108 Human ADA	671	7	2.3	454	8	ADJ84724	ADj84724 T. thermo
599	7	2.3	379	8	ADRI6112	Adri6112 Human ADA	672	7	2.3	454	8	ADM77512	ADm77512 DNA polym
600	7	2.3	379	8	ADRI6132	Adri6132 Human ADA	673	7	2.3	454	8	ADM66179	ADm66179 T. thermo
601	7	2.3	379	8	ADRI6130	Adri6130 Human ADA	674	7	2.3	454	8	ADOO4232	ADOO4232 T. thermo
602	7	2.3	379	8	ADRI6131	Adri6131 Human ADA	675	7	2.3	454	8	ADP82309	ADP82309 DNA polym
603	7	2.3	379	8	ADRI6127	Adri6127 Human ADA	676	7	2.3	455	2	AAW33698	AAw33698 AL-2-long
604	7	2.3	379	8	ADRI6121	Adri6121 Human ADA	677	7	2.3	456	7	ABO70671	ABO70671 Pseudomon
605	7	2.3	379	8	ADRI6129	Adri6129 Human ADA	678	7	2.3	458	2	AAAS4834	AAAS4834 Human der
606	7	2.3	379	8	ADRI6129	Adri6129 Human ADA	679	7	2.3	458	8	ADJ48714	ADj48714 O11-aesoc
607	7	2.3	383	8	ADN19022	ADn19022 Bacterial	680	7	2.3	458	8	ADM37054	ADM37054 Human alp
608	7	2.3	385	7	ABO73264	ABO73264 Pseudomon	681	7	2.3	458	8	ADO29176	ADO29176 Mouse GPC
609	7	2.3	390	6	ABM67643	ABM67643 Phototzhab	682	7	2.3	459	7	ABO80782	ABO80782 Pseudomon

683	7	2.3	460	3	AAB54132	Aab54132	Human	pan	756	7	2.3	505	8	ADM93490	Adm93490	Human	NOV
684	7	2.3	461	7	ABO75710	AbO75710	Pseudomon		757	7	2.3	505	8	ADM93504	Adm93504	Human	NOV
685	7	2.3	462	8	ADM37052	Adm37052	Human	alp	758	7	2.3	505	8	ADM93484	Adm93484	Human	NOV
686	7	2.3	464	2	AAW85045	AAW85045	Gamma	sub	759	7	2.3	506	7	ABO69644	AbO69644	Pseudomon	
687	7	2.3	464	2	AAV50004	AAV50004	Thermus	t	760	7	2.3	507	7	ABO68722	AbO68722	Pseudomon	
688	7	2.3	464	8	ADJ67774	AdJ67774	T. thermo		761	7	2.3	508	4	AAW79842	AAW79842	Human	pro
689	7	2.3	464	8	ADJ67986	AdJ67986	T. thermo		762	7	2.3	511	4	ABE65414	ABE65414	Human	pro
690	7	2.3	464	8	ADK01064	AdK01064	DNA	polym	763	7	2.3	513	8	ADJ42667	AdJ42667	Plant	tra
691	7	2.3	464	8	ADJ79283	AdJ79283	T. thermo		764	7	2.3	513	8	ADDO02916	ADDO02916	Thalae	lec
692	7	2.3	464	8	ADJ84723	AdJ84723	T. thermo		765	7	2.3	514	8	ADH41601	ADH41601	Novel	hum
693	7	2.3	464	8	ADM77511	AdM77511	DNA	polym	766	7	2.3	515	3	AAW42076	AAW42076	HSV-2	str
694	7	2.3	464	8	ADM66178	AdM66178	T. thermo		767	7	2.3	515	3	AAW42510	AAW42510	Human	ORF
695	7	2.3	464	8	ADO04231	AdO04231	T. thermo		768	7	2.3	515	8	ADN47628	ADN47628	Thermococ	
696	7	2.3	464	8	ADP82308	AdP82308	DNA	polym	769	7	2.3	522	6	AAE35267	AAE35267	Human	P45
697	7	2.3	465	4	AAB95721	Aab95721	Human	pro	770	7	2.3	523	7	AAW78858	AAW78858	Human	pro
698	7	2.3	465	5	ABG90332	ABg90332	Human	pol	771	7	2.3	524	4	AAW39649	AAW39649	Human	pol
699	7	2.3	465	5	ABG64595	ABg64595	Human	alb	772	7	2.3	524	7	ADE28737	AdE28737	Human	NOV
700	7	2.3	465	5	AAE21637	Aae21637	Human	gen	773	7	2.3	524	8	ADM93482	Adm93482	Human	NOV
701	7	2.3	465	5	ADL77862	AdL77862	Albumin	f	774	7	2.3	526	4	AAW80094	AAW80094	Human	pro
702	7	2.3	467	6	ADP76730	AdP76730	Streptomy		775	7	2.3	526	4	AAW80116	AAW80116	Human	pro
703	7	2.3	467	6	ABO78829	AbO78829	Pseudomon		776	7	2.3	527	4	AAU64492	AAU64492	Proplionib	
704	7	2.3	468	5	AAU72939	Aau72939	Neisseria		777	7	2.3	527	5	ABB91194	ABb91194	Herbicida	
705	7	2.3	469	6	ADA54968	Ada54968	Human	pro	778	7	2.3	527	6	ABM64701	ABm64701	Propionib	
706	7	2.3	470	7	ADM26441	AdM26441	Hyperther		779	7	2.3	527	6	ABM61011	ABm61011	Propionib	
707	7	2.3	470	8	ADL90192	AdL90192	Human	enz	780	7	2.3	528	2	AAV05909	AAV05909	Thermophi	
708	7	2.3	470	8	ADS41716	AdS41716	Bacterial		781	7	2.3	529	2	AAW85044	AAW85044	Tau	subun
709	7	2.3	472	7	ABO83322	AbO83322	Pseudomon		782	7	2.3	529	2	AAV50003	AAV50003	Thermus	t
710	7	2.3	476	8	ABO58882	AbO58882	Human	gen	783	7	2.3	529	2	AAV50025	AAV50025	Thermus	t
711	7	2.3	477	5	ABB93927	ABb93927	Herbicida		784	7	2.3	529	8	ADJ67772	AdJ67772	T. thermo	
712	7	2.3	477	7	ABO78770	AbO78770	Pseudomon		785	7	2.3	529	8	ADJ67984	AdJ67984	T. thermo	
713	7	2.3	479	4	AAB92879	Aab92879	Human	pro	786	7	2.3	529	8	ADK01062	AdK01062	DNA	polym
714	7	2.3	479	7	ADP76665	AdP76665	Novel	hum	787	7	2.3	529	8	ADJ79281	AdJ79281	T. thermo	
715	7	2.3	480	7	ADP74132	AdP74132	Human	nov	788	7	2.3	529	8	ADJ84721	AdJ84721	T. thermo	
716	7	2.3	482	7	ABO82746	AbO82746	Pseudomon		789	7	2.3	529	8	ADM77509	AdM77509	DNA	polym
717	7	2.3	484	7	ABO75503	AbO75503	Pseudomon		790	7	2.3	529	8	ADM66176	AdM66176	T. thermo	
718	7	2.3	485	7	ABEO7854	ABeo7854	Novel	pro	791	7	2.3	529	8	ADDO4229	ADdo4229	T. thermo	
719	7	2.3	485	8	ABO58389	ABo58389	Human	gen	792	7	2.3	529	8	ADP82306	AdP82306	Thermus	t
720	7	2.3	486	7	ABO82658	ABo82658	Pseudomon		793	7	2.3	537	8	ADP29732	AdP29732	Human	sec
721	7	2.3	490	7	ABO73969	ABo73969	Pseudomon		794	7	2.3	537	8	ADP29769	AdP29769	Human	sec
722	7	2.3	496	7	ABO77922	ABo77922	Pseudomon		795	7	2.3	537	8	ADP29752	AdP29752	Human	sec
723	7	2.3	499	7	ABO70875	ABo70875	Pseudomon		796	7	2.3	538	4	AAW41590	AAW41590	Human	pol
724	7	2.3	501	7	ADE28781	AdE28781	Human	NOV	797	7	2.3	543	7	ADDA6553	ADda6553	Human	pro
725	7	2.3	501	7	ADE28783	AdE28783	Human	NOV	798	7	2.3	547	4	AAW41435	AAW41435	Human	pol
726	7	2.3	501	7	ADE28779	AdE28779	Human	NOV	799	7	2.3	548	4	ABBS9192	ABbs9192	Drosophili	
727	7	2.3	501	7	ABO68984	ABo68984	Pseudomon		800	7	2.3	550	2	AAW98558	AAW98558	H. pylori	
728	7	2.3	501	7	ABO81139	ABo81139	Pseudomon		801	7	2.3	552	5	ADJ16903	AdJ16903	Human	NOV
729	7	2.3	501	8	ABO68049	ABo68049	Pseudomon		802	7	2.3	553	4	AAW61323	AAW61323	Human	tra
730	7	2.3	501	8	ADM93524	Adm93524	Human	NOV	803	7	2.3	553	4	AAW39804	AAW39804	Human	pol
731	7	2.3	501	8	ADM93526	Adm93526	Human	NOV	804	7	2.3	553	4	AAW95285	AAW95285	Human	pro
732	7	2.3	501	8	ADM93526	Adm93526	Human	NOV	805	7	2.3	553	4	ABO68683	ABo68683	Pseudomon	
733	7	2.3	504	3	AAW16593	AAw16593	Arabidops		806	7	2.3	554	8	ADNO4972	ADno4972	Antibiot	
734	7	2.3	505	4	ABG03717	ABg03717	Novel	hum	807	7	2.3	560	7	ABO77361	ABo77361	Pseudomon	
735	7	2.3	505	4	ABE28775	ABe28775	Human	NOV	808	7	2.3	560	8	ABM85018	ABm85018	Human	dia
736	7	2.3	505	7	ADE28753	AdE28753	Human	NOV	809	7	2.3	561	2	AAW63701	AAW63701	Human	hsk
737	7	2.3	505	7	ADE28757	AdE28757	Human	NOV	810	7	2.3	561	5	ADT16582	ADt16582	Human	NOV
738	7	2.3	505	7	ADE28739	AdE28739	Human	NOV	811	7	2.3	561	8	ADN42236	ADn42236	Human	NOV
739	7	2.3	505	7	ADE28743	AdE28743	Human	NOV	812	7	2.3	565	4	AAW39201	AAW39201	Human	pol
740	7	2.3	505	7	ADE28747	AdE28747	Human	NOV	813	7	2.3	565	5	ADH48764	ADh48764	NOV19	pro
741	7	2.3	505	7	ADE28749	AdE28749	Human	NOV	814	7	2.3	568	6	ABU43107	ABu43107	Protein	e
742	7	2.3	505	7	ADE28741	AdE28741	Human	NOV	815	7	2.3	568	7	ADBO7846	ADbo7846	Novel	pro
743	7	2.3	505	7	ADE28751	AdE28751	Human	NOV	816	7	2.3	568	7	ABO73715	ABo73715	Pseudomon	
744	7	2.3	505	7	ADE28745	AdE28745	Human	NOV	817	7	2.3	569	4	ABG02057	ABg02057	Novel	hum
745	7	2.3	505	7	ADE28755	AdE28755	Human	NOV	818	7	2.3	569	6	ABU21949	ABu21949	Protein	e
746	7	2.3	505	8	ADE28759	AdE28759	Human	NOV	819	7	2.3	572	7	ABO75250	ABo75250	Pseudomon	
747	7	2.3	505	8	ADM93486	Adm93486	Human	NOV	820	7	2.3	573	4	AAW79110	AAW79110	Human	pro
748	7	2.3	505	8	ADM93488	Adm93488	Human	NOV	821	7	2.3	574	3	AAW11086	AAW11086	Arabidops	
749	7	2.3	505	8	ADM93500	Adm93500	Human	NOV	822	7	2.3	574	4	ABG03206	ABg03206	Novel	hum
750	7	2.3	505	8	ADM93498	Adm93498	Human	NOV	823	7	2.3	576	5	ABP39110	ABp39110	Staphyloc	
751	7	2.3	505	8	ADM93494	Adm93494	Human	NOV	824	7	2.3	576	8	ADSO7323	ADso7323	Staphyloc	
752	7	2.3	505	8	ADM93496	Adm93496	Human	NOV	825	7	2.3	582	5	ABG61896	ABg61896	Prostate	
753	7	2.3	505	8	ADM93502	Adm93502	Human	NOV	826	7	2.3	582	5	ABJ05557	ABj05557	Breast	ca
754	7	2.3	505	8	ADM93520	Adm93520	Human	NOV	827	7	2.3	582	7	ADM93509	Adm93509	Cancer/an	
755	7	2.3	505	8	ADM93492	Adm93492	Human	NOV	828	7	2.3	582	7	ADM93575	Adm93575	Cancer/an	

829	7	2.3	582	7	ADN39535	Adn39535 Cancer/an	902	7	2.3	681	8	AD009782	AD009782 Rat SGLT
830	7	2.3	582	7	ADN39440	Adn39440 Cancer/an	903	7	2.3	681	8	AD009827	AD009827 Hamster S
831	7	2.3	585	7	ABU05348	Abu05348 Pancreas-	904	7	2.3	684	4	ABG14126	ABG14126 Human hum
832	7	2.3	585	8	ADH42375	Adh42375 Novel hum	905	7	2.3	684	6	ABJ37930	ABJ37930 NOXV prot
833	7	2.3	587	7	ABO69534	AbO69534 Pseudomon	906	7	2.3	684	7	ABO83596	ABO83596 Pseudomon
834	7	2.3	588	4	AAB96513	Aab96513 Putative	907	7	2.3	686	8	ADP29724	ADP29724 Human bec
835	7	2.3	590	7	ABO70381	AbO70381 Pseudomon	908	7	2.3	687	6	ABR56332	ABR56332 XM_047529
836	7	2.3	591	4	ABG17270	AbG17270 Novel hum	909	7	2.3	688	6	ABR21490	ABR21490 Protein e
837	7	2.3	593	7	ABO74594	AbO74594 Pseudomon	910	7	2.3	688	8	ADP29389	ADP29389 Human sec
838	7	2.3	594	7	AAG15592	Aag15592 Arabidops	911	7	2.3	690	3	AAV50844	AAV50844 A. oryzae
839	7	2.3	596	4	AAE06614	Aae06614 Human pro	912	7	2.3	690	3	AAV50835	AAV50835 A. oryzae
840	7	2.3	596	4	AAE08088	Aae08088 Human tra	913	7	2.3	691	8	ADS45043	ADS45043 Bacterial
841	7	2.3	596	5	ABG31594	AbG31594 Human tra	914	7	2.3	694	4	ABU36802	ABU36802 Protein e
842	7	2.3	596	5	ABR80588	ABr80588 Human sbg	915	7	2.3	696	6	ADAS5119	ADAS5119 Human pro
843	7	2.3	596	5	AAO14199	Aao14199 Human tra	916	7	2.3	696	6	ABU00092	ABU00092 Human nov
844	7	2.3	596	5	AD115578	Ad115578 Human NOV	917	7	2.3	700	8	ADR310686	ADR310686 Mouse goo
845	7	2.3	596	6	ABR99498	ABr99498 Amino aci	918	7	2.3	702	7	ABO82863	ABO82863 Pseudomon
846	7	2.3	596	6	ABU10299	Abu10299 Novel hum	919	7	2.3	703	3	AAH14781	AAH14781 Aspergill
847	7	2.3	596	6	ABU10300	Abu10300 Rabbit so	920	7	2.3	704	6	ABJ37934	ABJ37934 NOXV prot
848	7	2.3	596	6	ADH42377	Adh42377 Novel hum	921	7	2.3	709	9	ADD01163	ADD01163 Human nuc
849	7	2.3	596	8	ADN42332	Adn42332 Human nov	922	7	2.3	710	4	ABG20114	ABG20114 Rat YTS21
850	7	2.3	597	8	AD115900	Ad115900 Rabbit NO	923	7	2.3	712	2	AAW30749	AAW30749 Rat YTS21
851	7	2.3	597	8	ABM85015	Abm85015 Human dia	924	7	2.3	712	7	ADE56302	ADE56302 Rat Prote
852	7	2.3	598	8	ADH42373	Adh42373 Novel hum	925	7	2.3	715	7	ABO83994	ABO83994 Pseudomon
853	7	2.3	599	8	ABO71716	AbO71716 Pseudomon	926	7	2.3	716	3	AAG40451	AAG40451 Arabidops
854	7	2.3	599	8	ADQ66342	AdQ66342 Novel hum	927	7	2.3	720	5	ABP69719	ABP69719 Human pol
855	7	2.3	600	4	AAB85503	Aab85503 Human pro	928	7	2.3	721	6	ABJ26419	ABJ26419 Aspergill
856	7	2.3	600	5	AAE24147	Aae24147 Human kin	929	7	2.3	722	7	ABO69735	ABO69735 Pseudomon
857	7	2.3	600	6	ABU37929	AbJ37929 NOXV prot	930	7	2.3	724	7	ABO82969	ABO82969 Pseudomon
858	7	2.3	602	7	ABO81712	AbO81712 Pseudomon	931	7	2.3	726	8	ADR310684	ADR310684 Mouse goo
859	7	2.3	604	7	ADG74672	AdG74672 Human kin	932	7	2.3	731	8	ADP98881	ADP98881 C. albica
860	7	2.3	605	6	ABU24004	AbU24004 Protein e	933	7	2.3	734	8	ADN99796	ADN99796 Novel hum
861	7	2.3	606	8	ADE98284	Ade98284 Cancer-li	934	7	2.3	735	6	AAE37016	AAE37016 Human nuc
862	7	2.3	606	8	ABM85014	Abm85014 Human dia	935	7	2.3	738	6	AAE35065	AAE35065 Human tra
863	7	2.3	607	2	AAW09422	Aaw09422 Banana po	936	7	2.3	739	7	ADDE0809	ADDE0809 Novel pro
864	7	2.3	607	8	ABM84840	Abm84840 Human dia	937	7	2.3	741	4	AAE05188	AAE05188 Human dru
865	7	2.3	612	5	AD116580	Ad116580 Human NOV	938	7	2.3	743	6	ABJ37932	ABJ37932 NOXV prot
866	7	2.3	612	8	ADH42379	AdH42379 Novel hum	939	7	2.3	745	6	AAE35064	AAE35064 Human tra
867	7	2.3	612	8	ADN42324	Adn42324 Human nov	940	7	2.3	746	8	ADQ09511	ADQ09511 Human gen
868	7	2.3	616	6	ABP57705	Abp57705 Saccharop	941	7	2.3	746	8	ADQ2537	ADQ2537 Protein e
869	7	2.3	632	7	ABO75844	AbO75844 Pseudomon	942	7	2.3	747	3	ADN21011	ADN21011 Bacterial
870	7	2.3	633	7	AAW93900	Aaw93900 Human pol	943	7	2.3	747	3	AAAG40450	AAAG40450 Arabidops
871	7	2.3	633	8	AD132008	Ad132008 Human pro	944	7	2.3	749	7	AD121213	AD121213 Novel hum
872	7	2.3	633	8	ABM85017	Abm85017 Human dia	945	7	2.3	750	9	AAU01898	AAU01898 Mycobacte
873	7	2.3	635	7	ABO82900	AbO82900 Pseudomon	946	7	2.3	752	4	ABG28100	ABG28100 Novel hum
874	7	2.3	637	7	ABU25819	AbU25819 Aspergill	947	7	2.3	752	5	AAE15783	AAE15783 Human tra
875	7	2.3	643	6	ABR99497	ABr99497 Amino aci	948	7	2.3	760	5	AAE22157	AAE22157 Human TRN
876	7	2.3	643	8	ADSA2943	Adsa2943 Bacterial	949	7	2.3	760	7	ADE11758	Ade11758 Human sec
877	7	2.3	644	4	AAU33234	Aau33234 Novel hum	950	7	2.3	763	2	AAV24094	AAV24094 Mouse EPC
878	7	2.3	646	6	ABU20967	Abu20967 Protein e	951	7	2.3	768	5	ABP41137	ABP41137 Human ova
879	7	2.3	649	3	AAB12140	Aab12140 Hydrophob	952	7	2.3	787	5	ADR43728	ADR43728 Human pro
880	7	2.3	649	8	ABM85016	Abm85016 Human dia	953	7	2.3	787	8	ADH41599	ADH41599 Novel hum
881	7	2.3	650	5	ABR92769	ABr92769 HeBicida	954	7	2.3	787	8	ADQ09512	ADQ09512 Human gen
882	7	2.3	655	7	ABO68366	AbO68366 Pseudomon	955	7	2.3	787	8	ADQ22538	ADQ22538 Protein e
883	7	2.3	658	7	ABO71749	AbO71749 Pseudomon	956	7	2.3	787	8	ADSL0714	ADSL0714 Human the
884	7	2.3	659	7	ABO81607	AbO81607 Pseudomon	957	7	2.3	794	7	ADP77181	ADP77181 KALPA_2/
885	7	2.3	664	5	AAU85407	Aau85407 Human pro	958	7	2.3	801	5	ABP74123	ABP74123 Human TRI
886	7	2.3	664	5	ABR99496	ABr99496 Amino aci	959	7	2.3	802	4	AAH47105	AAH47105 First epi
887	7	2.3	672	7	ABO73661	AbO73661 Pseudomon	960	7	2.3	802	5	ABR78299	ABR78299 Amino aci
888	7	2.3	674	5	ABR93334	ABr93334 Pancreas-	961	7	2.3	802	7	ADH62503	ADH62503 Human MAP
889	7	2.3	674	5	ABU05342	AbU05342 Pancreas-	962	7	2.3	803	8	ADQ19759	ADQ19759 Human sof
890	7	2.3	674	5	ABU05347	AbU05347 Pancreas-	963	7	2.3	809	4	AAH41064	AAH41064 Human pol
891	7	2.3	674	5	ABU05346	AbU05346 Pancreas-	964	7	2.3	812	4	AAAB47106	AAAB47106 Second sp
892	7	2.3	674	6	AAE35063	Aae35063 Human tra	965	7	2.3	812	4	ABR00942	ABR00942 Gene 216
893	7	2.3	674	7	ADB85297	AdB85297 Human Na-	966	7	2.3	812	5	ABR78300	ABR78300 Amino aci
894	7	2.3	674	8	ADQ09778	AdQ09778 Human SGL	967	7	2.3	812	5	AAO14377	AAO14377 Human met
895	7	2.3	678	5	ABU05343	AbU05343 Pancreas-	968	7	2.3	812	5	AAU98885	AAU98885 Human pro
896	7	2.3	678	5	AD116902	Ad116902 Murine NO	969	7	2.3	812	6	ABU55870	ABU55870 Human 216
897	7	2.3	681	8	ADQ09780	AdQ09780 Mouse SGL	970	7	2.3	812	7	ADH62505	ADH62505 Human MAP
898	7	2.3	681	5	AAO14202	Aao14202 Human tra	971	7	2.3	812	8	ADH41611	ADH41611 Novel hum
899	7	2.3	681	5	ABU05344	AbU05344 Pancreas-	972	7	2.3	812	8	ADJ36972	ADJ36972 Human gen
900	7	2.3	681	6	AAE36062	Aae36062 Human tra	973	7	2.3	812	8	ADL81550	ADL81550 Human gen
901	7	2.3	681	8	ADJ81711	AdJ81711 Human SMI	974	7	2.3	813	4	AAU29256	AAU29256 Human PRO

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975 7 2.3 813 6 ABUS632 ABUS632 Human PRO
976 7 2.3 813 6 ABUS8180 ABUS8180 Novel hum
977 7 2.3 813 6 ABUS8495 ABUS8495 Human sec
978 7 2.3 813 6 ABUS6369 ABUS6369 Human sec
979 7 2.3 813 6 ABUS6759 ABUS6759 Human sec
980 7 2.3 813 6 ABUS9699 ABUS9699 Human sec
981 7 2.3 813 6 ABUS2938 ABUS2938 Human PRO
982 7 2.3 813 6 ABUS9059 ABUS9059 Human PRO
983 7 2.3 813 6 ABUS6308 ABUS6308 Human sec
984 7 2.3 813 6 ABUS6361 ABUS6361 Novel hum
985 7 2.3 813 6 ABUS2792 ABUS2792 Human sec
986 7 2.3 813 6 ABUS0869 ABUS0869 Human sec
987 7 2.3 813 6 ABUS0292 ABUS0292 Human sec
988 7 2.3 813 6 ABUS7075 ABUS7075 Human sec
989 7 2.3 813 6 ABUS4837 ABUS4837 Human sec
990 7 2.3 813 6 ABUS8510 ABUS8510 Human PRO
991 7 2.3 813 6 ABUS9870 ABUS9870 Novel hum
992 7 2.3 813 6 ABUS98185 ABUS98185 Novel hum
993 7 2.3 813 6 ABUS91891 ABUS91891 Novel hum
994 7 2.3 813 6 ABUS8584 ABUS8584 Human PRO
995 7 2.3 813 6 ABUS6425 ABUS6425 Human sec
996 7 2.3 813 6 ABUS67638 ABUS67638 Human sec
997 7 2.3 813 6 ABUS80666 ABUS80666 Human PRO
998 7 2.3 813 6 ABUS9584 ABUS9584 Human sec
999 7 2.3 813 6 ABUS98974 ABUS98974 Human sec
1000 7 2.3 813 6 ABUS16497 ABUS16497 Human sec
```

## ALIGNMENTS

RESULT 1  
AAB60386 standard; protein; 303 AA.

```
AC AAB60386;
XX
XX 24-APR-2001 (first entry)
XX
DE Human apoptosis-associated factor NT2RM1000558 (portion), SEQ ID NO:2.
XX
XX Human; apoptosis-associated factor; NT2RM1000558; death effector domain;
KM DED; caspase family cleavage domain; pro-apoptotic; drug screening;
KM cell proliferation; ischaemic disease; chronic viral disease.
XX
OS Homo sapiens.
XX
XX WO200104300-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-JP004516.
XX
XX 08-JUL-1999; 99JP-00194179.
PR 18-OCT-1999; 99US-0159586P.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
PI WPI; 2001-138348/14.
XX
XX N-PSDB; AAF27407.
XX
XX Polynucleotide encoding an apoptosis-associated factor protein with death
PT effector domain and caspase family-cleavage domain, useful in regulating
PT diseases with cell proliferation.
XX
XX Claim 1; Page 43-44; 53pp; Japanese.
XX
XX The invention relates to a novel human apoptosis-associated factor
CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death
CC effector domain (DED) and a caspase family cleavage domain and is capable
CC of inducing apoptosis in cells. The invention also relates to nucleic
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CC acids encoding the protein (AAF27407, AAF27408); variants of the protein
CC (particularly dominant negative variants); vectors and host cells
CC comprising a nucleic acid which encodes an apoptosis-associated factor
CC of the invention; the recombinant production of the protein; an antibody
CC against the protein; and methods of screening for compounds which can
CC regulate apoptosis. The apoptosis-related factor is useful in regulating
CC diseases associated with cell proliferation and in screening drug
CC candidates e.g., for regulating cell proliferation or cell death in
CC ischaemic diseases and chronic viral diseases. The present sequence
CC represents a substantial proportion of the human apoptosis-associated
CC factor NT2RM1000558
XX
SQ Sequence 303 AA;
Query Match 100.0%; Score 303; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.8e-264;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MALSGSTPAPCWEDECLDYGMLSLRMEVVGQUTTECELELAFLLDEAPGAAAGLA 60
|||
DB 1 MALSGSTPAPCWEDECLDYGMLSLRMEVVGQUTTECELELAFLLDEAPGAAAGLA 60
|||
QY 61 RASGGLLELELRRCQCGESNRLTGQLRVLAARDLPHLARKRRPVSPEYSYGT 120
|||
DB 61 RASGGLLELELRRCQCGESNRLTGQLRVLAARDLPHLARKRRPVSPEYSYGT 120
|||
QY 121 SSSKRTGSCRRRRQSSSSANSQOGWETGSPPTKQRGRSGRPGGARRRRGAPAPQ 180
|||
DB 121 SSSKRTGSCRRRRQSSSSANSQOGWETGSPPTKQRGRSGRPGGARRRRGAPAPQ 180
|||
QY 181 QOSEPARPSEGGVTCDIRLRVAEYCEHPALGCVASRRPOLARQDLVFEQATVLR 240
|||
DB 181 QOSEPARPSEGGVTCDIRLRVAEYCEHPALGCVASRRPOLARQDLVFEQATVLR 240
|||
QY 241 SRDLGSVCDIKFSELSYLDAPMGDYLSGALLQALRGVFTLALREAVGREAVLLVSD 300
|||
DB 241 SRDLGSVCDIKFSELSYLDAPMGDYLSGALLQALRGVFTLALREAVGREAVLLVSD 300
|||
QY 301 EAD 303
|||
DB 301 EAD 303
```

## RESULT 2

AAB60387 standard; protein; 326 AA.

```
AC AAB60387;
XX
XX 24-APR-2001 (first entry)
XX
DE Human apoptosis-associated factor NT2RM1000558, SEQ ID NO:4.
XX
XX Human; apoptosis-associated factor; NT2RM1000558; death effector domain;
KM DED; caspase family cleavage domain; pro-apoptotic; drug screening;
KM cell proliferation; ischaemic disease; chronic viral disease.
XX
XX Homo sapiens.
XX
XX WO200104300-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-JP004516.
XX
XX 08-JUL-1999; 99JP-00194179.
PR 18-OCT-1999; 99US-0159586P.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
PI WPI; 2001-138348/14.
XX
```

DR N-PSDB; AAF27408.  
 XX Polynucleotide encoding an apoptosis-associated factor protein with death  
 PT effector domain and caspase family-cleavage domain, useful in regulating  
 PT diseases with cell proliferation.  
 XX  
 XX  
 PS Claim 3; Page 47-48; 53pp; Japanese.  
 XX  
 XX The invention relates to a novel human apoptosis-associated factor  
 CC (AAB60386, AAB60387), designated NT2RM100558, which contains a death  
 CC effector domain (DED) and a caspase family cleavage domain and is capable  
 CC of inducing apoptosis in cells. The invention also relates to nucleic  
 CC acids encoding the protein (AAF27407, AAF27408); variants of the protein  
 CC (particularly dominant negative variants); vectors and host cells  
 CC comprising a nucleic acid which encodes an apoptosis-associated factor  
 CC of the invention; the recombinant production of the protein; an antibody  
 CC against the protein; and methods of screening for compounds which can  
 CC regulate apoptosis. The apoptosis-related factor is useful in regulating  
 CC diseases associated with cell proliferation and in screening drug  
 CC candidates e.g., for regulating cell proliferation or cell death in  
 CC ischaemic diseases and chronic viral diseases. The present sequence  
 CC represents the human apoptosis-associated factor NT2RM100558  
 XX  
 XX Sequence 326 AA;  
 SQ  
 Query Match 100.0%; Score 303; DB 4; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-264; Indels 0; Gaps 0;  
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALSGTAPCWEDECDYVGMGLHMFVEVGGQLTECELELLAFLDEAPGAAGLA 60  
 DB 1 MALSGTAPCWEDECDYVGMGLHMFVEVGGQLTECELELLAFLDEAPGAAGLA 60  
 QY 61 PARSGLELLERGGCGGSENLRLGQLRLVLAARDLPHLARRRRPVSPERYSGTS 120  
 DB 61 PARSGLELLERGGCGGSENLRLGQLRLVLAARDLPHLARRRRPVSPERYSGTS 120  
 QY 121 SSSKRTGSCRRRRQSSSSANSQCGQWETGSPPTKQRSGRPSGARRRRRGAPAPQ 180  
 DB 121 SSSKRTGSCRRRRQSSSSANSQCGQWETGSPPTKQRSGRPSGARRRRRGAPAPQ 180  
 QY 181 QOSEPARSSGKVTCDIRLRVRAVCEHGPALBEGVASRRPQALARQLDVFQATAVLR 240  
 DB 181 QOSEPARSSGKVTCDIRLRVRAVCEHGPALBEGVASRRPQALARQLDVFQATAVLR 240  
 QY 241 SRDGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVRVLLVSD 300  
 DB 241 SRDGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVFLTEALREAVRVLLVSD 300  
 QY 301 EAD 303  
 DB 301 EAD 303  
 RESULT 3  
 AAB15551  
 ID AAB15551 standard; protein; 304 AA.  
 XX  
 XX AAB15551;  
 XX  
 XX 28-FEB-2001 (first entry)  
 XX  
 XX Apoptosis related protein encoded by gene 1 clone HLDOK36.  
 DE  
 XX  
 XX Cytostatic; antiinflammatory; immunosuppressive; antisclerotic; cardiatic;  
 KM virucidal; anti-AIDS; vasotropic; anti-ischaemic; antiparkinsonian;  
 KM anti-Alzheimer; gene therapy; human; apoptosis; fusion protein; cancer;  
 KM colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;  
 KM autoimmune disorder; multiple sclerosis; viral infection.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200056752-A2.  
 PN

XX  
 PD 28-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US006642.  
 XX  
 XX 24-MAR-1999; 99US-0126018P.  
 XX  
 XX 17-JUN-1999; 99US-0139638P.  
 PR 18-AUG-1999; 99US-0149449P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PT Ruben SM, Ni J, Young PA;  
 PI WPI; 2000-587660/55.  
 DR N-PSDB; AAA95790.  
 XX  
 XX  
 XX Nucleic acid encoding human apoptosis associated protein, useful for the  
 PT prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's  
 PT disease, inflammation and ischemic injury.  
 XX  
 XX  
 PS Claim 11; Page 252-253; 273pp; English.  
 XX  
 XX The invention relates to the isolation of genes encoding a human  
 CC apoptosis-related proteins. The nucleotide sequences AAA95790-A95798  
 CC encode the human apoptosis related proteins AAB15551-B15559. The genes  
 CC can be used to generate fusion proteins by linking to the gene for the  
 CC human immunoglobulin G Fc (IgG Fc) portion (AAA95799) for increasing the  
 CC stability of the fusion protein as compared to the human protein only.  
 CC The gene and encoded protein may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate apoptosis associated  
 CC protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,  
 CC melanomas and lymphomas), inflammation, autoimmune disorders (e.g.  
 CC multiple sclerosis) and viral infections (e.g. herpes)  
 XX  
 XX Sequence 304 AA;  
 SQ  
 Query Match 73.9%; Score 224; DB 3; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-193;  
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 80 ESNRLRLGQLRLVLAARDLPHLAKRRRPSPERYSGTSSSKRTGSCRRRRQSSS 139  
 DB 58 ESNRLRLGQLRLVLAARDLPHLAKRRRPSPERYSGTSSSKRTGSCRRRRQSSS 117  
 QY 140 ANSQCGQWETGSPPTKQRSGRPSGARRRRRGAPAPQOSEPARSSGKVTCDIR 199  
 DB 118 ANSQCGQWETGSPPTKQRSGRPSGARRRRRGAPAPQOSEPARSSGKVTCDIR 177  
 QY 200 LRVRAVCEHGPALBEGVASRRPQALARQLDVFQATAVLRSDLSGVVCDIKFSELSYL 259  
 DB 178 LRVRAVCEHGPALBEGVASRRPQALARQLDVFQATAVLRSDLSGVVCDIKFSELSYL 237  
 QY 260 DAFMGDYLSGALLQALRGVFLTEALREAVRVLLVSD 303  
 DB 238 DAFMGDYLSGALLQALRGVFLTEALREAVRVLLVSD 281  
 RESULT 4  
 AAE24860  
 ID AAE24860 standard; protein; 318 AA.  
 XX  
 XX AAE24860;  
 XX  
 XX 22-OCT-2002 (first entry)  
 XX  
 XX Human DED4 (death effector domain) protein.  
 DE  
 XX  
 XX Human; death domain; DD; death effector domain; DED; Chlamydia infection;  
 KM NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
 KM inflammation; allergy; autoimmunity; allograft rejection; cell division;  
 KM immune-based pathology; fibrosis; arthritis; graft versus host disease;  
 KM immunosuppressive; gene therapy; antisense therapy.  
 XX



OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 53..74  
 FT Region /note= "Nuclear localisation sequence"  
 XX  
 PN W0200240680-A2.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 15-NOV-2001; 2001WO-US044844.  
 XX  
 PR 17-NOV-2000; 2000US-00715893.  
 PR 29-JUN-2001; 2001US-0301889P.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
 PI Stenmer-Liëwen F;  
 XX  
 XX WPI; 2002-500222/53.  
 DR N-PSDB; AAD40080.  
 XX  
 PT New polypeptide comprising a death domain or death effector domain,  
 PT useful for discovery of drugs that suppress infection, inflammation,  
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
 XX  
 PS Claim 3; Page 186-187; 2099p; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising a death  
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention  
 CC is useful for identifying a binding agent, preferably a protein or a drug  
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC  
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or  
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and  
 CC detecting the association of the domain and the candidate binding agent,  
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or  
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass  
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the  
 CC level of a cell process such as cell proliferation, cell adhesion, cell  
 CC stress response, responses to microbial infection, cell apoptosis, cell  
 CC immunoglobulin class switching, in particular apoptosis within a cell.  
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.  
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the  
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The  
 CC invention is useful for modulating the activity of oncogenic proteins,  
 CC for treating a pathology caused by the oncogenic proteins and for  
 CC treating bacterial infections by modulating the activity of bacterial  
 CC proteins. The protein and antibody specific for it are useful for  
 CC discovery of drugs that suppress infection, inflammation, allergy,  
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein  
 CC is useful for treating immune-based pathologies, pathologies associated  
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,  
 CC arthritis, graft versus host disease. The invention is used in antisense  
 CC therapy and gene therapy. The present sequence is human DED4 protein  
 XX  
 SQ Sequence 318 AA;  
 Query Match 73.9%; Score 224; DB 5; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-193;  
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 80 ESNRLRLGQLRLVLAARDLLPHLARKRRRPVSPERYSGTSSSKRTGSCRRRRQSSS 139  
 DB 80 ESNRLRLGQLRLVLAARDLLPHLARKRRRPVSPERYSGTSSSKRTGSCRRRRQSSS 139  
 QY 140 ANSQQGWETGSPPTKQRGRSGRRPGSGARRRGAAGAQAQQQSEPARPSSSEGVTTDIR 199  
 DB 140 ANSQQGWETGSPPTKQRGRSGRRPGSGARRRGAAGAQAQQQSEPARPSSSEGVTTDIR 199  
 QY 200 LRVRAECCEGPALEQGVASRRPQALAROLDVFGQATAVVRSRLGSGVCDIKFSELSYL 259  
 DB 200 LRVRAECCEGPALEQGVASRRPQALAROLDVFGQATAVVRSRLGSGVCDIKFSELSYL 259

QY 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303  
 DB 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303  
 RESULT 5  
 ID AAE38903 standard; protein; 318 AA.  
 XX  
 AC AAE38903;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human DED4 protein.  
 XX  
 KW Human, death domain; DD; death effector domain; DED; cell proliferation;  
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;  
 KW neural growth factor receptor-interacting death domain; cell adhesion;  
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;  
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;  
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;  
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;  
 KW keloid.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 12..112  
 FT Domain /note= "Death effector domain of DED-4"  
 FT Peptide /note= "Nuclear localisation sequence"  
 FT 53..74  
 XX  
 PN US2003049702-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 15-NOV-2001; 2001US-00001254.  
 XX  
 PR 17-NOV-2000; 2000US-00715893.  
 PR 17-NOV-2000; 2000US-0367360P.  
 PR 29-JUN-2001; 2001US-0301889P.  
 XX  
 XX (REED/) REED J C.  
 XX (GODZ/) GODZIK A.  
 XX (PAWL/) PAWLOWSKI K.  
 XX (FIOR/) FIORENTINO L.  
 XX (LEES/) LEE S H.  
 XX (ROTH/) ROTH W.  
 XX (STEN/) STENMER-LIEWEN F.  
 XX  
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
 PI Stenmer-Liëwen F;  
 XX  
 DR WPI; 2002-500222/53.  
 DR N-PSDB; AAD59062.  
 XX  
 PT New polypeptide comprising a death domain or death effector domain,  
 PT useful for discovery of drugs that suppress infection, inflammation,  
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
 XX  
 PS Claim 2; Page 44-45; 99p; English.  
 XX  
 CC The present invention provides novel death domain (DD) and death effector  
 CC domain (DED) proteins and nucleic acids encoding them. The invention also  
 CC provides death domain containing protein such as Chlamydia trachomatis  
 CC death domain containing protein (CTDD) DD and neural growth factor  
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for  
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED  
 CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate  
 CC binding agent and identifying an effective agent (e.g. protein or drug)  
 CC that modulates the association of a DD, DED or NB-ARC domain with protein  
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for

modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DBs, DEDs and NB-ARC domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. CC DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human DED4 CC protein. The DED4 gene is located on chromosome 19

XX Sequence 318 AA;

Query Match 73.9%; Score 224; DB 5; Length 318;  
Best Local Similarity 100.0%; Pred. No. 3.2e-193;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ESNRLIGQLRVARHDLPHLARKRRPVSPPRYSGTSSSKRTGSGRRROSS 139  
DB 80 ESNRLIGQLRVARHDLPHLARKRRPVSPPRYSGTSSSKRTGSGRRROSS 139  
QY 140 ANSOOGWETGSPPTKQORSRGRPSGARRRRGAPAPQOSEPARPSSEGVTCDIR 199  
DB 140 ANSOOGWETGSPPTKQORSRGRPSGARRRRGAPAPQOSEPARPSSEGVTCDIR 199  
QY 200 LRVAAEYCEHGPALGEGVARRRPPALARQDLVFGQATVLRSDLGSVCDIKFSELSYL 259  
DB 200 LRVAAEYCEHGPALGEGVARRRPPALARQDLVFGQATVLRSDLGSVCDIKFSELSYL 259  
QY 260 DAFMGDYLSGALLQALRGVFTLEALREAVGREAVRLVSVDEAD 303  
DB 260 DAFMGDYLSGALLQALRGVFTLEALREAVGREAVRLVSVDEAD 303

RESULT 6  
ABB07263  
ID ABB07263 standard; protein; 326 AA.

XX ABB07263;  
DT 26-MAR-2002 (first entry)  
DE Human apoptosis regulator (APRG) polypeptide (Incyte ID. 3102521CD1).  
XX APRG; apoptosis regulator; cytosolic; antiatherosclerotic; osteopathic;  
KW antiarteriosclerotic; hepatotropic; antipsoptic; antihelminthic; human;  
KW antiallergic; antianemic; antiaschemic; antihypertrophic; anti-HIV; cancer;  
KW antiinflammatory; antidiabetic; antipain; nephrotropic; ophthalmological;  
KW immunosuppressive; dermatological; antitumor; antirheumatic; fungicide;  
KW antitachytic; antibacterial; virucide; antiparasitic; protozoacide;  
KW tranquilizer; vulnerary; gynecological; vasotropic; gene therapy.

XX Homo sapiens.

OS WO200192527-A2.

PN 06-DEC-2001.

PD 30-MAY-2001; 2001WO-US017581.

PF 01-JUN-2000; 2000US-0209407P.

PR 30-NOV-2000; 2000US-0250326P.

XX (INCYTE GENOMICS INC.

PA Tang YT, Azimzai Y, Yue H, Burford N, Ding L, Elliott VS;

PI Paterson C, Baughn MR;

XX WPI; 2002-114350/15.  
DR N-PSDB; ABA94362.

XX Novel human apoptosis regulator polypeptides and polynucleotides for  
PT diagnosing, preventing, treating cell proliferative, immunological and  
PT reproductive disorders and for identifying modulators of therapeutic use.  
PS Claim 1; Page 97-98; 103pp; English.

The invention provides human apoptosis regulator (APRG) polypeptides and polynucleotides. The APRG polypeptides, polynucleotides and modulators are useful for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. The cell proliferative disorders include cancer, actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis, and immunological disorders include acquired immunodeficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, ankylosing spondylitis, amyloidosis, allergies, anemia, osteoporosis, autoimmune hemolytic anemia, asthma, autoimmune thyroiditis, Crohn's disease, contact dermatitis, diabetes mellitus, gout, Graves' disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, urethritis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma. Reproductive disorders include disorders of prolactin production, infertility, endometriosis, polycystic ovary syndrome, ectopic pregnancies, galactorrhea, abnormal sperm physiology, disruptions of spermatogenesis, cancer of testis and prostate, impotence, carcinoma of male breast and gynecomastia. The APRG polynucleotides are useful for creating knockin humanized animals or transgenic animals to model human disease and to detect and quantify gene expression in biopsied tissues in which expression of APRG is correlated with disease. APRG, fragments of it and antibodies specific for APRG are useful as elements on a microarray which is useful to monitor or measure protein-protein interactions, drug-target interactions and gene expression profiles. The present sequence represents a human APRG polypeptide

XX Sequence 326 AA;

Query Match 73.9%; Score 224; DB 5; Length 326;  
Best Local Similarity 100.0%; Pred. No. 3.3e-193;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ESNRLIGQLRVARHDLPHLARKRRPVSPPRYSGTSSSKRTGSGRRROSS 139  
DB 80 ESNRLIGQLRVARHDLPHLARKRRPVSPPRYSGTSSSKRTGSGRRROSS 139  
QY 140 ANSOOGWETGSPPTKQORSRGRPSGARRRRGAPAPQOSEPARPSSEGVTCDIR 199  
DB 140 ANSOOGWETGSPPTKQORSRGRPSGARRRRGAPAPQOSEPARPSSEGVTCDIR 199  
QY 200 LRVAAEYCEHGPALGEGVARRRPPALARQDLVFGQATVLRSDLGSVCDIKFSELSYL 259  
DB 200 LRVAAEYCEHGPALGEGVARRRPPALARQDLVFGQATVLRSDLGSVCDIKFSELSYL 259  
QY 260 DAFMGDYLSGALLQALRGVFTLEALREAVGREAVRLVSVDEAD 303  
DB 260 DAFMGDYLSGALLQALRGVFTLEALREAVGREAVRLVSVDEAD 303

XX Homo sapiens.

OS WO200192527-A2.

PN 06-DEC-2001.

PD 30-MAY-2001; 2001WO-US017581.

PF 01-JUN-2000; 2000US-0209407P.

PR 30-NOV-2000; 2000US-0250326P.

XX (INCYTE GENOMICS INC.

PA Tang YT, Azimzai Y, Yue H, Burford N, Ding L, Elliott VS;

PI Paterson C, Baughn MR;

XX WPI; 2002-114350/15.  
DR N-PSDB; ABA94362.

PN W02003054195-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 20-DEC-2002; 2002W0-JP013371.  
XX  
PR 20-DEC-2001; 2001JP-00387854.  
XX  
PR 18-JUL-2002; 2002JP-00209458.  
XX  
PA (MORG ) MORINAGA MILK IND CO LTD.  
XX  
PI Shizu S, Hageshita H, Nomaguchi K, Yamada M, Hayaasawa H;  
XX  
DR WPI; 2003-569246/53.  
XX  
DR N-PSDB; ADCT9259.  
PT DNA encoding cell death proteins for treatment of kidney, large intestine  
PT and prostate cancers and leukemia.  
PS  
PS Claim 1; Page 20-21; 26pp; Japanese.  
XX  
CC The present sequence represents a human death effector domains (DED)  
CC containing DNA-binding protein (DEDD) protein, designated DEDD2, that  
CC causes cell death. Also described: (1) primer and probe for investigation  
CC of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has  
CC cytoskeletal activity. DEDD2 can be used in the diagnosis and treatment of  
CC cancers of the kidney, large intestine and prostate, and acute and  
CC chronic myeloid leukemia.  
XX  
SQ Sequence 326 AA;  
Query Match 73.9%; Score 224; DB 7; Length 326;  
Best Local Similarity 100.0%; Pred. No. 3.3e-193;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 80 ESNRLRLGQLRLVLRARHDLPHLARKRRRPPVSPRYSGTSSSKRTGSCRRRROSSS 139  
DB 80 ESNRLRLGQLRLVLRARHDLPHLARKRRRPPVSPRYSGTSSSKRTGSCRRRROSSS 139  
QY 140 ANSQOGQWETGSPPTKQRORSRGRPSGARRRRRGAAPAPQOSEPARPSEKVTCDIR 199  
DB 140 ANSQOGQWETGSPPTKQRORSRGRPSGARRRRRGAAPAPQOSEPARPSEKVTCDIR 199  
QY 200 LRVRAEYCEHPALQEGVARRRPPQALARQLDVFQATAVLRSDLSGVCDIKFSELSYL 259  
DB 200 LRVRAEYCEHPALQEGVARRRPPQALARQLDVFQATAVLRSDLSGVCDIKFSELSYL 259  
QY 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303  
DB 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303  
RESULT 8  
AAG73852  
ID AAG73852 standard; protein; 366 AA.  
XX  
AC AAG73852;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen protein SEQ ID NO:4616.  
XX  
KM Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KM colorectal carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN W0200122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000W0-US026524.  
XX

PR 29-SEP-1999; 99US-0157137P.  
XX  
PR 03-NOV-1999; 99US-0163280P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
DR WPI; 2001-225357/24.  
XX  
DR N-PSDB; AAH33283.  
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
PT useful for preventing, diagnosing and/or treating colorectal cancers.  
XX  
PS  
PS Claim 11; Page 6413-6414; 9803pp; English.  
XX  
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patients own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922  
XX  
SQ Sequence 366 AA;  
Query Match 73.9%; Score 224; DB 4; Length 366;  
Best Local Similarity 100.0%; Pred. No. 3.7e-193;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 80 ESNRLRLGQLRLVLRARHDLPHLARKRRRPPVSPRYSGTSSSKRTGSCRRRROSSS 139  
DB 120 ESNRLRLGQLRLVLRARHDLPHLARKRRRPPVSPRYSGTSSSKRTGSCRRRROSSS 179  
QY 140 ANSQOGQWETGSPPTKQRORSRGRPSGARRRRRGAAPAPQOSEPARPSEKVTCDIR 199  
DB 140 ANSQOGQWETGSPPTKQRORSRGRPSGARRRRRGAAPAPQOSEPARPSEKVTCDIR 239  
QY 200 LRVRAEYCEHPALQEGVARRRPPQALARQLDVFQATAVLRSDLSGVCDIKFSELSYL 259  
DB 200 LRVRAEYCEHPALQEGVARRRPPQALARQLDVFQATAVLRSDLSGVCDIKFSELSYL 259  
QY 240 LRVRAEYCEHPALQEGVARRRPPQALARQLDVFQATAVLRSDLSGVCDIKFSELSYL 299  
DB 240 LRVRAEYCEHPALQEGVARRRPPQALARQLDVFQATAVLRSDLSGVCDIKFSELSYL 299  
RESULT 9  
AAB58420  
ID AAB58420 standard; protein; 319 AA.  
XX  
AC AAB58420;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Lung cancer associated polypeptide sequence SEQ ID 758.  
XX  
XX Human; lung cancer associated protein; neuroprotective; cytoskeletal;  
XX cardioactive; immunomodulatory; muscular active; vulnerability;  
XX gastrointestinal; nephroretropic; antifibrotic; gynecological;  
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
XX proliferative disorder; wound healing; infectious disease.  
XX



QY 230 DVEGQATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 289  
DB 146 DVEGQATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 205  
QY 290 REAVRLVSVDEAD 303  
DB 206 REAVRLVSVDEAD 219

RESULT 11  
ID ABB06038 standard; protein; 361 AA.  
AC ABB06038;  
XX  
XX 10-MAY-2002 (first entry)  
DE Human NS protein sequence SEQ ID NO:130.

Human; cytostatic; osteopathic; gynaecological; neuroprotective;  
KM antihemmatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;  
KM vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;  
KM anorectic; muscular; antinfertility; cardiovascular; anticoagulant;  
KM antifibrinolytic; hypotension; antiaschmatic; immunomodulator; cardiant;  
KM anticonvulsant; antidiabetic; tranquilliser; antidepressant; neuroleptic;  
KM gastrointestinal; virucide; anticancer; cerebroprotective; nootropic;  
KM contraceptive; vaccine; gene therapy; cancer; osteoporosis; dysomnia;  
KM endometriosis; degenerative disease; multiple sclerosis; psoriasis;  
KM rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;  
KM inflammation; skin disorder; obesity; muscular dystrophy; AIDS;  
KM infertility; cardiovascular disease; coagulation disease; hypertension;  
KM ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;  
KM diabetes; anxiety; depression; schizophrenia; viral disease; stroke;  
KM gastric ulcer; Alzheimer's disease.

OS Homo sapiens.  
PN MO200206315-A2.  
XX  
XX 24-JAN-2002.  
PD  
XX 17-JUL-2001; 2001WO-11000653.  
PF  
XX 18-JUL-2000; 2000IL-00137345.  
PR  
XX 15-DEC-2000; 2000IL-00140354.  
XX  
XX (COMP-) COMPUGEN LTD.  
PA  
XX Mintz L, Freilich S, Bernstein J;  
PI  
XX WPI; 2002-155037/20.  
DR  
XX N-PSDB; ABL39692.  
PS  
XX  
PT One hundred and twenty eight novel nucleic acid sequences, useful for  
treating and diagnosing e.g. cancer, asthma and Alzheimer's.  
XX  
XX Claim 6; Page 149-151; 290pp; English.

ABL39691 to ABL39818 represent novel human nucleic acid sequences  
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences  
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,  
CC antihemmatic, antiarthritic, antipsoriatic, ophthalmological, virucide,  
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,  
CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular, cardiant,  
CC anticoagulant, antifibrinolytic, hypotension, antiaschmatic, cardiant,  
CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, anticancer,  
CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,  
CC nootropic and contraceptive activities. The NS can be used in vaccines,  
CC gene therapy and antitense therapy. Nucleic acid, expression vectors and  
CC antibodies from the present invention can be used for treating and  
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative  
CC diseases, dysomnia, multiple sclerosis, rheumatoid arthritis, psoriasis,

CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,  
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular  
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune  
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,  
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,  
CC Alzheimer's disease and as a contraceptive  
XX  
XX Sequence 361 AA;  
SQ

Query Match 38.6%; Score 117; DB 5; Length 361;  
Best Local Similarity 100.0%; Pred. No. 1,1e-96;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 AAPAPQOSEPARPSSEGVTCIDIRVRAEYCEHGPALGQVARRPOLARQOLDVFGQ 234  
DB 202 AAPAPQOSEPARPSSEGVTCIDIRVRAEYCEHGPALGQVARRPOLARQOLDVFGQ 261

QY 235 ATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 291  
DB 262 ATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 318

RESULT 12  
ID ABB06039 standard; protein; 368 AA.  
AC ABB06039;  
XX  
XX 10-MAY-2002 (first entry)  
DE Human NS protein sequence SEQ ID NO:131.

Human; cytostatic; osteopathic; gynaecological; neuroprotective;  
KM antihemmatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;  
KM vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;  
KM anorectic; muscular; antinfertility; cardiovascular; anticoagulant;  
KM antifibrinolytic; hypotension; antiaschmatic; immunomodulator; cardiant;  
KM anticonvulsant; antidiabetic; tranquilliser; antidepressant; neuroleptic;  
KM gastrointestinal; virucide; anticancer; cerebroprotective; nootropic;  
KM contraceptive; vaccine; gene therapy; cancer; osteoporosis; dysomnia;  
KM endometriosis; degenerative disease; multiple sclerosis; psoriasis;  
KM rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;  
KM inflammation; skin disorder; obesity; muscular dystrophy; AIDS;  
KM infertility; cardiovascular disease; coagulation disease; hypertension;  
KM ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;  
KM diabetes; anxiety; depression; schizophrenia; viral disease; stroke;  
KM gastric ulcer; Alzheimer's disease.

OS Homo sapiens.  
PN MO200206315-A2.  
XX  
XX 24-JAN-2002.  
PD  
XX 17-JUL-2001; 2001WO-11000653.  
PF  
XX 18-JUL-2000; 2000IL-00137345.  
PR  
XX 15-DEC-2000; 2000IL-00140354.  
XX  
XX (COMP-) COMPUGEN LTD.  
PA  
XX Mintz L, Freilich S, Bernstein J;  
PI  
XX WPI; 2002-155037/20.  
DR  
XX N-PSDB; ABL39693.  
PS  
XX  
PT One hundred and twenty eight novel nucleic acid sequences, useful for  
treating and diagnosing e.g. cancer, asthma and Alzheimer's.  
XX  
XX Claim 6; Page 151-152; 290pp; English.

ABL39691 to ABL39818 represent novel human nucleic acid sequences  
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences

CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,  
CC antineumatic, antiarthritic, antiparatic, ophthalmological, vitucide,  
CC vasorectic, antiaeriosclerotic, antinflammatory, dermatological,  
CC anorectic, muscular, anti-HIV, antifertility, cardiovascular.  
CC antioestrogenic, anticonvulsant, hypotension, transthematic, cardiant,  
CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antituber,  
CC antidepressant, gastroenteric, neuroleptic, cerebroprotective,  
CC neurotic and contraceptive activities. The NS can be used in vaccines,  
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and  
CC antipodides from the present invention can be used for treating and  
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative  
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,  
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,  
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular  
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune  
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,  
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,  
CC Alzheimer's disease and as a contraceptive

CC  
XX  
SQ Sequence 368 AA;

Query Match 38.6%; Score 117; DB 5; Length 368;  
Best Local Similarity 100.0%; Pred. No. 1.1e-96;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APAPOQSQSPAPSPSGKVTCDRLRVRAVCEHGPALREGVYASRRPOLARQDVFQ 234  
DB 209 APAPOQSQSPAPSPSGKVTCDRLRVRAVCEHGPALREGVYASRRPOLARQDVFQ 268

QY 235 ATAVLRGRDLSVVCIDIKFSELSYLDAPMGDYLSGALLQALRGVFLTEALREAVGRE 291  
DB 269 ATAVLRGRDLSVVCIDIKFSELSYLDAPMGDYLSGALLQALRGVFLTEALREAVGRE 325

#### RESULT 13

AAE24855 ID AAE24855 standard; protein; 101 AA.

XX AAE24855;

DT 22-OCT-2002 (first entry)

DE Human DED4 DED (death effector domain) protein.

KM Human; death domain; DD; death effector domain; DED; Chlamydia infection;  
KM NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;  
KM inflammation; allergy; autoimmunity; allograft rejection; cell division;  
KM immune-based pathology; fibrosis; arthritis; graft versus host disease;  
KM immunosuppressive; gene therapy; antisense therapy.

OS Homo sapiens.

XX WO200240680-A2.

PN 23-MAY-2002.

PD 15-NOV-2001; 2001MO-US044844.

XX 17-NOV-2000; 2000US-00715893.

PR 29-JUN-2001; 2001US-0301889P.

XX (BURN-) BURHAM INST.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

DR N-PSDB; AAD40075.

XX WPI; 2002-500222/53.

PT New polypeptide comprising a death domain or death effector domain,  
XX useful for discovery of drugs that suppress infection, inflammation,  
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 1; Page 175; 2099P; English.

XX The invention relates to an isolated polypeptide comprising a death  
CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention  
CC is useful for identifying a binding agent, preferably a protein or a drug  
CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC  
CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or  
CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and  
CC detecting the association of the domain and the candidate binding agent,  
CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or  
CC chemical crosslinking, nuclear magnetic resonance (NMR), mass  
CC spectroscopy (MS) and FPA. The invention is useful for modulating the  
CC level of a cell process such as cell proliferation, cell adhesion, cell  
CC stress responses, responses to microbial infection and B cell  
CC immunoglobulin class switching, in particular apoptosis within a cell.  
CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.  
CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the  
CC CTDD DD protein is useful for detecting a Chlamydia infection. The  
CC invention is useful for modulating the activity of oncogenic proteins,  
CC for treating a pathology caused by the oncogenic proteins and for  
CC treating bacterial infections by modulating the activity of bacterial  
CC proteins. The protein and antibody specific for it are useful for  
CC discovery of drugs that suppress infection, inflammation, allergy,  
CC sepsis, autoimmunity, allograft rejection and other diseases. The protein  
CC is useful for treating immune-based pathologies, pathologies associated  
CC with cell division, inflammatory diseases such as sepsis, fibrosis,  
CC arthritis, graft versus host disease. The invention is used in antisense  
CC therapy and gene therapy. The present sequence is human DED4 DED protein  
XX

SQ Sequence 101 AA;

Query Match 22.1%; Score 67; DB 5; Length 101;  
Best Local Similarity 100.0%; Pred. No. 4.3e-52;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 WEDECDIDYGMSTLRMPFVVGQUTRECELELAPLDEAPAGGLARAGLEELLE 71  
DB 1 WEDECDIDYGMSTLRMPFVVGQUTRECELELAPLDEAPAGGLARAGLEELLE 60

QY 72 LERRGQC 78  
DB 61 LERRGQC 67

#### RESULT 14

AAE38898 ID AAE38898 standard; protein; 101 AA.

XX AAE38898;

DT 18-DEC-2003 (first entry)

DE Human DED4 DED protein.

KM Human; death domain; DD; death effector domain; DED; cell proliferation;  
KM Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;  
KM neural growth factor receptor-interacting death domain; cell adhesion;  
KM vasotrophic; microbial infection; inflammation; allograft rejection; CTDD;  
KM cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;  
KM apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;  
KM neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;  
KM ketoid.

OS Homo sapiens.

XX US2003049702-A1.

PN 13-MAR-2003.

PD 15-NOV-2001; 2001US-00001254.

XX 17-NOV-2000; 2000US-00715893.

PR 17-NOV-2000; 2000US-0367360P.



PR 29-JUN-2001; 2001US-0301889P.  
XX (REED/) REED J C.  
XX (GODZ/) GODZIK A.  
PA (PAMI/) PAWLOWSKI K.  
PA (FIOR/) FIORENTINO L.  
PA (LEES/) LEE S H.  
PA (ROTH/) ROTH W.  
XX (STEN/) STENNER-LIEWEN F.  
XX  
PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
PI Stenner-Liwen F;  
XX  
DR WPI; 2002-500222/53.  
DR N-PSDB; AAD59057.  
XX  
XX  
PT New polypeptide comprising a death domain or death effector domain,  
PT useful for discovery of drugs that suppress infection, inflammation,  
PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
XX  
XX  
PS Claim 1; Page 35; 99p; English.  
XX  
XX The present invention provides novel death domain (DD) and death effector  
XX domain (DED) proteins and nucleic acids encoding them. The invention also  
XX provides death domain containing protein such as Chlamydia trachomatis  
XX death domain containing protein (CTDD) DD and neural growth factor  
XX receptor-interacting death domain (NIDD) DD. The invention is useful for  
XX identifying a binding agent (e.g. protein or drug) that binds a DD, DED  
XX or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate  
XX binding agent and identifying an effective agent (e.g. protein or drug)  
XX that modulates the association of a DD, DED or NB-ARC domain with protein  
XX that binds the DD, DED or NB-ARC domain. The invention is also useful for  
XX modulating the level of cell process such as apoptosis, cell adhesion,  
XX cell proliferation, cell stress responses, responses to microbial  
XX infection and B cell immunoglobulin class switching. DEDs, DEDs and NB-ARC  
XX domains and/or anti-DD, anti-DD or anti-NB-ARC domain antibodies are  
XX useful for discovery of drugs that suppress infection, autoimmunity,  
XX inflammation, allergy, allograft rejection, sepsis and other diseases.  
XX DD, DED or NB-ARC domain proteins are used to treat infection, allergy,  
XX autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte  
XX hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,  
XX inflammatory hyperplasia and smooth muscle cell proliferation in arterios  
XX following balloon angioplasty (restenosis). The invention is also used in  
XX antibody therapy and gene therapy. The present sequence is human DED4 DD  
XX protein. The DED4 gene is located on chromosome 1  
XX  
SQ Sequence 101 AA;  
Query Match 22.1%; Score 67; DB 5; Length 101;  
Best Local Similarity 100.0%; Pred. No. 4.3e-52;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 12 WEDECDLDYVGMGLSRMFVVGQGLTECELELLAFLLDPAAGAGLARRSGLELLLE 71  
DB 1 WEDECDLDYVGMGLSRMFVVGQGLTECELELLAFLLDPAAGAGLARRSGLELLLE 60  
QY 72 LERRGQC 78  
DB 61 LERRGQC 67  
RESULT 15  
ID AAM41591  
ID AAM41591 standard; protein; 217 AA.  
XX  
XX AAM41591;  
AC  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 6522.  
XX  
XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
XX Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
XX  
XX  
XX 26-JUL-2001.  
XX  
XX  
XX 26-DEC-2000; 2000WO-US034263.  
XX  
XX  
XX 23-DEC-1999; 99US-00471275.  
XX  
XX 21-JAN-2000; 2000US-00488725.  
XX  
XX 25-APR-2000; 2000US-00552317.  
XX  
XX 20-JUN-2000; 2000US-00598042.  
XX  
XX 19-JUL-2000; 2000US-00620312.  
XX  
XX 03-AUG-2000; 2000US-00653450.  
XX  
XX 14-SEP-2000; 2000US-00662191.  
XX  
XX 19-OCT-2000; 2000US-00693036.  
XX  
XX 29-NOV-2000; 2000US-00727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
XX Zhou P, Goodrich R, Drmanac RT;  
XX  
XX WPI; 2001-442253/47.  
XX  
XX N-PSDB; AA160747.  
XX  
XX Novel nucleic acids and polypeptides, useful for treating disorders such  
XX as central nervous system injuries.  
XX  
XX  
XX Example 2; SEQ ID NO 6522; 10078p; English.  
XX  
XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
XX encoded polypeptides (AAM38642-AAM42213) with noctropic,  
XX immunosuppressant and cyostatic activity. The polynucleotides are useful  
XX in gene therapy. A composition containing a polypeptide or polynucleotide  
XX of the invention may be used to treat diseases of the peripheral nervous  
XX system, such as peripheral nervous injuries, peripheral neuropathy and  
XX localised neuropathies and central nervous system diseases, such as  
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
XX utilisation of the activities such as: Immune system suppression,  
XX activation/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
XX assays for receptor activity, arthritis and inflammation, leukaemia and  
XX C.N.S disorders. Note: The sequence data for this patent did not form  
XX part of the printed specification  
XX  
SQ Sequence 217 AA;  
Query Match 21.8%; Score 66; DB 4; Length 217;  
Best Local Similarity 100.0%; Pred. No. 6.7e-51;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 80 ESNRLIGQLLVLAHDLPLHARRRPVPERVYGTSSSKRTGSCRRRSSSS 139  
DB 109 ESNRLIGQLLVLAHDLPLHARRRPVPERVYGTSSSKRTGSCRRRSSSS 168  
QY 140 ANSQQC 145  
DB 169 ANSQQC 174  
Search completed: February 12, 2005, 16:37:45  
Job time : 125 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: February 12, 2005, 15:25:44 ; Search time 74 Seconds  
(without alignments)  
1583.627 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 1550  
Sequence: 1 MALSGSTAPPCWEDECDLY.....LREAVGRAVLLVSVDEAD 303

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 366760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1550	100.0	303	4 AAB60386	Aab60386 Human apo
2	1550	100.0	326	4 AAB60387	Aab60387 Human apo
3	1543	99.5	318	5 AAE24860	Aae24860 Human DED
4	1543	99.5	318	5 AAE38903	Aae38903 Human DED
5	1543	99.5	326	5 ABB07263	Abb07263 Human apo
6	1543	99.5	326	7 ADC79260	Adc79260 Human DED
7	1543	99.5	366	4 AAG73852	Aag73852 Human DED
8	1413	91.2	304	4 AAB15551	Aab15551 Apoptosis
9	1404	90.6	319	3 AAB58420	Aab58420 Lung canc
10	1090.5	70.4	361	5 ABB06038	Abb06038 Human NS
11	1090.5	70.4	368	5 ABB06039	Abb06039 Human NS
12	987	63.7	242	4 AAM25705	Aam25705 Human pro
13	950.5	61.3	277	4 AAM39805	Aam39805 Human pro
14	854	55.1	217	4 AAM41591	Aam41591 Human pro
15	622.5	40.2	318	4 AAB94040	Aab94040 Human pro
16	614.5	39.6	318	2 AAW91022	Aaw91022 Human FLA
17	614.5	39.6	318	3 AAE26087	Aae26087 Human FLA
18	614.5	39.6	318	5 AAB93016	Aab93016 Human pro
19	613.5	39.6	318	2 AAW90109	Aaw90109 Mouse FLA
20	608.5	39.3	318	2 AAY51023	Aay51023 Murine DE
21	608.5	39.3	318	5 AAE26088	Aae26088 Mouse FLA
22	514	33.2	101	5 AAE38898	Aae38898 Human DED
23	514	33.2	101	5 AAE38898	Aae38898 Human DED
24	514	33.2	101	5 AAE38898	Aae38898 Human DED
25	136	8.8	340	3 AAY84360	Aay84360 Amino aci

26	136	8.8	397	8 ADP24485	Adp24485 PRO poly
27	135.5	8.7	398	7 ABO72356	Ab072356 Pseudomon
28	124	8.0	289	7 ABO77445	Ab077445 Pseudomon
29	124	8.0	599	7 ABO68504	Ab068504 Pseudomon
30	123.5	8.0	404	7 ABO84268	Ab084268 Pseudomon
31	122	7.9	450	7 ABO83695	Ab083695 Pseudomon
32	121.5	7.8	182	7 ABO84091	Ab084091 Pseudomon
33	120	7.7	165	7 ABO73027	Ab073027 Pseudomon
34	119.5	7.7	1041	7 ABO76891	Ab076891 Pseudomon
35	119	7.7	891	7 ABO81878	Ab081878 Pseudomon
36	119	7.7	1938	6 ABE76679	Abp76679 Streptomy
37	117.5	7.6	334	7 ABO78408	Ab078408 Pseudomon
38	117.5	7.6	372	7 ABO74480	Ab074480 Pseudomon
39	117	7.5	549	7 ABO69003	Ab069003 Pseudomon
40	117	7.5	589	7 ABO73107	Ab073107 Pseudomon
41	116.5	7.5	407	7 ABO71933	Ab071933 Pseudomon
42	116.5	7.5	557	7 ABO79337	Ab079337 Pseudomon
43	116	7.5	735	7 ABO83426	Ab083426 Pseudomon
44	115.5	7.5	574	7 ABO70112	Ab070112 Pseudomon
45	115.5	7.5	582	7 ABO77436	Ab077436 Pseudomon

## ALIGNMENTS

RESULT 1	
AAB60386	
ID	AAB60386 standard; protein; 303 AA.
XX	
AC	AAB60386;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Human apoptosis-associated factor NT2RM1000558 (portion), SEQ ID NO:2.
XX	
KM	Human; apoptosis-associated factor; NT2RM1000558; death effector domain;
XX	DED; caspase family cleavage domain; pro-apoptotic; drug screening;
KM	cell proliferation; ischaemic disease; chronic viral disease.
XX	
OS	Homo sapiens.
XX	
PN	WO200104300-A1.
XX	
PD	18-JAN-2001.
XX	
PF	06-JUL-2000; 2000WO-JP004516.
XX	
PR	08-JUL-1999; 99JP-00194179.
XX	
PA	18-OCT-1999; 99US-0159586P.
XX	
FI	(HELI-) HELIX RES INST.
XX	
DR	Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
XX	WPI; 2001-138348/14.
PT	N-PSDB; AAF27407.
XX	
PT	Polynucleotide encoding an apoptosis-associated factor protein with death
XX	effector domain and caspase family-cleavage domain, useful in regulating
PT	diseases with cell proliferation.
XX	
PS	Claim 1; Page 43-44; 53pp; Japanese.
XX	
CC	The invention relates to a novel human apoptosis-associated factor
CC	(AAB60386, AAB60387), designated NT2RM1000558, which contains a death
CC	effector domain (DED) and a caspase family cleavage domain and is capable
CC	of inducing apoptosis in cells. The invention also relates to nucleic
CC	acids encoding the protein (AAF27407, AAF27408); variants of the protein
CC	(particularly dominant negative variants); vectors and host cells
CC	comprising a nucleic acid which encodes an apoptosis-associated factor
CC	of the invention; the recombinant production of the protein; an antibody
CC	against the protein; and methods of screening for compounds which can
CC	regulate apoptosis. The apoptosis-related factor is useful in regulating

CC diseases associated with cell proliferation and in screening drug  
 CC candidates e.g., for regulating cell proliferation or cell death in  
 CC ischemic diseases and chronic viral diseases. The present sequence  
 CC represents a substantial proportion of the human apoptosis-associated  
 CC factor NT2RM1000558  
 CC  
 XX

Sequence 303 AA;

Query Match 100.0%; Score 1550; DB 4; Length 303;

Best Local Similarity 100.0%; Pred. No. 1e-144; Indels 0; Gaps 0;

Matches 303; Conservative 0; Mismatches 0;

QY 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQUTCELELAFLLDEAPGAGGLA 60

DB 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQUTCELELAFLLDEAPGAGGLA 60

QY 61 PARSGLELLELERRGCGESNRLQQLRLVLAHDLPHLAKRRRPPVSPERYSGTS 120

DB 61 PARSGLELLELERRGCGESNRLQQLRLVLAHDLPHLAKRRRPPVSPERYSGTS 120

QY 121 SSSKRTGSCRRRQSSSSANSOQOMETGSPPTKQRRSGRSGARRRRGAPAPQ 180

DB 121 SSSKRTGSCRRRQSSSSANSOQOMETGSPPTKQRRSGRSGARRRRGAPAPQ 180

QY 181 QOSEPARPSSEKVTCDIRLVRAYCEHGPALLEGVARRPQALAROLDVFGQATAVLR 240

DB 181 QOSEPARPSSEKVTCDIRLVRAYCEHGPALLEGVARRPQALAROLDVFGQATAVLR 240

QY 241 SRDLGSVVCIDIKFSELSYLDLFWGDIYSGLLQALRGVFLTEALREAVGREAVRLVSV 300

DB 241 SRDLGSVVCIDIKFSELSYLDLFWGDIYSGLLQALRGVFLTEALREAVGREAVRLVSV 300

QY 301 EAD 303

DB 301 EAD 303

RESULT 2

AAB60387

ID AAB60387 standard; protein; 326 AA.

AC AAB60387;

DT 24-APR-2001 (first entry)

DE Human apoptosis-associated factor NT2RM1000558, SEQ ID NO.4.

XX Human; apoptosis-associated factor; NT2RM1000558; death effector domain;

KW DED; caspase family cleavage domain; pro-apoptotic; drug screening;

KW cell proliferation; ischemic disease; chronic viral disease.

XX Homo sapiens.

OS Homo sapiens.

XX WO200104300-A1.

PD 18-JAN-2001.

XX 06-JUL-2000; 2000WO-JP004516.

PF 08-JUL-1999; 99JP-00194179.

PR 18-OCT-1999; 99US-0159586P.

XX (HELI-) HELIX RES INST.

XX Oca T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;

XX WPI, 2001-138348/14.

DR N-PSDB; AAF27408.

XX Polynucleotide encoding an apoptosis-associated factor protein with death

PT effector domain and caspase family-cleavage domain, useful in regulating

PT diseases with cell proliferation.

PS Claim 3; Page 47-48; 53pp; Japanese.

XX The invention relates to a novel human apoptosis-associated factor

CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death

CC effector domain (DED) and a caspase family cleavage domain and is capable

CC of inducing apoptosis in cells. The invention also relates to nucleic

CC acids encoding the protein (AAF27407, AAF27408); variants of the protein

CC (particularly dominant negative variants); vectors and host cells

CC comprising a nucleic acid which encodes an apoptosis-associated factor

CC of the invention; the recombinant production of the protein; an antibody

CC against the protein; and methods of screening for compounds which can

CC regulate apoptosis. The apoptosis-related factor is useful in regulating

CC diseases associated with cell proliferation and in screening drug

CC candidates e.g., for regulating cell proliferation or cell death in

CC ischemic diseases and chronic viral diseases. The present sequence

CC represents the human apoptosis-associated factor NT2RM1000558

XX

Sequence 326 AA;

Query Match 100.0%; Score 1550; DB 4; Length 326;

Best Local Similarity 100.0%; Pred. No. 1.1e-144; Indels 0; Gaps 0;

Matches 303; Conservative 0; Mismatches 0;

QY 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQUTCELELAFLLDEAPGAGGLA 60

DB 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQUTCELELAFLLDEAPGAGGLA 60

QY 61 PARSGLELLELERRGCGESNRLQQLRLVLAHDLPHLAKRRRPPVSPERYSGTS 120

DB 61 PARSGLELLELERRGCGESNRLQQLRLVLAHDLPHLAKRRRPPVSPERYSGTS 120

QY 121 SSSKRTGSCRRRQSSSSANSOQOMETGSPPTKQRRSGRSGARRRRGAPAPQ 180

DB 121 SSSKRTGSCRRRQSSSSANSOQOMETGSPPTKQRRSGRSGARRRRGAPAPQ 180

QY 181 QOSEPARPSSEKVTCDIRLVRAYCEHGPALLEGVARRPQALAROLDVFGQATAVLR 240

DB 181 QOSEPARPSSEKVTCDIRLVRAYCEHGPALLEGVARRPQALAROLDVFGQATAVLR 240

QY 241 SRDLGSVVCIDIKFSELSYLDLFWGDIYSGLLQALRGVFLTEALREAVGREAVRLVSV 300

DB 241 SRDLGSVVCIDIKFSELSYLDLFWGDIYSGLLQALRGVFLTEALREAVGREAVRLVSV 300

QY 301 EAD 303

DB 301 EAD 303

RESULT 3

AAE24860

ID AAE24860 standard; protein; 318 AA.

AC AAE24860;

DT 22-OCT-2002 (first entry)

DE Human DED4 (death effector domain) protein.

XX Human; death domain; DD; death effector domain; DED; Chlamydia infection;

KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;

KW inflammation; allergy; autoimmunity; allograft rejection; cell division;

KW immune-based pathology; fibrosis; arthritis; graft versus host disease;

KW immunosuppressive; gene therapy; anticense therapy.

XX Homo sapiens.

OS Homo sapiens.

XX Key

XX Region

XX Location/Qualifiers

XX 53..74

XX /note= "Nuclear localisation sequence"

XX WO200240680-A2.

XX 23-MAY-2002.

XX 15-NOV-2001; 2001WO-US044844.  
 XX PF 17-NOV-2000; 2000US-00715893.  
 XX PR 29-JUN-2001; 2001US-0301889P.  
 XX (BURN-) BURNHAM INST.  
 XX PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
 XX PI Stenner-Liewen F;  
 XX DR WPI; 2002-500222/53.  
 XX DR N-PSDB; AAD40080.  
 XX  
 PT New polypeptide comprising a death domain or death effector domain,  
 PT useful for discovery of drugs that suppress infection, inflammation,  
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.  
 XX  
 PS Claim 3; Page 186-187; 209pp; English.

The invention relates to an isolated polypeptide comprising a death domain (DD), death effector domain (DED) or NB-ARC domain. The invention is useful for identifying a binding agent, preferably a protein or a drug that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or NIDD (NGFR-interacting Death Domain), with a candidate binding agent and detecting the association of the domain and the candidate binding agent, by yeast two hybrid assay, immunoprecipitation, SPR, ultraviolet (UV) or chemical crosslinking, nuclear magnetic resonance (NMR), mass spectroscopy (MS) and FPA. The invention is useful for modulating the level of a cell process such as cell proliferation, cell adhesion, cell stress responses, responses to microbial infection, cell apoptosis, cell immunoglobulin class switching, in particular apoptosis within a cell. Antibody specifically reactive with CTDD DD of C. trachomatis, C. muridarum, C. pneumoniae, and C. peitraci or a nucleic acid encoding the CTDD DD protein is useful for detecting a Chlamydia infection. The invention is useful for modulating the activity of oncogenic proteins, for treating a pathology caused by the oncogenic proteins and for treating bacterial infections by modulating the activity of bacterial proteins. The protein and antibody specific for it are useful for discovery of drugs that suppress infection, inflammation, allergy, sepsis, autoimmunity, allograft rejection and other diseases. The protein is useful for treating immune-based pathologies, pathologies associated with cell division, inflammatory diseases such as sepsis, fibrosis, arthritis, graft versus host disease. The invention is used in antisense therapy and gene therapy. The present sequence is human DED4 protein

Sequence 318 AA;

Query Match 99.5%; Score 1543; DB 5; Length 318;  
 Best Local Similarity 99.7%; Pred. No. 5-5e-144;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTAPPCWBEBCLDYGMLSLHNFVVGQLTCELELLAFLIDEAPGAAGGLA 60  
 DB 1 MALSGSTAPPCWBEBCLDYGMLSLHNFVVGQLTCELELLAFLIDEAPGAAGGLA 60  
 QY 61 PARSGLELLEERRGGCGESNLRLGQLRLTAHHDLPHARRRRPVSERRSYGTS 120  
 DB 61 PARSGLELLEERRGGCGESNLRLGQLRLTAHHDLPHARRRRPVSERRSYGTS 120  
 QY 121 SSSKRTGSSCRRRRQSSSSANSQCGWETGSPPTKRQRRSRPGSGARRRRRGAAPAPQ 180  
 DB 121 SSSKRTGSSCRRRRQSSSSANSQCGWETGSPPTKRQRRSRPGSGARRRRRGAAPAPQ 180  
 QY 181 QOSEPARSSBGGKTCIDRLRVRAYCEHGPALGEGVASRRPQALARQLDVGQATAVLR 240  
 DB 181 QOSEPARSSBGGKTCIDRLRVRAYCEHGPALGEGVASRRPQALARQLDVGQATAVLR 240  
 QY 241 SRDLGSVVCIDIKFSELSYLDFAWGDYLSGALLQALRGVFTALAEAVGREAVRLVVD 300  
 DB 241 SRDLGSVVCIDIKFSELSYLDFAWGDYLSGALLQALRGVFTALAEAVGREAVRLVVD 300

QY 301 EAD 303  
 DB 301 EAD 303

RESULT 4  
 ID AAE38903  
 AA AAE38903 standard; protein; 318 AA.

AA AAE38903;

18-DEC-2003 (first entry)

Human DED4 protein.

Human; death Domain; DD; death effector domain; DED; cell proliferation;  
 Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;  
 neural growth factor receptor-interacting protein; cell adhesion;  
 vasotropic; microbial infection; inflammation; allograft rejection; CTDD;  
 cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;  
 apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;  
 neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;  
 keloid.

Homo sapiens.

Key Location/Qualifiers

Domain 12..112

Peptide /note= "Death effector domain of DED-4"

53..74

/note= "Nuclear localisation sequence"

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

(REED/) REED J C.

(GODZ/) GODZIK A.

(PAWL/) PAWLOWSKI K.

(FIOR/) FIORENTINO L.

(LEES/) LEE S H.

(ROTH/) ROTH W.

(STEN/) STENNER-LIEWEN F.

Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;  
 Stenner-Liewen F;

WPI; 2002-500222/53.

N-PSDB; AAD59062.

New polypeptide comprising a death domain or death effector domain,  
 useful for discovery of drugs that suppress infection, inflammation,  
 allergy, sepsis, autoimmunity, allograft rejection and other diseases.

Claim 2; Page 44-45; 99pp; English.

The present invention provides novel death Domain (DD) and death effector domain (DED) proteins and nucleic acids encoding them. The invention also provides death domain containing protein such as Chlamydia trachomatis death domain containing protein (CTDD) DD and neural growth factor receptor-interacting death domain (NIDD) DD. The invention is useful for identifying a binding agent (e.g. protein or drug) that binds a DD, DED or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate binding agent and identifying an effective agent (e.g. protein or drug) that modulates the association of a DD, DED or NB-ARC domain with protein that binds the DD, DED or NB-ARC domain. The invention is also useful for modulating the level of cell process such as apoptosis, cell adhesion,

cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. Dbs, Deds and NB-ARC domains and/or anti-DB, anti-DED or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human DED4 protein. The DED4 gene is located on chromosome 19

Sequence 318 AA;

Query Match 99.5%; Score 1543; DB 5; Length 318;  
Best Local Similarity 99.7%; Pred. No. 5,5e-144;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGLA 60  
DB 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGLA 60  
QY 61 PARSGLELLELERRGQCGESNLRLLGQLRLAARDLLPHLARKRRPVSPERSYSGTS 120  
DB 61 PARSGLELLELERRGQCGESNLRLLGQLRLAARDLLPHLARKRRPVSPERSYSGTS 120  
QY 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKRRSRGSPSGARRRRRGAAPAPQ 180  
DB 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKRRSRGSPSGARRRRRGAAPAPQ 180  
QY 181 QOSEPARPSSSEKVTCDIRLRVAEYCEHGPALGCVASRRPQALARQIDVFQATAYLR 240  
DB 181 QOSEPARPSSSEKVTCDIRLRVAEYCEHGPALGCVASRRPQALARQIDVFQATAYLR 240  
QY 241 SSDLGSVVDIKFSELSYLDAPFWGDLGALLQALRGVFLTEALRAVGEAVRLVSYD 300  
DB 241 SSDLGSVVDIKFSELSYLDAPFWGDLGALLQALRGVFLTEALRAVGEAVRLVSYD 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 5  
ABR07263  
ID ABR07263 standard; protein; 326 AA.

AC ABR07263;  
XX  
XX  
DT 26-MAR-2002 (first entry)  
DE Human apoptosis regulator (APRG) polypeptide (Incyte ID. 3102521CD1).  
XX  
XX APRG; apoptosis regulator; cytosolic; antiatherosclerotic; osteopathic;  
XX antiarteriosclerotic; hepatotropic; antiposrotatic; antelimitic; human;  
XX anti-allergic; antianemic; antiaesthetic; antithyroid; anti-HIV; cancer;  
XX anti-inflammatory; antidiabetic; antignout; nephrotropic; ophthalmological;  
XX immunosuppressive; dermatological; anticancer; antirheumatic; fungicide;  
XX antitubercic; antibacterial; virucide; antiparasitic; procoagulate;  
XX tranquilizer; vulnerary; gynecological; vasotrophic; gene therapy.

OS Homo sapiens.  
XX  
XX WO200192527-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 30-MAY-2001; 2001WO-US017581.  
XX  
XX 01-JUN-2000; 2000US-0209407P.  
XX  
XX 30-NOV-2000; 2000US-0250326P.

PA (INCY-) INCYTE GENOMICS INC.

XX Tang YT, Azimzai Y, Yue H, Burford N, Ding L, Elliott VS;  
PI Paterson C, Baughn MR;  
XX WPI; 2002-114350/15.  
DR N-PSDB; ABA94362.

XX Novel human apoptosis regulator polypeptides and polynucleotides for  
PT diagnosing, preventing, treating cell proliferative, immunological and  
PT reproductive disorders and for identifying modulators of therapeutic use.  
XX  
XX Claim 1; Page 97-98; 103pb; English.

XX The invention provides human apoptosis regulator (APRG) polypeptides and  
XX polynucleotides. The APRG polypeptides, polynucleotides and modulators  
XX are useful for diagnosis, treatment and prevention of cell proliferative,  
XX immunological and reproductive disorders. The cell proliferative  
XX disorders include cancers, actinic keratosis, arteriosclerosis,  
XX atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis, and  
XX immunological disorders include acquired immunodeficiency syndrome  
XX (AIDS), adult respiratory distress syndrome, Addison's disease,  
XX ankylosing spondylitis, amyloidosis, allergies, anemia, osteoporosis,  
XX autoimmune hemolytic anemia, asthma, autoimmune thyroiditis, Crohn's  
XX disease, contact dermatitis, diabetes mellitus, gout, Graves' disease,  
XX glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus  
XX erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis,  
XX urethritis, viral, bacterial, fungal, parasitic, protozoal, helminthic  
XX infections and trauma. Reproductive disorders include disorders of  
XX prolactin production, infertility, endometriosis, polycystic ovary  
XX syndrome, ectopic pregnancies, galactorrhea, abnormal sperm physiology,  
XX disruptions of spermatogenesis, cancer of testis and prostate, impotence,  
XX carcinoma of male breast and gynecomastia. The APRG polynucleotides are  
XX useful for creating knockin humanized animals or transgenic animals to  
XX model human disease and to detect and quantify gene expression in  
XX biopsied tissues in which expression of APRG is correlated with disease.  
XX APRG fragments of it and antibodies specific for APRG are useful as  
XX elements on a microarray which is useful to monitor or measure protein-  
XX protein interactions, drug-target interactions and gene expression  
XX profiles. The present sequence represents a human APRG polypeptide

Sequence 326 AA;

Query Match 99.5%; Score 1543; DB 5; Length 326;  
Best Local Similarity 99.7%; Pred. No. 5,7e-144;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGLA 60  
DB 1 MALSGSTPAPCWEDECDYDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGLA 60  
QY 61 PARSGLELLELERRGQCGESNLRLLGQLRLAARDLLPHLARKRRPVSPERSYSGTS 120  
DB 61 PARSGLELLELERRGQCGESNLRLLGQLRLAARDLLPHLARKRRPVSPERSYSGTS 120  
QY 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKRRSRGSPSGARRRRRGAAPAPQ 180  
DB 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKRRSRGSPSGARRRRRGAAPAPQ 180  
QY 181 QOSEPARPSSSEKVTCDIRLRVAEYCEHGPALGCVASRRPQALARQIDVFQATAYLR 240  
DB 181 QOSEPARPSSSEKVTCDIRLRVAEYCEHGPALGCVASRRPQALARQIDVFQATAYLR 240  
QY 241 SSDLGSVVDIKFSELSYLDAPFWGDLGALLQALRGVFLTEALRAVGEAVRLVSYD 300  
DB 241 SSDLGSVVDIKFSELSYLDAPFWGDLGALLQALRGVFLTEALRAVGEAVRLVSYD 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 6

ADC79260  
ID ADC79260 standard; protein; 326 AA.  
XX  
AC ADC79260;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human DEDD2 protein SEQ ID NO:2.  
XX  
KW human; death effector domains containing DNA-binding protein;  
KM DED-containing DNA-binding protein; DEDD2; cell death; gene therapy;  
XX cytostatic; cancer; chronic myeloid leukaemia.  
OS Homo sapiens.  
XX  
PN WO2003054195-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 20-DEC-2002; 2002WO-JP013371.  
XX  
PR 20-DEC-2001; 2001JP-00387854.  
XX 18-JUL-2002; 2002JP-00209458.  
XX  
PA (MORG ) MORINAGA MILK IND CO LTD.  
XX  
PI Suzu S, Hageshita H, Nomaguchi K, Yamada M, Hayasawa H;  
XX  
DR WPI; 2003-569246/53.  
XX N-PSDB; ADC79259.  
XX  
PT DNA encoding cell death proteins for treatment of kidney, large intestine  
XX and prostate cancers and leukemia.  
XX  
PS Claim 1; Page 20-21; 26pp; Japanese.  
XX  
CC The present sequence represents a human death effector domains (DED)  
CC containing DNA-binding protein (DEDD) protein, designated DEDD2, that  
CC causes cell death. Also described: (1) primer and probe for investigation  
CC of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has  
CC cytostatic activity. DEDD2 can be used in the diagnosis and treatment of  
CC cancers of the kidney, large intestine and prostate, and acute and  
CC chronic myeloid leukaemia.  
XX  
SQ Sequence 326 AA;  
Query Match 99.5%; Score 1543; DB 7; Length 326;  
Best Local Similarity 99.7%; Pred. No. 5.7e-144;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MALSGSTPAPCWEDECDLDYGMGLSLHRMFEVVGQLTECELELAFLLDEAPGAAGLA 60  
DB 1 MALSGSTPAPCWEDECDLDYGMGLSLHRMFEVVGQLTECELELAFLLDEAPGAAGLA 60  
QY 61 PARSGLELLLEBRGGCGESNLRLGQLRVLARHDLPHLARRRRPVSPERYSYGTS 120  
DB 61 PARSGLELLLEBRGGCGESNLRLGQLRVLARHDLPHLARRRRPVSPERYSYGTS 120  
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKORRSRPGGARRRRRGAAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKORRSRPGGARRRRRGAAPAPQ 180  
QY 181 QOSEPARPSSEKVTCDIRLVRAEYCEHGPALGEGVASRRRPOALLRQUDVFGQATAYLR 240  
DB 181 QOSEPARPSSEKVTCDIRLVRAEYCEHGPALGEGVASRRRPOALLRQUDVFGQATAYLR 240  
QY 241 SRDLGSVVCIDIKFSELSYIDAFWGYLSGALLQALRGVFLTEALREAVGRRVLLVSD 300  
DB 241 SRDLGSVVCIDIKFSELSYIDAFWGYLSGALLQALRGVFLTEALREAVGRRVLLVSD 300  
QY 301 EAD 303  
DB 301 EAD 303

RESULT 7  
AAG73852  
ID AAG73852 standard; protein; 366 AA.  
XX  
AC AAG73852;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen protein SEQ ID NO:4616.  
XX  
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KM colorectal carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN WO200122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-US026524.  
XX  
PR 29-SEP-1999; 99US-0157137P.  
XX 03-NOV-1999; 99US-0163280P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX  
DR WPI; 2001-235357/24.  
XX N-PSDB; AAG73283.  
XX  
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
XX useful for preventing, diagnosing and/or treating colorectal cancers.  
XX  
PS Claim 1; Page 6413-6414; 9803pp; English.  
XX  
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patient's own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated P, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922  
XX  
SQ Sequence 366 AA;  
Query Match 99.5%; Score 1543; DB 4; Length 366;  
Best Local Similarity 99.7%; Pred. No. 6.6e-144;  
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MALSGSTPAPCWEDECDLDYGMGLSLHRMFEVVGQLTECELELAFLLDEAPGAAGLA 60  
DB 41 MALSGSTPAPCWEDECDLDYGMGLSLHRMFEVVGQLTECELELAFLLDEAPGAAGLA 100  
QY 61 PARSGLELLLEBRGGCGESNLRLGQLRVLARHDLPHLARRRRPVSPERYSYGTS 120  
DB 101 PARSGLELLLEBRGGCGESNLRLGQLRVLARHDLPHLARRRRPVSPERYSYGTS 160  
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKORRSRPGGARRRRRGAAPAPQ 180

Db 161 SSKRTGSGCRRRRSSANSQOGWETGSPPTKQRSGRRGPGARRRRRCAPAPQ 220  
 QY 181 QOSEPARPSSGKYTCIDIRLRVRAVCEHGPALCEQVARSRRPQALARQLDVFGQATAVLR 240  
 Db 221 QOSEPARPSSGKYTCIDIRLRVRAVCEHGPALCEQVARSRRPQALARQLDVFGQATAVLR 280  
 QY 241 SRDGSVVCIDIKFSELSYLDAFMGDYLQALRGVFLTEALREAVGREAVRLVSYVD 300  
 Db 281 SRDGSVVCIDIKFSELSYLDAFMGDYLQALRGVFLTEALREAVGREAVRLVSYVD 340  
 QY 301 EAD 303  
 Db 341 EAD 343

RESULT 8  
 AAB15551  
 ID AAB15551 standard; protein; 304 AA.

AC AAB15551;

DT 28-FEB-2001 (first entry)

DE Apoptosis related protein encoded by gene 1 clone HLDOK36.

XX Cytostatic; antiinflammatory; immunosuppressive; antisclerotic; cardiant;  
 XX antiviral; anti-AIDS; vasotropic; anti-ischaemic; antiparkinsonian;  
 XX anti-Alzheimer; gene therapy; human; apoptosis; fusion protein; cancer;  
 XX colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;  
 XX autoimmune disorder; multiple sclerosis; viral infection.

OS Homo sapiens.

PN WO200056752-A2.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000WO-US006642.

PR 24-MAR-1999; 99US-0126018P.

PR 17-JUN-1999; 99US-0139638P.

PR 18-AUG-1999; 99US-0149449P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Ni J, Young PA;

DR WPI; 2000-587660/55.

DR N-PSDB; AAA95790.

PT Nucleic acids encoding human apoptosis associated protein, useful for the

PT prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's

PT disease, inflammation and ischemic injury.

PS Claim 11; Page 252-253; 273pp; English.

XX The invention relates to the isolation of genes encoding 9 human

CC apoptosis-related proteins. The nucleotide sequences AAA95790-A95798

CC encode the human apoptosis related proteins AAB15551-B15559. The genes

CC can be used to generate fusion proteins by linking to the gene for the

CC human immunoglobulin G Fc (IgG Fc) portion (AAA95799) for increasing the

CC stability of the fusion protein as compared to the human protein only.

CC The gene and encoded protein may be used in the prevention, treatment and

CC diagnosis of diseases associated with inappropriate apoptosis associated

CC protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,

CC melanomas and lymphomas), inflammation, autoimmune disorders (e.g.

CC multiple sclerosis) and viral infections (e.g. herpes)

XX Sequence 304 AA;

XX Query Match 91.2%; Score 1413; DB 3; Length 304;

XX Best Local Similarity 99.6%; Pred. No. 3.9e-11;

XX Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 MSLHMEFVVGQLTCECELELAFLDEAPGAAGLAPARSGLLELLEERRQCGESN 82  
 Db 1 MSLHMEFVVGQLTCECELELAFLDEAPGAAGLAPARSGLLELLEERRQCGESN 60  
 QY 83 LRLGLGLRLVLAHDDLPHLARRRRPVSPERYSGTSSSKRTGSGCRRRRSSANS 142  
 Db 61 LRLGLGLRLVLAHDDLPHLARRRRPVSPERYSGTSSSKRTGSGCRRRRSSANS 120  
 QY 143 QCGWETGSPPTKQRSGRRPQALARQLDVFGQATAVLRSDIGSVCDIKFSELSYDAF 262  
 Db 121 QCGWETGSPPTKQRSGRRPQALARQLDVFGQATAVLRSDIGSVCDIKFSELSYDAF 180  
 QY 203 RAECYCEHGPALCEQVARSRRPQALARQLDVFGQATAVLRSDIGSVCDIKFSELSYDAF 262  
 Db 181 RAECYCEHGPALCEQVARSRRPQALARQLDVFGQATAVLRSDIGSVCDIKFSELSYDAF 240  
 QY 263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSYDEAD 303  
 Db 241 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSYDEAD 281

RESULT 9  
 AAB58420  
 ID AAB58420 standard; protein; 319 AA.

AC AAB58420;

DT 14-MAR-2001 (first entry)

DE Lung cancer associated polypeptide sequence SEQ ID 758.

XX Human; lung cancer associated protein; neuroprotective; cytoskeletal;  
 XX cardioactive; immunomodulatory; muscular active; vulnary;  
 XX gastrointestinal; nephrotoxic; antiinfective; gynecological;  
 XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
 XX proliferative disorder; wound healing; infectious disease.

OS Homo sapiens.

PN WO200055180-A2.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US005918.

PR 12-MAR-1999; 99US-0124270P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (ROSE/) ROSEN C A.

DR Ruben SM;

DR WPI; 2000-587514/55.

DR N-PSDB; AAF18296.

PT Lung cancer associated gene sequences, referred to as lung cancer

PT antilegms, useful for treatment, prevention, and diagnosis of disorders

PT such as lung cancer.

PS Claim 11; Page 1275-1276; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer

CC associated proteins represented in AAB58106 - AAB58548. Lung cancer

CC associated proteins and polynucleotide sequences; their agonists, and

CC antagonists may have neuroprotective; cytoskeletal; cardiovascular

CC immunomodulatory; muscular active general; vulnary; gastrointestinal

CC general; nephrotoxic; antiinfective; gynecological; or antibacterial

CC activity. The invention also includes antibodies specific for the protein

CC or polynucleotide sequences. The lung cancer associated polynucleotide

CC sequences may be used for detection of lung cancer, chromosome

CC identification, as chromosome markers, and for numerous other diagnostic

CC or research purposes. The proteins may be used to treat disorders such as

CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,  
 CC cardiovascular, renal, and proliferative disorders. The proteins may also  
 CC be used in the treatment of wounds and infectious diseases.  
 CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are  
 CC used in the course of the invention for the identification and  
 CC characterization of the polynucleotide and protein sequences

XX Sequence 319 AA;

Query Match 90.6%; Score 1404; DB 3; Length 319;  
 Best Local Similarity 99.6%; Pred. No. 3.2e-130;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPPCWBEDECDYGYMLSLHMFVVGQGLTECELELAFLLDEAPGAAGLA 60  
 DB 41 MALSGTAPPCWBEDECDYGYMLSLHMFVVGQGLTECELELAFLLDEAPGAAGLA 100  
 QY 61 PARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 120  
 DB 101 PARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 160  
 QY 121 SSSKRTGSCRRRRSSSSANGQGWETGSPPTKRORRSRGRPSGARRRRGAAPAPQ 180  
 DB 161 SSSKRTGSCRRRRSSSSANGQGWETGSPPTKRORRSRGRPSGARRRRGAAPAPQ 220  
 QY 181 QGSEPARPSSSEKVTCDIRLVRVAYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240  
 DB 221 QGSEPARPSSSEKVTCDIRLVRVAYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 280  
 QY 241 SRDLGSVVCIDIKFSELSYLDAPFWGDLGALLQ 273  
 DB 281 SRDLGSVVCIDIKFSELSYLDAPFWGDLGALLQ 313

RESULT 10  
 ABB06038  
 ID ABB06038 standard; protein; 361 AA.

XX ABB06038;  
 DT 10-MAY-2002 (first entry)

DE Human NS protein sequence SEQ ID NO:130.

XX Human; cytosolic; osteopathic; gynaecological; neuroprotective;  
 KW antifibrotic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;  
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;  
 KW anorectic; muscular; antidiabetic; cardiovascular; anticoagulant;  
 KW antifibrinolytic; hypotension; antiaesthetic; immunomodulator; cardiac;  
 KW gastrointestinal; antidiabetic; tranquilizer; antidepressant; neuroleptic;  
 KW gastrointestinal; virucide; antitumor; cerebroprotective; nootropic;  
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;  
 KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;  
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;  
 KW infertility; cardiovascular disease; coagulation disease; hypertension;  
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;  
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;  
 KW gastric ulcer; Alzheimer's disease.

XX Homo sapiens.

OS WO200206315-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-IL000653.

XX 18-JUL-2000; 2000IL-00137345.  
 PR 15-DEC-2000; 2000IL-00140354.

XX (COMP-) COMPUGEN LTD.

PI Mintz L, Freilich S, Bernstein J,  
 XX WPI; 2002-155037/20.  
 DR N-PsDB; ABL39692.

PT One hundred and twenty eight novel nucleic acid sequences, useful for  
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.

XX Claim 6, Page 149-151; 290pp; English.

CC ABL39692 to ABL38818 represent novel human nucleic acid sequences  
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences  
 CC (NS) can have cytosolic, osteopathic, gynaecological, neuroprotective,  
 CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,  
 CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,  
 CC anorectic, muscular, anti-HIV, antifertility, cardiovascular,  
 CC anticoagulant, antifibrinolytic, hypotension, antiaesthetic, cardiac,  
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antitumor,  
 CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,  
 CC nootropic and contraceptive activities. The NS can be used in vaccines,  
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and  
 CC antibodies from the present invention can be used for treating and  
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative  
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,  
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,  
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular  
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune  
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,  
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,  
 CC Alzheimer's disease and as a contraceptive

XX Sequence 361 AA;

Query Match 70.4%; Score 1090.5; DB 5; Length 361;  
 Best Local Similarity 73.9%; Pred. No. 4.3e-99;  
 Matches 229; Conservative 11; Mismatches 31; Indels 39; Gaps 4;

QY 1 MALSGTAPPCWBEDECDYGYMLSLHMFVVGQGLTECELELAFLLDEAPGAAGLA 60  
 DB 29 MALSGTAPPCWBEDECDYGYMLSLHMFVVGQGLTECELELAFLLDEAPGAAGLA 88  
 QY 61 PARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 120  
 DB 89 PARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 133  
 QY 121 SSSKRTGSCRRRRSSSSANGQGWETGSPPTKRORRSRGRPSGARRRRGAAPAPQ 168  
 DB 134 SSSKRTGSCRRRRSSSSANGQGWETGSPPTKRORRSRGRPSGARRRRGAAPAPQ 188  
 QY 169 SSSKRTGSCRRRRSSSSANGQGWETGSPPTKRORRSRGRPSGARRRRGAAPAPQ 221  
 DB 189 SSSKRTGSCRRRRSSSSANGQGWETGSPPTKRORRSRGRPSGARRRRGAAPAPQ 248  
 QY 222 PQLARQLDVFGQATAVLRSDLSVVCIDIKFSELSYLDAPFWGDLGALLQALRGVFLT 281  
 DB 249 PQLARQLDVFGQATAVLRSDLSVVCIDIKFSELSYLDAPFWGDLGALLQALRGVFLT 308  
 QY 282 EALREAVGRE 291  
 DB 309 EALREAVGRE 318

RESULT 11

ABBO6039  
 ID ABB06039 standard; protein; 368 AA.

XX ABB06039;  
 DT 10-MAY-2002 (first entry)

DE Human NS protein sequence SEQ ID NO:131.

XX Human; cytosolic; osteopathic; gynaecological; neuroprotective;



KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;  
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;  
 KW antitubercular; antineoplastic; antidiabetic; immunomodulator; cardiant;  
 KW antifibrinolytic; hypotension; antispasmodic; antidiabetic; auroleptic;  
 KW anticonvulsant; antidiabetic; tranquilizer; antidepressant; neuroleptic;  
 KW gastroenteric; antidiabetic; antitumor; cerebroprotective; nootropic;  
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; psoriasis;  
 KW endometriosis; degenerative disease; multiple sclerosis; glaucoma;  
 KW rheumatoid arthritis; cataract; restenosis; muscular dystrophy; AIDS;  
 KW inflammation; skin disorder; obesity; coagulation disease; hypertension;  
 KW interstitial; cardiovascular disease; epilepsy; angina; neurodegeneration;  
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;  
 KW gastric ulcer; Alzheimer's disease.  
 KW Homo sapiens.  
 OS WO200206315-A2.  
 PN 24-JAN-2002.  
 XX 17-JUL-2001; 2001WO-IL000653.  
 XX 18-JUL-2000; 2000IL-00137345.  
 XX 15-DEC-2000; 2000IL-00140354.  
 PR (COMP-) COMPUGEN LTD.  
 PA Mintz L, Freilich S, Bernstein J;  
 PI WPI: 2002-155037/20.  
 DR N-PSDB; ABL39693.  
 PT One hundred and twenty eight novel nucleic acid sequences, useful for  
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.  
 PS Claim 6, Page 151-152; 290pp; English.  
 CC ABL39691 to ABL39818 represent novel human nucleic acid sequences  
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences  
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,  
 CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,  
 CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,  
 CC anorectic, muscular, anti-HIV, antineoplastic, cardiovascular,  
 CC anticonvulsant, antifibrinolytic, hypotension, antispasmodic, cardiant,  
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antitumor,  
 CC antidepressant, gastroenteric, neuroleptic, cerebroprotective,  
 CC nootropic and contraceptive activities. The NS can be used in vaccines,  
 CC gene therapy and antitumor therapy. Nucleic acids, expression vectors and  
 CC antibodies from the present invention can be used for treating and  
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative  
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,  
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,  
 CC glaucoma, obesity, muscular dystrophy, AIDS, interstitial, cardiovascular  
 CC disease, coagulation disease, ischemia, hypertension, asthma, immune  
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,  
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,  
 CC Alzheimer's disease and as a contraceptive  
 CC  
 XX Sequence 368 AA:  
 SQ  
 Query Match 70.4%; Score 1090.5; DB 5; Length 368;  
 Best Local Similarity 73.9%; Pred. No. 4.4e-99;  
 Matches 229; Conservative 11; Mismatches 31; Indels 39; Gaps 4;  
 QY 1 MALSGSTPAPCWEDECDYVYGMGLSRHMEFVVGQGLTECELELILAFLLDEAPAGAGLA 60  
 DB 36 MALSGSTPAPCWEDECDYVYGMGLSRHMEFVVGQGLTECELELILAFLLDEAPAGAGYA 95  
 QY 61 PARSGLELLELERRGGGSENLRLGQLAVLARHDLPLHARRRRPVPPEYSGTYS 120  
 DB 96 PARSGLELLELERRGGGSENLRLGQLAVLARHDLPLHARRRRPVPPEYSGTYS 140

QY 121 SSKRTGSGCRRRRROSSSSANSQOQ-----WETGSPPTKR-----QRSGRGPSSGCA-- 168  
 DB 141 -----AAGCGLQAIAMAPALORGRVAVANVGAVQILSRFGSGQAPPPSSGTAES 195  
 QY 169 -----RRRRRGAAPAPQOQSEPPAPSSSEKVTCTIRLVRAYEYEHGPALEQVASRR 221  
 DB 196 GPAMWMCQTAAERAPAPAPQOQSEPPAPSSSEKVTCTIRLVRAYEYEHGPALEQVASRR 255  
 QY 222 PQLARQLDVFQGTATVRSRDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRGVFLT 281  
 DB 256 PQLARQLDVFQGTATVRSRDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRGVFLT 315  
 QY 282 EALREAVGRE 291  
 DB 316 EALREAVGRE 325  
 RESULT 12  
 ID AAM25705  
 ID AAM25705 standard; protein: 242 AA.  
 AC AAM25705;  
 XX 16-OCT-2001 (first entry)  
 DT Human protein sequence SEQ ID NO.1220.  
 DE Human; cancer; HIV infection; human immunodeficiency virus;  
 XX antineoplastic; antirheumatic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; vitruide;  
 KW anti-HIV; fungicide; antimetabolite; cardiovascular; antianemic; anaemia;  
 KW antitubercular; haemostatic; antidiabetic; antitumor; antispasmodic; infection;  
 KW dermatological; antiallergic; antispasmodic; antidiabetic; cytostatic;  
 KW neuroprotective; gene therapy; antitumor; antispasmodic; antidiabetic;  
 KW immunostimulant; rheumatoid arthritis; septic shock; pancreatitis;  
 KW antianaphylactic; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW cardiac dysfunction; neuropathology; severe combined immunodeficiency;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopenia; osteoporosis; multiple sclerosis; depression;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder.  
 KW Homo sapiens.  
 OS WO200153455-A2.  
 PN 26-JUL-2001.  
 XX 22-DEC-2000; 2000WO-US035017.  
 XX 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-00552317.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI: 2001-457603/49.  
 DR N-PSDB; AAM99646.  
 XX Isolated human polynucleotides encoding polypeptides, useful for the  
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.  
 PT Claim 20; Page 253; 1217pp; English.  
 PS AAM99166 to AAM9994 encode the human proteins given in AAM25225 to  
 CC AAM25963. The proteins can have activities based on the tissues and cells  
 CC they are expressed in, such as: antineoplastic; antirheumatic; cardiant;  
 CC antitubercular; haemostatic; antidiabetic; antitumor; antispasmodic;  
 CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; vitruide; antianaphylactic; autoimmunity;  
 CC cardiovascular; antianemic; antitubercular; haemostatic; vulnery;

```
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antididiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders  
CC  
CC  
SQ Sequence 242 AA;  
  
Query Match 63.7%; Score 987; DB 4; Length 242;  
Best Local Similarity 97.0%; Pred. No. 4,6e-89;  
Matches 196; Conservative 1; Mismatches 3; Indels 2; Gaps 1;  
  
QY 104 RRRRRP--VSPERYVTGSSSSKRTGSGRRRRSSSSSSNSOQGWETGSPPTKQRRR 161  
DB 18 RSHRTPESVSPERYVTGSSSSKRTGSGRRRRSSSSSSNSOQGWETGSPPTKQRRR 77  
QY 162 GRPSCGARRRRRGAPAPAPQOQSEPARPSEGGKVTCDIRLVAAEYCEHPALGQVAAAR 221  
DB 78 GRPSCGARRRRRGAPAPAPQOQSEPARPSEGGKVTCDIRLVAAEYCEHPALGQVAAAR 137  
QY 222 PQLARQLDVGQATVATRSRDLSGVCDIKFSELSYLDAPMGDYLSGALLQALRGVFLT 281  
DB 138 PQLARQLDVGQATVATRSRDLSGVCDIKFSELSYLDAPMGDYLSGALLQALRGVFLT 197  
QY 282 EALREAVGRBAVRLIVSDEAD 303  
DB 198 EALREAVGRBAVRLIVSDEAD 219  
  
RESULT 13  
ID AAM39805 standard; protein; 277 AA.  
XX AAM39805;  
AC  
XX  
XX  
DT 22-OCT-2001 (first entry)  
XX  
XX  
DE Human polypeptide SEQ ID NO 2950.  
XX  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN MO300153312-A1.  
XX  
XX  
PD 26-JUL-2001.  
XX  
XX  
PF 26-DEC-2000; 2000MO-US034263.  
XX  
XX  
XX 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.
```

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XX  
PA (HYGE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Dmanac RT;  
XX  
XX WPI; 2001-442253/47.  
DR N-PEDB; AAI58961.  
PT Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX  
XX  
PS Example 4; SEQ ID NO 2950; 10078bp; English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM36642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localized neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
CC  
CC  
SQ Sequence 277 AA;  
  
Query Match 61.3%; Score 950.5; DB 4; Length 277;  
Best Local Similarity 95.9%; Pred. No. 2,3e-85;  
Matches 187; Conservative 2; Mismatches 1; Indels 5; Gaps 1;  
  
QY 1 MALSGTPAPCMEDECDYGMLSIHMFVVGQGLTECELELAFLDPAAGGLA 60  
DB 1 MALSGTPAPCMEDECDYGMLSIHMFVVGQGLTECELELAFLDPAAGGLS 60  
QY 61 PARSGLELLLEERRGCGESNLRLGQLLVLARHDLPHLARRRPVPERSYGTG 120  
DB 61 PARSGLELLLEERRGCGESNLRLGQLLVLARHDLPHLARRRPVPERSYGTG 120  
QY 121 SSSKRTGSCRRRRSSSSSSNSOQGWETGSPPTKQRRSGRPGARRRRRGAPAPQ 180  
DB 121 SSSKRTGSCRRRRSSSSSSNSOQGWETGSPPTKQRRSGRPGARRRRRGAPAPQ 175  
QY 181 QOSEPARPSSSEKVT 195  
DB 176 QOSEPARPSSSEKVT 190  
  
RESULT 14  
ID AAM41591 standard; protein; 217 AA.  
XX AAM41591;  
AC  
XX  
XX  
DT 22-OCT-2001 (first entry)  
XX  
XX  
DE Human polypeptide SEQ ID NO 6522.  
XX  
XX  
XX  
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
XX  
OS Homo sapiens.  
XX
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PN WO200153312-A1.  
 XX 26-JUL-2001.  
 XX 26-DEC-2000; 2000WO-US034263.  
 XX 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-00552317.  
 PR 20-JUN-2000; 2000US-00598042.  
 PR 19-JUL-2000; 2000US-00620312.  
 PR 03-AUG-2000; 2000US-00653450.  
 PR 14-SEP-2000; 2000US-00662191.  
 PR 19-OCT-2000; 2000US-00693036.  
 PR 29-NOV-2000; 2000US-00727344.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,  
 PI Zhou P, Goodrich R, Drmanac RT;  
 XX WPI; 2001-442253/47.  
 DR N-PSDB; AAI60747.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 PT Example 2; SEQ ID NO 6522; 10078pp; English.  
 XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
 CC encoded polypeptides (AAM3642-AA42213) with neurotrophic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilization of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification  
 CC  
 CC Sequence 217 AA;  
 XX  
 SQ  
 Query Match 55.1%; Score 854; DB 4; Length 217;  
 Best Local Similarity 90.5%; Pred. No. 5.9e-76;  
 Matches 171; Conservative 2; Mismatches 10; Indels 6; Gaps 2;

QY 1 MALSGSTPAPCWEDECDLYYGMLSHRFVVGQUTCECELLAFLIDEAPGAAGGA 60  
 DB 30 MALSGSTPAPCWEDECDLYYGMLSHRFVVGQUTCECELLAFLIDEAPGAAGGA 89  
 QY 61 PARSGELLEERRGCGESNRLGQLRLVLAARDLLPHLARKRRRPVSPERYSGTS 120  
 DB 90 PARSGELLEERRGCGESNRLGQLRLVLAARDLLPHLARKRRRPVSPERYSGTS 149  
 QY 121 SSSKRTGSCRRRRSSSSANSOQGWETGSPPTKQRRSRGPPSGARRRRRG-APAAP 179  
 DB 150 SSSKRTGSCRRRRSSSSANSOQGWETGSPPTKQRRSRGPPSGARRRRRGPOPHPS 204  
 QY 180 QOQSEPPAP 188  
 DB 205 SSGSPDLP 213

RESULT 15  
 AAB94040  
 ID AAB94040 standard; protein; 318 AA.  
 XX

AC AAB94040;  
 XX 26-JUN-2001 (first entry)  
 DT Human protein sequence SEQ ID NO:14195.  
 DE Human protein sequence SEQ ID NO:14195.  
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 KW Homo sapiens.  
 OS  
 PN EP1074617-A2.  
 XX 07-FEB-2001.  
 PD  
 XX 28-JUL-2000; 2000EP-00116126.  
 PF  
 XX 29-JUL-1999; 99JP-00248036.  
 PR 27-AUG-1999; 99JP-00300253.  
 PR 11-JAN-2000; 2000JP-00118776.  
 PR 02-MAY-2000; 2000JP-00183767.  
 PR 09-JUN-2000; 2000JP-00241899.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J,  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX WPI; 2001-318749/34.  
 DR  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-  
 PT length cDNAs defined in the specification, and for the detection and/or  
 PT diagnosis of the abnormality of the proteins encoded by the full-length  
 PT cDNAs.  
 PS Claim 8; SEQ ID NO 14195; 2537pp + Sequence listing; English.  
 XX The present invention describes primer sets for synthesising 5602 full-  
 CC length cDNAs defined in the specification. Where a primer set comprises:  
 CC (a) an oligo-dr primer and an oligonucleotide complementary to the  
 CC complementary strand of a polynucleotide which comprises one of the 5602  
 CC nucleotide sequences defined in the specification; where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the  
 CC specification. The primer sets can be used in antisense therapy and in  
 CC gene therapy. The primers are useful for synthesising polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893  
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent  
 CC oligonucleotides, all of which are used in the exemplification of the  
 CC present invention  
 CC  
 CC Sequence 318 AA;  
 XX  
 SQ  
 Query Match 40.2%; Score 622.5; DB 4; Length 318;  
 Best Local Similarity 45.2%; Pred. No. 8.4e-53;  
 Matches 136; Conservative 54; Mismatches 90; Indels 21; Gaps 6;

QY 12 WEDECDLYYGMLSHRFVVGQUTCECELLAFLIDEAPGAAGGAPARSGLELL 70  
 DB 12 WPEHGEQHGGLXSLRWFVDYVTHLTHRDVLTSLFVDVIDDHERGL--INRGDFLL 69  
 QY 71 ELERRGCGESNRLGQLRLVLAARDLLPHLARKRRRPVSP---ERYSGTS---SSK 124  
 DB 70 ALERRGCGESNRFVYQLRLITTRHDLIPYVTLKRRRAVCPDLVKKYLEETISRYVTR 129

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Qy 125 RTGSCRRRRQSSSSANSQOQO--WETGSPPTKORRSRGRPSGGARRRRRGAPAPQOQ 182
Db 130 ALSDEPRPPQPSKTVPPHYPVVCCPTSGPQMCSSKRPARGATLGSQRKR----- 180
Qy 183 SEPARPSSEKVTCDIRLVRRAEYCEHGPALQGVASRRPQALRQLDVFGQATVLRSR 242
Db 181 -KPVTPDPEKEKQTCIRLVRRAEYCOHETALQGNVFSNRQDPLERQFERFNOANTILKSR 239
Qy 243 DLGSVVCIDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEA 302
Db 240 DLGSTICDIXFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEA 299
Qy 303 D 303
Db 300 D 300

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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:31:06 ; Search time 72 Seconds  
(without alignments)  
2155.000 Million cell updates/sec

Title: US-10-030-271-2  
Perfect score: 303  
Sequence: 1 MALSGSTPAFCWEDECLDY.....LREAVGRAVRLVSVDEAD 303

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	224	73.9	326	1 DED2_HUMAN	Q8W2F8 homo sapien
2	117	38.6	330	1 DED2_MOUSE	Q8QZV0 mus musculu
3	23	7.6	168	2 O8BRM3	Q8BRM9 mus musculu
4	14	4.6	369	2 O919M3	Q919M3 brachydanto
5	13	4.3	318	1 DEDD_HUMAN	Q75618 homo sapien
6	13	4.3	318	1 DEDD_MOUSE	Q92113 mus musculu
7	13	4.3	318	1 DEDD_RAT	Q92113 mus musculu
8	13	4.3	404	2 Q6DH2	Q6DH2 brachydanto
9	11	3.6	243	2 Q6GNZ8	Q6GNZ8 xenopus lae
10	10	3.3	218	2 Q91W13	Q91W13 molluscum c
11	10	3.3	235	2 Q98222	Q98222 molluscum c
12	10	3.3	244	2 Q6DHV2	Q6DHV2 brachydanto
13	9	3.0	127	2 Q9Y9Y9	Q9Y9Y9 aeropyrum p
14	9	3.0	222	2 Q671V3	Q671V3 oryza sativ
15	9	3.0	227	2 Q706G3	Q706G3 anopheles g
16	9	3.0	241	2 Q6MEX0	Q6MEX0 paracelamyd
17	9	3.0	385	2 Q6M204	Q6M204 corynebacte
18	9	3.0	395	2 Q8NLT5	Q8NLT5 corynebacte
19	9	3.0	478	2 Q82HT1	Q82HT1 streptomyce
20	9	3.0	629	2 Q871T5	Q871T5 neurospora
21	9	3.0	5835	2 Q631K8	Q631K8 burkholderi
22	8	2.6	72	2 Q8H7Z8	Q8H7Z8 oryza sativ
23	8	2.6	75	2 Q8HUG7	Q8HUG7 agrobacteri
24	8	2.6	93	2 Q9FLF2	Q9FLF2 enterococcu
25	8	2.6	101	2 Q6UPP9	Q6UPP9 human immun
26	8	2.6	105	2 Q92KX5	Q92KX5 rhizobium m
27	8	2.6	106	2 Q86VG6	Q86VG6 homo sapien
28	8	2.6	113	2 Q8G7A6	Q8G7A6 bifidobacte
29	8	2.6	125	2 Q9BRA0	Q9BRA0 homo sapien
30	8	2.6	125	2 Q9D2U5	Q9D2U5 mus musculu
31	8	2.6	129	2 Q653U5	Q653U5 oryza sativ

32	8	2.6	134	2 Q7GVZ3	Q7GVZ3 giardia lam
33	8	2.6	142	2 Q6ERC3	Q6ERC3 oryza sativ
34	8	2.6	150	2 Q981A0	Q981A0 rhizobium l
35	8	2.6	159	2 Q6H586	Q6H586 oryza sativ
36	8	2.6	161	2 Q94EB4	Q94EB4 oryza sativ
37	8	2.6	163	2 Q6K7X6	Q6K7X6 oryza sativ
38	8	2.6	165	2 Q8S751	Q8S751 oryza sativ
39	8	2.6	165	2 Q87GH6	Q87GH6 oryza sativ
40	8	2.6	170	2 Q9S187	Q9S187 arabidopsis
41	8	2.6	186	2 Q7M020	Q7M020 bordetella
42	8	2.6	186	2 Q7MCE0	Q7MCE0 bordetella
43	8	2.6	186	2 Q7MQE6	Q7MQE6 bordetella
44	8	2.6	195	2 Q7D907	Q7D907 mycobacteri
45	8	2.6	197	2 Q0S575	Q0S575 mycobacteri
46	8	2.6	197	2 Q7U0W4	Q7U0W4 mycobacteri
47	8	2.6	223	2 Q84R51	Q84R51 oryza sativ
48	8	2.6	224	2 Q6SA89	Q6SA89 mycobacteri
49	8	2.6	224	2 Q6SA92	Q6SA92 mycobacteri
50	8	2.6	224	2 Q6SA93	Q6SA93 mycobacteri
51	8	2.6	224	2 Q69644	Q69644 mycobacteri
52	8	2.6	224	2 Q744E3	Q744E3 mycobacteri
53	8	2.6	224	2 Q7TVY9	Q7TVY9 mycobacteri
54	8	2.6	224	2 Q9CB91	Q9CB91 mycobacteri
55	8	2.6	225	2 Q744Y5	Q744Y5 mycobacteri
56	8	2.6	227	2 Q8RQX9	Q8RQX9 corynebacte
57	8	2.6	227	2 Q6N2U0	Q6N2U0 corynebacte
58	8	2.6	227	2 Q79V17	Q79V17 corynebacte
59	8	2.6	227	2 Q8FTU1	Q8FTU1 corynebacte
60	8	2.6	229	2 Q653P9	Q653P9 oryza sativ
61	8	2.6	231	2 Q8N922	Q8N922 homo sapien
62	8	2.6	245	2 Q67UJ2	Q67UJ2 oryza sativ
63	8	2.6	248	2 Q86SM7	Q86SM7 homo sapien
64	8	2.6	271	2 Q7XHN7	Q7XHN7 oryza sativ
65	8	2.6	279	2 Q66554	Q66554 aquifex aeo
66	8	2.6	282	1 P811_YEAST	P811_YEAST saccharomyc
67	8	2.6	314	2 Q92178	Q92178 oryza sativ
68	8	2.6	324	2 Q8Z178	Q8Z178 lactococcus
69	8	2.6	333	2 Q65XW6	Q65XW6 oryza sativ
70	8	2.6	339	1 HXD9_MOUSE	P28357 mus musculu
71	8	2.6	342	1 HXD9_HUMAN	P28356 homo sapien
72	8	2.6	342	2 Q86ST1	Q86ST1 homo sapien
73	8	2.6	346	2 Q73W29	Q73W29 mycobacteri
74	8	2.6	352	2 Q6Z1A4	Q6Z1A4 oryza sativ
75	8	2.6	354	2 Q6ZK4	Q6ZK4 oryza sativ
76	8	2.6	356	2 Q91314	Q91314 aeromonas h
77	8	2.6	361	2 Q7TMA4	Q7TMA4 mus musculu
78	8	2.6	363	2 Q69949	Q69949 streptomyce
79	8	2.6	364	2 Q8BCN1	Q8BCN1 xanthomonas
80	8	2.6	369	2 Q8BPE0	Q8BPE0 xanthomonas
81	8	2.6	386	2 Q94HU7	Q94HU7 oryza sativ
82	8	2.6	392	2 Q7MXU4	Q7MXU4 porphyromon
83	8	2.6	417	2 Q9CEH2	Q9CEH2 lactococcus
84	8	2.6	419	2 Q9ZAU1	Q9ZAU1 lactococcus
85	8	2.6	441	2 Q8H513	Q8H513 oryza sativ
86	8	2.6	444	2 Q942J2	Q942J2 oryza sativ
87	8	2.6	454	2 Q94DV6	Q94DV6 oryza sativ
88	8	2.6	473	2 Q8BPM7	Q8BPM7 xanthomonas
89	8	2.6	475	1 VTRC_RABIT	P22458 streptococcus
90	8	2.6	497	2 Q82BP9	Q82BP9 streptococcus
91	8	2.6	510	2 Q941U8	Q941U8 oryza sativ
92	8	2.6	526	2 Q73YQ3	Q73YQ3 mycobacteri
93	8	2.6	528	2 Q8U666	Q8U666 agrobacteri
94	8	2.6	573	2 Q994E5	Q994E5 porcine ade
95	8	2.6	579	2 Q755M9	Q755M9 ashyba goss
96	8	2.6	607	2 Q943P2	Q943P2 oryza sativ
97	8	2.6	632	2 Q70LFS	Q70LFS hordeum vul
98	8	2.6	633	1 MUA_TERTH	P40631 tetrahymena
99	8	2.6	678	2 Q82N52	Q82N52 streptomyce
100	8	2.6	685	2 Q9P0N9	Q9P0N9 azospirillum
101	8	2.6	693	2 Q829A5	Q829A5 streptomyce
102	8	2.6	701	2 Q6FBA3	Q6FBA3 acinetobact
103	8	2.6	761	1 PQOF_KLEPN	P27508 klebsiella
104	8	2.6	814	2 Q9ETL8	Q9ETL8 caenorhabdit

105	8	2.6	846	2	06PD17	06pd17 mus musculu
106	8	2.6	847	2	06TNV2	06tnv2 brachydanio
107	8	2.6	848	2	09AD04	09ad04 streptomyc
108	8	2.6	849	2	09VT98	09vt98 dirosophila
109	8	2.6	850	2	07YU08	07yu08 dirosophila
110	8	2.6	881	2	09VT99	09vt99 dirosophila
111	8	2.6	887	2	09ZS86	09zs86 arabidopsis
112	8	2.6	890	2	08LMT7	08lmt7 oryza sativ
113	8	2.6	901	2	09CS85	09cs85 arabidopsis
114	8	2.6	908	2	07ZVL4	07zvl4 brachydanio
115	8	2.6	909	2	06TUB6	06tub6 oryza sativ
116	8	2.6	910	2	093Y01	093y01 arabidopsis
117	8	2.6	924	2	022207	022207 arabidopsis
118	8	2.6	928	2	09T0B6	09t0b6 arabidopsis
119	8	2.6	934	2	06P5E8	06p5e8 mus musculu
120	8	2.6	937	2	09T0B8	09t0b8 arabidopsis
121	8	2.6	950	2	09PWC6	09pwc6 gallus gall
122	8	2.6	951	2	08H557	08h557 oryza sativ
123	8	2.6	952	2	09R085	09r085 rattus norv
124	8	2.6	953	2	080TY6	080ty6 mus musculu
125	8	2.6	963	2	08BP4	08bp4 homo sapien
126	8	2.6	973	2	08AVB6	08avb6 xenopus lae
127	8	2.6	981	1	UB15_HUMAN	09y4e8 homo sapien
128	8	2.6	981	1	UB15_MOUSE	08t5h1 mus musculu
129	8	2.6	981	1	080UK9	080uk9 mus musculu
130	8	2.6	1004	2	08ZJMS	08zjms streptomyc
131	8	2.6	1005	2	06W5R0	06w5r0 streptomyc
132	8	2.6	1021	1	CARA_MOUSE	P58660 mus musculu
133	8	2.6	1028	1	Q9ZSB5	Q9zsb5 arabidopsis
134	8	2.6	1032	1	CARA_HUMAN	Q9bwt7 homo sapien
135	8	2.6	1044	2	07QVN9	07qvn9 giardia lam
136	8	2.6	1093	2	0872P9	0872p9 neurospora
137	8	2.6	1095	2	0913U4	0913u4 pseudomonas
138	8	2.6	1098	2	07R1Z8	07r1z8 plasmodium
139	8	2.6	1332	2	0813U1	0813u1 plasmodium
140	8	2.6	1406	1	UBP6_HUMAN	P35125 homo sapien
141	8	2.6	1604	1	UBP2_HUMAN	08nta0 homo sapien
142	8	2.6	1733	1	VN1A_PRIVK	P33385 pseudorabie
143	8	2.6	1790	2	08W0J4	08w0j4 oryza sativ
144	8	2.6	1958	2	069340	069340 suid herpes
145	8	2.6	5216	2	Q7N239	Q7n239 photorhabd
146	8	2.3	35	1	SMS_LAMFL	Q9prx0 lampetra fl
147	7	2.3	47	2	Q23578	Q23578 caenorhabdi
148	7	2.3	52	2	06T1Q2	06t1q2 dirosophila
149	7	2.3	55	2	0842D8	0842d8 oryza sativ
150	7	2.3	56	2	07NWX2	07nwx2 oryza sativ
151	7	2.3	57	2	06KSW3	06ksw3 oryza sativ
152	7	2.3	58	2	0621W3	0621w3 chromobacte
153	7	2.3	64	2	0621W3	0621w3 burkholderi
154	7	2.3	64	2	06UDZ9	06udz9 human cytom
155	7	2.3	70	2	07M6G6	07m6g6 human cytom
156	7	2.3	73	2	0856U2	0856u2 mycobacteri
157	7	2.3	73	2	084039	084039 oryza sativ
158	7	2.3	73	2	08W0B8	08w0b8 oryza sativ
159	7	2.3	74	2	06YZR4	06yzt4 oryza sativ
160	7	2.3	75	2	07PWT3	07pwt3 anopheles g
161	7	2.3	81	2	08EUP5	08epj5 xanthomonas
162	7	2.3	85	2	06P5U4	06p5u4 homo sapien
163	7	2.3	86	2	06YTT5	06yts5 oryza sativ
164	7	2.3	87	2	06YUQ4	06yuq4 oryza sativ
165	7	2.3	88	2	0901H7	0901h7 human immun
166	7	2.3	90	2	067TMS	067tms oryza sativ
167	7	2.3	90	2	0851Q7	0851q7 oryza sativ
168	7	2.3	90	2	08H4N9	08h4n9 oryza sativ
169	7	2.3	91	2	07Z7E4	07z7e4 homo sapien
170	7	2.3	92	2	09S1X9	09s1x9 streptomyc
171	7	2.3	93	2	07S1V1	07s1v1 human immun
172	7	2.3	93	2	08ANAO	08ana0 human immun
173	7	2.3	94	2	06K7I2	06k7i2 oryza sativ
174	7	2.3	94	2	07SUI7	07sui7 human immun
175	7	2.3	94	2	07SUG3	07sug3 human immun
176	7	2.3	95	2	06YTR7	06ytr7 oryza sativ
177	7	2.3	95	2	08AMV7	08amv7 human immun
178	7	2.3	96	2	08T9V4	08t9v4 aedes aegypt
179	7	2.3	96	2	06JCC9	06jcc9 human immun
180	7	2.3	97	2	06Z2G4	06z2g4 oryza sativ
181	7	2.3	98	2	068Q09	068q09 human immun
182	7	2.3	99	2	0908Q9	0908q9 human immun
183	7	2.3	99	2	098X72	098x72 human immun
184	7	2.3	99	2	068Q06	068q06 human immun
185	7	2.3	99	2	068Q06	068q06 human immun
186	7	2.3	99	2	068Q08	068q08 human immun
187	7	2.3	99	2	068Q08	068q08 human immun
188	7	2.3	99	2	068Q08	068q08 human immun
189	7	2.3	99	2	068Q08	068q08 human immun
190	7	2.3	99	2	068Q08	068q08 human immun
191	7	2.3	99	2	068Q08	068q08 human immun
192	7	2.3	99	2	068Q08	068q08 human immun
193	7	2.3	99	2	068Q08	068q08 human immun
194	7	2.3	99	2	068Q08	068q08 human immun
195	7	2.3	99	2	068Q08	068q08 human immun
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197	7	2.3	99	2	068Q08	068q08 human immun
198	7	2.3	99	2	068Q08	068q08 human immun
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201	7	2.3	99	2	068Q08	068q08 human immun
202	7	2.3	99	2	068Q08	068q08 human immun
203	7	2.3	99	2	068Q08	068q08 human immun
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211	7	2.3	99	2	068Q08	068q08 human immun
212	7	2.3	99	2	068Q08	068q08 human immun
213	7	2.3	99	2	068Q08	068q08 human immun
214	7	2.3	99	2	068Q08	068q08 human immun
215	7	2.3	99	2	068Q08	068q08 human immun
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217	7	2.3	99	2	068Q08	068q08 human immun
218	7	2.3	99	2	068Q08	068q08 human immun
219	7	2.3	99	2	068Q08	068q08 human immun
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221	7	2.3	99	2	068Q08	068q08 human immun
222	7	2.3	99	2	068Q08	068q08 human immun
223	7	2.3	99	2	068Q08	068q08 human immun
224	7	2.3	99	2	068Q08	068q08 human immun
225	7	2.3	99	2	068Q08	068q08 human immun
226	7	2.3	99	2	068Q08	068q08 human immun
227	7	2.3	99	2	068Q08	068q08 human immun
228	7	2.3	99	2	068Q08	068q08 human immun
229	7	2.3	99	2	068Q08	068q08 human immun
230	7	2.3	99	2	068Q08	068q08 human immun
231	7	2.3	99	2	068Q08	068q08 human immun
232	7	2.3	99	2	068Q08	068q08 human immun
233	7	2.3	99	2	068Q08	068q08 human immun
234	7	2.3	99	2	068Q08	068q08 human immun
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239	7	2.3	99	2	068Q08	068q08 human immun
240	7	2.3	99	2	068Q08	068q08 human immun
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242	7	2.3	99	2	068Q08	068q08 human immun
243	7	2.3	99	2	068Q08	068q08 human immun
244	7	2.3	99	2	068Q08	068q08 human immun
245	7	2.3	99	2	068Q08	068q08 human immun
246	7	2.3	99	2	068Q08	068q08 human immun
247	7	2.3	99	2	068Q08	068q08 human immun
248	7	2.3	99	2	068Q08	068q08 human immun
249	7	2.3	99	2	068Q08	068q08 human immun
250	7	2.3	99	2	068Q08	068q08 human immun



251	7	2.3	143	2	069PH1	069ph1 oryza sativ	324	7	2.3	204	2	09H6X1	09hex1 homo sapien
252	7	2.3	144	2	08BDJ6	08bdj6 shewanella	325	7	2.3	205	2	08ASM4	08asm4 bacteroides
253	7	2.3	144	2	06ADL8	06adl8 leifsonia x	326	7	2.3	204	2	08BDR1	08bdr1 homo sapien
254	7	2.3	147	2	09AMT7	09amt7 oryza sativ	327	7	2.3	206	2	07YH1	07yhl1 mycobacteri
255	7	2.3	147	2	07NK38	07nk38 gloeobacter	328	7	2.3	207	2	09RUG1	09rug1 deinococcus
256	7	2.3	148	2	098B53	098b53 cyprinus ca	329	7	2.3	206	2	09L432	09l432 xanthomonas
257	7	2.3	150	2	07Z7E5	07z7e5 homo sapien	330	7	2.3	207	2	08P9K6	08p9k6 xanthomonas
258	7	2.3	150	2	07XXP0	07xxp0 chlorarachn	331	7	2.3	208	2	06H6A1	06h6a1 oryza sativ
259	7	2.3	152	2	05Z549	05z549 plasmid ppe	332	7	2.3	210	2	06S4X7	06s4x7 oryza sativ
260	7	2.3	152	2	08YMH3	08ymh3 anabaena sp	333	7	2.3	211	2	06Z801	06z801 oryza sativ
261	7	2.3	153	2	09Y9Z9	09y9z9 aeropyrum p	334	7	2.3	211	2	08RE54	08re54 fusobacteri
262	7	2.3	154	2	06ZAL6	06zal6 homo sapien	335	7	2.3	212	1	YLE1_HRCPU	028102 archaeoglob
263	7	2.3	155	2	09YAL6	09yal6 aeropyrum p	336	7	2.3	213	1	H1X_HUMAN	092522 homo sapien
264	7	2.3	157	2	07P2J9	07p2j9 chromobacte	337	7	2.3	213	2	08GTM2	08gtm2 brasica ol
265	7	2.3	158	2	074ZM7	074zm7 mycobacteri	338	7	2.3	215	2	084Z32	084z32 chlamydia t
266	7	2.3	160	2	08HXB4	08hxb4 maceca faec	339	7	2.3	215	2	08Y2Y9	08y2y9 ralbtonia b
267	7	2.3	160	2	06YVW7	06yvww7 oryza sativ	340	7	2.3	217	2	08YXK8	08yxk8 pseudomonas
268	7	2.3	162	2	06BD40	06bd40 drosophila	341	7	2.3	218	2	09DWM9	09dwm9 rat cytoleg
269	7	2.3	167	2	07OUG1	07oug1 giardia lam	342	7	2.3	219	2	09X7G3	09x7g3 methylolact
270	7	2.3	168	2	09CW76	09cw76 mus musculu	343	7	2.3	223	2	09D5P3	09d5p3 mus musculu
271	7	2.3	170	2	07MSU7	07msu7 mouse adeno	344	7	2.3	224	1	TEMB_CHLTR	084836 chlamydia t
272	7	2.3	170	2	09NBF9	09nbf9 philodina r	345	7	2.3	224	2	06Z9S6	06z9s6 oryza sativ
273	7	2.3	172	2	08LIT5	08lit5 oryza sativ	346	7	2.3	225	2	097PNO	097pno streptococc
274	7	2.3	173	2	07SV41	07sv41 physcomitre	347	7	2.3	225	2	08DP06	08dp06 streptococc
275	7	2.3	173	2	08N8Z9	08n8z9 homo sapien	348	7	2.3	227	2	08ZBU9	08zbu9 streptomyce
276	7	2.3	174	2	06KX41	06kx41 homo sapien	349	7	2.3	228	2	08LMC8	08lmc8 oryza sativ
277	7	2.3	174	2	06S6U7	06s6u7 oryza sativ	350	7	2.3	228	2	06JMT8	06jmt8 uncultured
278	7	2.3	174	2	06S8S9	06s8s9 burkholderi	351	7	2.3	231	2	08LMQ0	08lmq0 oryza sativ
279	7	2.3	178	2	08TCH5	08tch5 homo sapien	352	7	2.3	231	2	08GRN2	08grn2 oryza sativ
280	7	2.3	179	2	07Z7E3	07z7e3 homo sapien	353	7	2.3	231	2	06LFT7	06lft7 photobacter
281	7	2.3	180	2	09ZMF5	09zmf5 oryza sativ	354	7	2.3	233	2	08B100	08b100 chimpanzee
282	7	2.3	180	2	06CMV2	06cmv2 kluveromyc	355	7	2.3	233	2	08PBA5	08pba5 xanthomonas
283	7	2.3	180	2	07Z7E1	07z7e1 homo sapien	356	7	2.3	233	2	06DCP9	06dcp9 xenopus lae
284	7	2.3	182	2	09SE78	09se78 rhizobium l	357	7	2.3	234	2	048418	048418 bacterioph
285	7	2.3	182	2	06K310	06k310 oryza sativ	358	7	2.3	234	2	07Y292	07y292 phage phi 4
286	7	2.3	183	2	08WT05	08wt05 plasmodium	359	7	2.3	236	2	06Z3M7	06z3m7 oryza sativ
287	7	2.3	183	2	08L161	08l161 oryza sativ	360	7	2.3	236	2	07RMS9	07rms9 neurospora
288	7	2.3	184	1	GCHI_AQUAE	066603 aquifex aeo	361	7	2.3	236	2	06YV10	06yv10 oryza sativ
289	7	2.3	184	2	069JZ0	069jz0 oryza sativ	362	7	2.3	237	2	08SBS7	08sbs7 oryza sativ
290	7	2.3	184	2	06YXR8	06yxr8 oryza sativ	363	7	2.3	237	2	07G668	07g668 oryza sativ
291	7	2.3	184	2	08Z0U3	08z0u3 streptomyce	364	7	2.3	238	1	PYRE_COCCIM	093849 coccidioid
292	7	2.3	184	2	0640T0	0640t0 xenopus tro	365	7	2.3	240	2	06Q500	06q500 oryza sativ
293	7	2.3	186	1	ATPD_CYAPA	048082 cyanophora	366	7	2.3	240	2	07X185	07x185 oryza sativ
294	7	2.3	187	2	07R1F5	07r1f5 giardia lam	367	7	2.3	240	2	09LDM2	09ldm2 oryza sativ
295	7	2.3	187	2	09XVX5	09xvx5 caenorhabdi	368	7	2.3	240	2	08ZFC5	08zfc5 streptomyce
296	7	2.3	188	2	069PQ2	069pq2 oryza sativ	369	7	2.3	241	2	08PMU4	08pmu4 xanthomonas
297	7	2.3	188	2	067SY1	067sy1 symbiodacte	370	7	2.3	244	2	08LMA7	08lma7 oryza sativ
298	7	2.3	189	2	09LH28	09lh28 oryza sativ	371	7	2.3	246	1	NPD_DEIRA	09ryd4 deinococcus
299	7	2.3	190	2	06YX18	06yx18 oryza sativ	372	7	2.3	246	2	08ZAC3	08zac3 streptomyce
300	7	2.3	191	2	086D99	086d99 caenorhabdi	373	7	2.3	246	2	06ZYK2	06zyk2 pyrobaculum
301	7	2.3	192	2	07MR58	07mr58 wolfinella s	374	7	2.3	247	2	07PM81	07pm81 anopheles g
302	7	2.3	193	2	084PC6	084pc6 oryza sativ	375	7	2.3	249	1	MSX1_CHICK	028361 gallus gall
303	7	2.3	195	1	INOI_BOVIN	070752 boe laurus	376	7	2.3	250	2	09HFS1	09hfs1 candida alb
304	7	2.3	195	2	P28170	028561 ovis aries	377	7	2.3	252	2	09DMG9	09dmg9 rat cytoleg
305	7	2.3	195	2	028561	028561 ovis aries	378	7	2.3	253	2	084G27	084g27 streptomyce
306	7	2.3	195	2	07MZY7	07mzy7 ovis aries	379	7	2.3	253	2	064N05	064n05 bacteroides
307	7	2.3	195	2	06YSY8	06ysy8 oryza sativ	380	7	2.3	254	2	07XFD3	07xfd3 oryza sativ
308	7	2.3	195	2	08UH52	08uh52 agrobacteri	381	7	2.3	254	2	09AUNI	09aun1 oryza sativ
309	7	2.3	196	2	06KZB9	06kzb9 oryza sativ	382	7	2.3	255	2	06FV64	06fv64 candida gla
310	7	2.3	196	2	08VN19	08vn19 kluvera ci	383	7	2.3	255	2	09N0J3	09n0j3 ovis aries
311	7	2.3	197	1	IE68_HRV2	08v19 human herpe	384	7	2.3	255	2	08L1Z2	08l1z2 streptomyce
312	7	2.3	197	1	PADI_ECOS57	09x028 escherichia	385	7	2.3	256	2	09PEV1	09pev1 neurospora
313	7	2.3	197	2	07XZ04	07xz04 griffithsia	386	7	2.3	258	2	0688E7	0688e7 oryza sativ
314	7	2.3	197	2	09FR80	09fer0 escherichia	387	7	2.3	258	2	06R950	06r950 oryza sativ
315	7	2.3	197	2	083Q85	083qes shigella fl	388	7	2.3	258	2	08XR81	08xr81 ralbtonia b
316	7	2.3	199	2	07JZ15	07jz15 mycobacteri	389	7	2.3	259	2	06ZGS2	06zgs2 oryza sativ
317	7	2.3	200	1	YN02_SHIFL	029771 shigella fl	390	7	2.3	259	2	055780	055780 synechocyst
318	7	2.3	200	2	07XN13	07xn13 oryza sativ	391	7	2.3	259	2	0745X8	0745x8 thermus the
319	7	2.3	200	2	08VNT1	08vnt1 enterobacte	392	7	2.3	260	2	094A09	094a09 arabidopsis
320	7	2.3	200	2	0616A9	0616a9 escherichia	393	7	2.3	261	2	075181	075181 oryza sativ
321	7	2.3	200	2	06YANI	06yani pigmenticpha	394	7	2.3	262	2	07XIV8	07xiv8 oryza sativ
322	7	2.3	202	2	09V760	09v760 drosophila	395	7	2.3	263	2	08SB70	08sb70 oryza sativ
323	7	2.3	203	2	067VR0	067vr0 oryza sativ	396	7	2.3	263	2	06YVG2	06yvg2 oryza sativ

397	2.3	263	2	Q7G6R8	Q7g6e8 oryza sativ	470	7	2.3	314	2	Q6CX46	Q6cx46 kluyveromy
398	7	266	2	Q8S7I0	Q8s7i0 oryza sativ	471	7	2.3	314	2	Q39309	Q39309 brassica na
399	2.3	267	2	Q8XMM6	Q8xmm6 clostridium	472	7	2.3	315	2	Q6ASR7	Q6asr7 oryza sativ
400	7	268	1	FGF5_HUMAN	P12034 homo sapien	473	7	2.3	316	2	Q6ZJ42	Q6zj42 oryza sativ
401	2.3	268	2	Q8NF50	Q8nf50 homo sapien	474	7	2.3	318	2	Q75K64	Q75k64 oryza sativ
402	7	269	2	Q7Y0A3	Q7y0a3 oryza sativ	475	7	2.3	318	2	Q06629	Q06629 mycobacteri
403	2.3	269	2	Q6NHR3	Q6nhr3 corynebacte	476	7	2.3	318	2	Q6A9T1	Q6a9t1 propionibac
404	7	269	2	Q82900	Q829q0 streptomyce	477	7	2.3	318	2	Q7U185	Q7u185 mycobacteri
405	2.3	269	2	Q7EYMS	Q7eyms oryza sativ	478	7	2.3	319	2	Q7PVH4	Q7pvh4 anopheles g
406	7	270	2	Q84U22	Q84uz2 chlamydomon	479	7	2.3	320	2	Q8B6E9	Q8b6e9 streptomyce
407	2.3	270	1	REXA_HUMAN	000287 homo sapien	480	7	2.3	321	2	Q8NKK6	Q8nkk6 staphylococ
408	7	272	1	Q8TC10	Q8tc40 homo sapien	481	7	2.3	322	2	Q8KOR4	Q8kor4 staphylococ
409	2.3	272	2	Q8BAP1	Q8bap1 xanthomonas	482	7	2.3	322	2	Q6GAB1	Q6gab1 staphylococ
410	7	273	2	Q89UX0	Q89ux0 staphylococ	483	7	2.3	322	2	Q6GHV2	Q6ghv2 staphylococ
411	2.3	273	2	Q7A6S1	Q7a6s1 staphylococ	484	7	2.3	323	1	VATC_THETH	P74902 thermus the
412	7	276	2	Q98IB9	Q98ib9 rhizobium 1	485	7	2.3	323	2	Q8LBF8	Q8lbf8 arabidopsis
413	2.3	277	2	Q7RUC6	Q7ruc6 neurospora	486	7	2.3	323	2	Q9SBG3	Q9sbg3 arabidopsis
414	7	282	2	Q82TS3	Q82ts3 nitrosomona	487	7	2.3	323	2	Q9SCU7	Q9scu7 thermus the
415	2.3	278	1	HT22_ARATH	P46604 arabidopsis	488	7	2.3	324	2	Q8GHB2	Q8ghb2 streptomyce
416	7	279	2	Q6CPE1	Q6cppl kluyveromyce	489	7	2.3	324	2	Q8GMP5	Q8gmp5 aeromonas s
417	2.3	279	2	Q8ZSAB	Q8zsa8 streptomyce	490	7	2.3	325	2	Q84PV0	Q84pv0 oryza sativ
418	7	281	2	Q8UEW7	Q8uem7 agrobacteri	491	7	2.3	325	2	Q8NNY3	Q8nny3 corynebacte
419	2.3	281	2	Q8RZG6	Q8rzg6 oryza sativ	492	7	2.3	325	2	Q8NNY3	Q8nny3 prochloroco
420	7	282	2	Q8ZSAB	Q8zsa8 streptomyce	493	7	2.3	325	2	Q7V3Z3	Q7vgq4 halobacteri
421	2.3	282	1	AROE_CORGL	Q9x5c9 corynebacte	494	7	2.3	326	2	Q9HQD4	Q94jg3 oryza sativ
422	7	283	2	Q753B3	Q75b3 aebhya goes	495	7	2.3	326	2	Q94UG3	Q6K7C9 oryza sativ
423	2.3	284	2	Q71S18	Q71s8 gallus gall	496	7	2.3	327	2	Q6M413	Q6m413 corynebacte
424	7	285	2	Q82FB6	Q82fb6 streptomyce	497	7	2.3	327	2	Q73K65	Q73k65 treponema d
425	2.3	286	2	Q72JZ7	Q72jz7 thermus the	498	7	2.3	327	2	Q7XR65	Q7xr65 oryza sativ
426	7	287	2	Q6ZBE4	Q6zbe4 oryza sativ	499	7	2.3	328	2	Q7XR65	Q6eyt3 anabaena sp
427	2.3	289	2	Q7EYB7	Q7eyb7 oryza sativ	500	7	2.3	328	2	Q6SEB4	Q8y174 human immun
428	7	291	2	Q6ZFR8	Q6zfr8 oryza sativ	501	7	2.3	329	2	Q8Y174	Q911b6 arabidopsis
429	2.3	291	2	Q6ZFT1	Q6zft1 oryza sativ	502	7	2.3	330	2	Q8Q174	Q911b6 arabidopsis
430	7	292	2	Q94H41	Q94h41 oryza sativ	503	7	2.3	330	2	Q9L1H6	Q881j4 pseudomonas
431	2.3	293	2	Q7U8M8	Q7u8m8 synechococc	504	7	2.3	331	2	Q8B0T4	Q8b0t4 erwinia car
432	7	293	2	Q6WV7	Q6wv7 human immun	505	7	2.3	331	2	Q6D899	Q6d899 erwinia car
433	2.3	294	2	Q93HV7	Q93hv7 arthrobacte	506	7	2.3	331	2	Q91W20	Q91w20 mus musculu
434	7	294	2	Q7ZGT7	Q7zgt7 thermus the	507	7	2.3	332	2	Q6U922	Q6u922 human immun
435	2.3	294	2	Q80V25	Q80v25 mus musculu	508	7	2.3	332	2	Q6U9A0	Q6u9a0 human immun
436	7	294	2	Q918A3	Q918a3 xenopus lae	509	7	2.3	332	2	Q7ZLD6	Q7zld6 human immun
437	2.3	295	1	U966_HUMAN	Q918a3 xenopus lae	510	7	2.3	332	2	Q7ZLD7	Q7zld7 human immun
438	7	295	1	U966_MOUSE	Q6w14 homo sapien	511	7	2.3	332	2	Q7ZLD8	Q7zld8 human immun
439	2.3	295	2	Q8XKS7	Q8xks7 mus musculu	512	7	2.3	332	2	Q7ZLD9	Q7zld9 human immun
440	7	296	1	MURB_CHLNU	Q8xks7 rhlamdia s	513	7	2.3	332	2	Q7ZLE1	Q7zle1 human immun
441	2.3	296	1	Q8UGF8	Q8ugp8 agrobacteri	514	7	2.3	332	2	Q7ZLE2	Q7zle2 human immun
442	7	297	2	Q23263	Q23263 caenorhabdi	515	7	2.3	332	2	Q7ZLE3	Q7zle3 human immun
443	2.3	298	2	Q9CS83	Q9cs83 mus musculu	516	7	2.3	332	2	Q6P7C4	Q6p7c4 rictus norv
444	7	299	1	HEY1_MOUSE	Q9wv93 mus musculu	517	7	2.3	334	2	Q93642	Q93642 caenorhabdi
445	2.3	299	2	Q9LNT8	Q9lnz8 arabidopsis	518	7	2.3	336	2	Q8LFW6	Q8lfw6 gloeobacter
446	7	299	2	Q9DOR0	Q9d0r0 mus musculu	519	7	2.3	336	2	Q7NHHX	Q9jfd5 human immun
447	2.3	299	2	Q9QUM5	Q9qum5 m basic-hel	520	7	2.3	336	2	Q90JD5	Q6cw65 oryza sativ
448	7	300	2	Q66KK8	Q66kk8 xenopus tro	521	7	2.3	336	2	Q6ZCW6	Q6zcm6 oryza sativ
449	2.3	301	2	P74823	P74823 sphingomona	522	7	2.3	337	2	Q6ZCW6	Q6zcm6 oryza sativ
450	7	301	2	Q92NXX1	Q92nxx1 rhizobium m	523	7	2.3	337	2	Q6ZCW6	Q6zcm6 oryza sativ
451	2.3	301	2	Q88GP9	Q88gp9 pseudomonas	524	7	2.3	338	2	Q67K15	Q67k15 symbiodacte
452	7	302	2	Q84O12	Q84o12 pseudomonas	525	7	2.3	338	2	Q741W6	Q741w6 mycobacteri
453	2.3	303	2	Q759J3	Q759j3 aebhya goes	526	7	2.3	340	1	ERB3_HUMAN	Q15768 homo sapien
454	7	304	1	HEY1_CANFA	Q9e22 canis famil	527	7	2.3	340	1	Q98ZFP9	Q98zfp9 human immun
455	2.3	304	1	HEY1_HUMAN	Q9y5j3 homo sapien	528	7	2.3	340	2	Q7SMX0	Q7smx0 human immun
456	7	304	2	Q66PR6	Q66pr6 homo sapien	529	7	2.3	342	2	Q8RZ07	Q8rz07 oryza sativ
457	2.3	304	2	Q76018	Q76018 bos taurus	530	7	2.3	343	2	Q90J97	Q90j97 human immun
461	7	306	2	Q7NMG2	Q7nmg2 chromobacte	531	7	2.3	343	2	Q88YC7	Q88yc7 human immun
462	2.3	307	2	Q6K1Z4	Q6k1z4 oryza sativ	532	7	2.3	343	2	Q98YK7	Q98yk7 human immun
463	7	308	2	Q8NMM2	Q8nmm2 homo sapien	533	7	2.3	346	1	HM22_CAEEL	P41936 caenorhabdi
464	2.3	310	2	Q8SXX4	Q8sxx4 dirosophila	534	7	2.3	347	2	Q985B8	Q985b8 deinococcus
465	7	310	2	Q8ZCNS	Q8zcn3 streptomyce	535	7	2.3	347	2	Q904G5	Q904g5 human immun
466	2.3	311	2	Q8LNR3	Q8lnr3 oryza sativ	536	7	2.3	350	2	Q73MH1	Q73mh1 treponema d
467	7	312	2	Q62KE6	Q62ke6 burkholderi	537	7	2.3	350	2	Q8R5E6	Q8r5e6 mus musculu
468	2.3	312	2	Q63U79	Q63u79 burkholderi	538	7	2.3	353	2	Q845Y3	Q845y3 oryza sativ
469	7	313	2	Q6S6P3	Q6sep3 human immun	541	7	2.3	353	2	Q7NLE8	Q7nle8 gloeobacter
						542	7	2.3	354	2	Q90K81	Q90k81 human immun

543	7	2.3	355	2	Q9W311	Q9W311 drosophila	616	7	2.3	402	2	Q90F42	Q90F42 human immun
544	7	2.3	355	2	Q8KY5	Q8KY5 ruegeria sp	617	7	2.3	402	2	Q90I39	Q90I39 human immun
545	7	2.3	355	2	Q6KMG9	Q6KMG9 bacillus st	618	7	2.3	402	2	Q90IS5	Q90IS5 human immun
546	7	2.3	355	2	Q90L28	Q90L28 human immun	619	7	2.3	403	2	Q8ZSL7	Q8ZSL7 pyrobaculum
547	7	2.3	356	2	Q8H5D9	Q8H5D9 oryza sativ	620	7	2.3	403	2	Q7W717	Q7W717 bordetella
548	7	2.3	357	2	Q73W61	Q73W61 mycobacteri	621	7	2.3	403	2	Q7WIS4	Q7WIS4 bordetella
549	7	2.3	358	2	Q8GLP0	Q8GLP0 aeromonas h	622	7	2.3	404	2	Q96B18	Q96B18 homo sapien
550	7	2.3	358	2	Q8Z2L6	Q8Z2L6 enterococcu	623	7	2.3	405	2	Q7PYD4	Q7PYD4 anophelis g
551	7	2.3	359	2	Q9LUF4	Q9LUF4 arabidopsis	624	7	2.3	405	2	Q8HY80	Q8HY80 tupia glis
552	7	2.3	359	2	Q8ZG42	Q8ZG42 streptomyce	625	7	2.3	406	2	Q7NE93	Q7NE93 gloobacter
553	7	2.3	360	2	Q7S896	Q7S896 neuropsora	626	7	2.3	408	2	Q8JAP2	Q8JAP2 coxiella bu
554	7	2.3	360	2	Q8LMA1	Q8LMA1 oryza sativ	627	7	2.3	410	2	Q8ZCDO	Q8ZCDO streptomyce
555	7	2.3	360	2	Q7NR53	Q7NR53 chromobacte	628	7	2.3	412	2	Q20873	Q20873 caenorhabdi
556	7	2.3	360	2	Q89QF5	Q89QF5 bradyrhizob	629	7	2.3	412	2	Q6APF4	Q6APF4 leifsonia x
557	7	2.3	364	2	Q69Y83	Q69Y83 oryza sativ	630	7	2.3	413	2	Q9J1L1	Q9J1L1 arabidopsis
558	7	2.3	366	2	Q9JW11	Q9JW11 neisseria m	631	7	2.3	413	2	Q6H700	Q6H700 propionibac
559	7	2.3	366	2	Q9JXFB	Q9JXFB neisseria m	632	7	2.3	413	2	P89474	P89474 human hepe
560	7	2.3	367	2	Q90GF8	Q90GF8 mus musculi	633	7	2.3	414	1	SPYA_CALTA	SPYA_CALTA calithrix
561	7	2.3	368	2	Q8KJL2	Q8KJL2 mus musculi	634	7	2.3	414	2	Q44542	Q44542 caenorhabdi
562	7	2.3	369	2	Q8N8M0	Q8N8M0 homo sapien	635	7	2.3	414	2	Q70XK9	Q70XK9 gordonia we
563	7	2.3	371	2	Q39308	Q39308 braesica na	636	7	2.3	416	1	ELT1_CAEEL	ELT1_CAEEL
564	7	2.3	371	2	Q90IM4	Q90IM4 human immun	637	7	2.3	416	2	Q8CNE9	Q8CNE9 staphylococ
565	7	2.3	372	2	Q982M2	Q982M2 rhizobium l	638	7	2.3	417	2	Q7SV42	Q7SV42 physcomitre
566	7	2.3	373	2	Q6MCV4	Q6MCV4 paracchlamyd	639	7	2.3	418	1	THBG_MOUSE	THBG_MOUSE
567	7	2.3	374	2	Q9SFB3	Q9SFB3 arabidopsis	640	7	2.3	418	1	THBG_RAT	THBG_RAT
568	7	2.3	375	2	Q55851	Q55851 synechocyst	641	7	2.3	418	2	Q9QX71	Q9QX71
569	7	2.3	375	2	Q72H86	Q72H86 thermus the	642	7	2.3	420	2	Q9QX71	Q9QX71
570	7	2.3	375	2	Q98ZJ4	Q98ZJ4 human immun	643	7	2.3	421	2	Q9RQ37	Q9RQ37 staphylococ
571	7	2.3	378	2	Q7NM19	Q7NM19 chromobacte	644	7	2.3	421	2	Q70007	Q70007 streptomyce
572	7	2.3	378	2	Q8D501	Q8D501 vibrio vuln	645	7	2.3	421	2	Q8NVAS	Q8NVAS staphylococ
573	7	2.3	378	2	Q90JY4	Q90JY4 human immun	646	7	2.3	421	2	Q7A2M4	Q7A2M4 staphylococ
574	7	2.3	381	2	Q52563	Q52563 amycolatops	647	7	2.3	421	2	Q7A447	Q7A447 staphylococ
575	7	2.3	381	2	Q90J53	Q90J53 human immun	648	7	2.3	421	2	Q9X4D7	Q9X4D7 staphylococ
576	7	2.3	382	2	Q8S0V8	Q8S0V8 oryza sativ	649	7	2.3	421	2	Q6G760	Q6G760 staphylococ
577	7	2.3	382	2	Q9HXJ9	Q9HXJ9 pseudomonas	650	7	2.3	421	2	Q6GEH2	Q6GEH2 staphylococ
578	7	2.3	383	1	G1C2_YEAST	G1C2_YEAST saccharomyc	651	7	2.3	422	2	Q67J17	Q67J17 oryza sativ
579	7	2.3	384	1	R1R2_SPIRO	R1R2_SPIRO spilaula sol	652	7	2.3	423	1	PYRX_PSEAB	PYRX_PSEAB
580	7	2.3	384	1	Y039_MYCPN	Y039_MYCPN mycoplasma	653	7	2.3	423	2	Q8AH86	Q8AH86 human immun
581	7	2.3	384	2	Q7NBE2	Q7NBE2 photorhabdu	654	7	2.3	423	2	Q8AH83	Q8AH83 human immun
582	7	2.3	385	2	Q8RSC4	Q8RSC4 corynebacte	655	7	2.3	423	2	Q8AH11	Q8AH11 human immun
583	7	2.3	385	2	Q90GH4	Q90GH4 human immun	656	7	2.3	423	2	Q8AH17	Q8AH17 human immun
584	7	2.3	385	2	Q90J16	Q90J16 human immun	657	7	2.3	423	2	Q8AH18	Q8AH18 human immun
585	7	2.3	386	2	Q62003	Q62003 branchiosto	658	7	2.3	423	2	Q8AHM1	Q8AHM1 human immun
586	7	2.3	386	2	Q88G90	Q88G90 pseudomonas	659	7	2.3	423	2	Q8AHM9	Q8AHM9 human immun
587	7	2.3	387	1	YR24_CAEEL	YR24_CAEEL caenorhabdi	660	7	2.3	426	2	Q6BX74	Q6BX74 debaryomyce
588	7	2.3	387	2	Q6F8N5	Q6F8N5 acinetobact	661	7	2.3	427	2	Q7J269	Q7J269 mycobacteri
589	7	2.3	387	2	Q838Y6	Q838Y6 enterococcu	662	7	2.3	428	2	Q6X895	Q6X895 gallus gall
590	7	2.3	388	2	Q8XVY1	Q8XVY1 ralistonia s	663	7	2.3	430	2	Q67T20	Q67T20 syphilobacte
591	7	2.3	390	2	Q8AHM4	Q8AHM4 human immun	664	7	2.3	432	2	Q21857	Q21857 caenorhabdi
592	7	2.3	390	2	Q987E4	Q987E4 rhizobium l	665	7	2.3	432	2	Q8UBES	Q8UBES agrobacteri
593	7	2.3	391	2	Q7W043	Q7W043 bordetella	666	7	2.3	432	2	Q7UGK8	Q7UGK8 rhodopirell
594	7	2.3	392	2	Q01479	Q01479 caenorhabdi	667	7	2.3	432	2	Q7W3U8	Q7W3U8 bordetella
595	7	2.3	392	2	Q7R7J1	Q7R7J1 plasmodium	668	7	2.3	433	2	Q7WF78	Q7WF78 bordetella
596	7	2.3	394	2	Q80MJ7	Q80MJ7 human immun	669	7	2.3	433	2	Q87A55	Q87A55 xyella fas
597	7	2.3	394	2	Q90K14	Q90K14 human immun	670	7	2.3	433	2	Q9PAB9	Q9PAB9 xyella fas
598	7	2.3	396	2	Q59354	Q59354 pyrococcus	671	7	2.3	433	2	Q8AXK6	Q8AXK6 xenopus lae
599	7	2.3	396	2	Q9SDD5	Q9SDD5 oryza sativ	672	7	2.3	434	2	Q6VUAS	Q6VUAS uncultured
600	7	2.3	396	2	Q88P50	Q88P50 pseudomonas	673	7	2.3	434	2	Q648Y7	Q648Y7 uncultured
601	7	2.3	397	2	Q6AM78	Q6AM78 oryza sativ	674	7	2.3	434	2	Q64BJ1	Q64BJ1 uncultured
602	7	2.3	397	2	Q766V3	Q766V3 oryza sativ	675	7	2.3	434	2	Q6TPS1	Q6TPS1 human immun
603	7	2.3	397	2	Q7VSJ3	Q7VSJ3 bordetella	676	7	2.3	434	2	Q6TPS6	Q6TPS6 human immun
604	7	2.3	397	2	Q7W464	Q7W464 bordetella	677	7	2.3	435	1	Y0D7_CAEEL	Y0D7_CAEEL
605	7	2.3	397	2	Q7WFM1	Q7WFM1 bordetella	678	7	2.3	437	2	Q7CYG9	Q7CYG9 agrobacteri
606	7	2.3	398	2	Q90JK9	Q90JK9 human immun	679	7	2.3	437	2	Q81Z14	Q81Z14 nitrosomona
607	7	2.3	398	2	Q6AFD2	Q6AFD2 leifsonia x	680	7	2.3	437	2	Q8G6T2	Q8G6T2 bifidobacte
608	7	2.3	399	2	Q90HC8	Q90HC8 human immun	681	7	2.3	438	2	Q87856	Q87856 streptomyce
609	7	2.3	401	2	Q8NDP0	Q8NDP0 homo sapien	682	7	2.3	438	2	Q7VVB7	Q7VVB7 bordetella
610	7	2.3	401	2	Q95Q88	Q95Q88 caenorhabdi	683	7	2.3	443	2	Q804T6	Q804T6 brachydantio
611	7	2.3	401	2	Q9S221	Q9S221 streptomyce	684	7	2.3	444	1	TIG_AZOB	TIG_AZOB
612	7	2.3	401	2	Q90HP5	Q90HP5 human immun	685	7	2.3	445	1	TRX6_HUMAN	TRX6_HUMAN
613	7	2.3	401	2	Q90IB8	Q90IB8 human immun	686	7	2.3	445	2	Q7XHS6	Q7XHS6 oryza sativ
614	7	2.3	402	2	Q7S182	Q7S182 oryza sativ	687	7	2.3	446	2	Q69KW1	Q69KW1 oryza sativ
615	7	2.3	402	2	Q9ZVP2	Q9ZVP2 rhizobium m	688	7	2.3	446	2	Q69885	Q69885 streptomyce

689	7	2.3	447	2	Q72L17	Q72L17	thermus the
690	7	2.3	447	2	Q82EH0	Q82EH0	streptomyce
691	7	2.3	447	2	Q9X7Z6	Q9X7Z6	streptomyce
692	7	2.3	448	2	Q63KQ9	Q63KQ9	burkholderi
693	7	2.3	448	2	Q88XM9	Q88XM9	lactobacilli
694	7	2.3	449	2	Q72G82	Q72G82	thermus the
695	7	2.3	449	2	Q82A36	Q82A36	streptomyce
696	7	2.3	449	2	Q9A3Q1	Q9A3Q1	caulobacter
697	7	2.3	450	2	Q7W6X6	Q7W6X6	bordetella
698	7	2.3	450	2	Q7W1Y3	Q7W1Y3	bordetella
699	7	2.3	450	2	Q9ZL68	Q9ZL68	helicobacte
700	7	2.3	451	2	Q62EH4	Q62EH4	burkholderi
701	7	2.3	451	2	Q63P97	Q63P97	burkholderi
702	7	2.3	455	1	A2AC_CAVPO	A2AC_CAVPO	cavia porce
703	7	2.3	456	1	Q9CL30	Q9CL30	pasteurella
704	7	2.3	458	1	A2AC_MOUSE	A2AC_MOUSE	mus musculi
705	7	2.3	458	1	A2AC_RAT	A2AC_RAT	rattus norv
706	7	2.3	459	1	Q61OZ2	Q61OZ2	placophilus
707	7	2.3	461	2	Q82GP7	Q82GP7	streptomyce
708	7	2.3	461	2	Q9K3U6	Q9K3U6	streptomyce
709	7	2.3	462	1	A2AC_HUMAN	A2AC_HUMAN	homo sapien
710	7	2.3	464	1	IFE_BRALA	IFE_BRALA	branchiosto
711	7	2.3	465	2	Q94692	Q94692	schizosacch
712	7	2.3	465	2	Q81VS1	Q81VS1	homo sapien
713	7	2.3	465	2	Q9H7X1	Q9H7X1	homo sapien
714	7	2.3	466	2	Q9H3U5	Q9H3U5	homo sapien
715	7	2.3	466	2	Q84ZB8	Q84ZB8	oryza sativ
716	7	2.3	467	1	CLCA_VIBPA	CLCA_VIBPA	vibriol para
717	7	2.3	467	1	CLCA_VIBVU	CLCA_VIBVU	vibriol vuln
718	7	2.3	467	1	CLCA_VIBVU	CLCA_VIBVU	vibriol vuln
719	7	2.3	467	2	Q727H1	Q727H1	desulfovibr
720	7	2.3	468	1	CLCA_VIBCH	CLCA_VIBCH	vibriol chol
721	7	2.3	468	1	Q9NL06	Q9NL06	epitactreus
722	7	2.3	469	1	FXGA_HUMAN	FXGA_HUMAN	homo sapien
723	7	2.3	469	2	Q6A613	Q6A613	propionibac
724	7	2.3	469	2	Q7DD55	Q7DD55	neisseria m
725	7	2.3	469	2	Q9JRK0	Q9JRK0	neisseria m
726	7	2.3	470	2	Q8TW17	Q8TW17	methanopyru
727	7	2.3	470	2	Q7W7F2	Q7W7F2	bordetella
728	7	2.3	471	2	Q80TE3	Q80TE3	mus musculi
729	7	2.3	474	2	Q92ZJ7	Q92ZJ7	rhizobium m
730	7	2.3	475	2	Q9L094	Q9L094	streptomyce
731	7	2.3	477	2	Q9RGW9	Q9RGW9	arabidopsis
732	7	2.3	479	2	Q9GSU8	Q9GSU8	homo sapien
733	7	2.3	479	2	Q8LS17	Q8LS17	chlamydomon
734	7	2.3	482	2	Q7S0U9	Q7S0U9	neutrospora
735	7	2.3	484	2	Q9KYG5	Q9KYG5	streptomyce
736	7	2.3	485	2	Q73VA2	Q73VA2	mycobacteri
737	7	2.3	485	2	Q7ND75	Q7ND75	gloeobacter
738	7	2.3	486	2	Q94815	Q94815	oryza sativ
739	7	2.3	486	2	Q7XEU8	Q7XEU8	oryza sativ
740	7	2.3	488	2	Q9N9Z2	Q9N9Z2	dirosophila
741	7	2.3	489	2	Q7SEW1	Q7SEW1	ashbya gosb
742	7	2.3	489	2	Q72GQ1	Q72GQ1	desulfovibr
743	7	2.3	489	2	Q88988	Q88988	murid herpe
744	7	2.3	490	2	Q941W5	Q941W5	oryza sativ
745	7	2.3	490	2	P95098	P95098	mycobacteri
746	7	2.3	490	2	Q7TXC5	Q7TXC5	mycobacteri
747	7	2.3	491	2	P94289	P94289	bacillus ci
748	7	2.3	492	2	Q6A329	Q6A329	arabidopsis
749	7	2.3	493	2	Q7O2S8	Q7O2S8	anopheles g
750	7	2.3	496	2	Q91TMO	Q91TMO	tupaiaid her
751	7	2.3	497	2	Q87BA2	Q87BA2	xylella fas
752	7	2.3	497	2	Q9PEA3	Q9PEA3	xylella fas
753	7	2.3	499	2	Q82QV9	Q82QV9	streptomyce
754	7	2.3	499	2	Q88GH8	Q88GH8	pseudomonas
755	7	2.3	499	2	Q67C63	Q67C63	human immun
756	7	2.3	499	2	Q67C83	Q67C83	human immun
757	7	2.3	499	2	Q67C95	Q67C95	human immun
758	7	2.3	499	2	Q67CE7	Q67CE7	human immun
759	7	2.3	499	2	Q67CG3	Q67CG3	human immun
760	7	2.3	499	2	Q67C10	Q67C10	human immun
761	7	2.3	499	2	Q67C14	Q67C14	human immun
762	7	2.3	499	2	Q67CT2	Q67CT2	human immun
763	7	2.3	499	2	Q67CV4	Q67CV4	human immun
764	7	2.3	499	2	Q67DB6	Q67DB6	human immun
765	7	2.3	499	2	Q67DB6	Q67DB6	human immun
766	7	2.3	499	2	Q67DC6	Q67DC6	human immun
767	7	2.3	499	2	Q67D12	Q67D12	human immun
768	7	2.3	499	2	Q67D16	Q67D16	human immun
769	7	2.3	499	2	Q67D35	Q67D35	human immun
770	7	2.3	499	2	Q67DN2	Q67DN2	human immun
771	7	2.3	500	2	Q7URV7	Q7URV7	rhodospirilli
772	7	2.3	500	2	Q99KX9	Q99KX9	mus musculi
773	7	2.3	506	2	Q82Z84	Q82Z84	chlamydomon
774	7	2.3	507	2	Q69Z54	Q69Z54	mus musculi
775	7	2.3	508	1	CPT7_HORSE	CPT7_HORSE	equus cabal
776	7	2.3	510	2	Q8VJ78	Q8VJ78	mycobacteri
777	7	2.3	511	2	Q9V8Z9	Q9V8Z9	dirosophila
778	7	2.3	513	2	Q92M58	Q92M58	rhizobium m
779	7	2.3	514	2	Q7XED6	Q7XED6	oryza sativ
780	7	2.3	515	2	Q84HH8	Q84HH8	azarcus ev
781	7	2.3	515	2	Q62FQ6	Q62FQ6	burkholderi
782	7	2.3	515	2	Q63PJ0	Q63PJ0	burkholderi
783	7	2.3	516	2	Q8W080	Q8W080	oryza sativ
784	7	2.3	518	2	Q6PD24	Q6PD24	mus musculi
785	7	2.3	522	1	GUAA_XYLEA	GUAA_XYLEA	xylella fas
786	7	2.3	522	1	GUAA_XYLFT	GUAA_XYLFT	xylella fas
787	7	2.3	522	2	Q6V0D0	Q6V0D0	homo sapien
788	7	2.3	524	2	Q87V45	Q87V45	macaca fasc
789	7	2.3	524	2	Q87V45	Q87V45	pseudomonas
790	7	2.3	524	2	Q8K012	Q8K012	mus musculi
791	7	2.3	525	1	ALGG_AZQVI	ALGG_AZQVI	azotobacter
792	7	2.3	525	2	Q748H0	Q748H0	geobacter s
793	7	2.3	527	2	Q9SAB5	Q9SAB5	arabidopsis
794	7	2.3	528	2	Q96TW5	Q96TW5	hanseniella a
795	7	2.3	528	2	Q9FMW0	Q9FMW0	arabidopsis
796	7	2.3	529	2	Q7Q299	Q7Q299	anopheles g
797	7	2.3	529	2	Q31001	Q31001	thermus the
798	7	2.3	533	1	RP65_AMERT	RP65_AMERT	ambystoma t
799	7	2.3	533	2	Q6EBG1	Q6EBG1	lupinus alb
800	7	2.3	538	2	Q9LSB3	Q9LSB3	arabidopsis
801	7	2.3	542	2	Q6NNU8	Q6NNU8	dirosophila
802	7	2.3	542	2	Q93YR0	Q93YR0	arabidopsis
803	7	2.3	543	2	Q6DJU4	Q6DJU4	homo sapien
804	7	2.3	543	2	Q8W3B4	Q8W3B4	oryza sativ
805	7	2.3	545	2	Q75M59	Q75M59	oryza sativ
806	7	2.3	545	2	Q9AJR4	Q9AJR4	streptomyce
807	7	2.3	550	2	Q73YZ0	Q73YZ0	mycobacteri
808	7	2.3	551	2	Q6AUP1	Q6AUP1	oryza sativ
809	7	2.3	551	2	Q87AL4	Q87AL4	xylella fas
810	7	2.3	552	2	Q9NPZ7	Q9NPZ7	homo sapien
811	7	2.3	553	2	Q7VVK5	Q7VVK5	bordetella
812	7	2.3	553	2	Q7WS12	Q7WS12	bordetella
813	7	2.3	553	2	Q7W512	Q7W512	bordetella
814	7	2.3	554	2	Q9UHY0	Q9UHY0	homo sapien
815	7	2.3	557	2	Q70Q44	Q70Q44	xenopus lae
816	7	2.3	558	2	Q6NN42	Q6NN42	dirosophila
817	7	2.3	558	2	Q8KDW0	Q8KDW0	chlorobium
818	7	2.3	560	2	Q6ZMF6	Q6ZMF6	burkholderi
819	7	2.3	560	1	KCVL_HUMAN	KCVL_HUMAN	homo sapien
820	7	2.3	566	2	Q81XM4	Q81XM4	homo sapien
821	7	2.3	566	2	Q6GC11	Q6GC11	mint vein b
822	7	2.3	567	2	Q6PSX0	Q6PSX0	homo sapien
823	7	2.3	568	2	Q91DD4	Q91DD4	oryza sativ
824	7	2.3	568	2	Q8PC69	Q8PC69	xanthomonas
825	7	2.3	568	2	Q8CMS2	Q8CMS2	stephylococ
826	7	2.3	576	2	Q9XA04	Q9XA04	streptomyce
827	7	2.3	578	2	Q6SKZ4	Q6SKZ4	arabidopsis
828	7	2.3	578	2	Q65KX2	Q65KX2	arabidopsis
829	7	2.3	581	2	Q6C8A4	Q6C8A4	yarrowia li
830	7	2.3	581	2	Q6CXV1	Q6CXV1	oryza sativ
831	7	2.3	583	2	Q9G414	Q9G414	murid herpe
832	7	2.3	584	2	Q92YK4	Q92YK4	rhizobium m
833	7	2.3	584	2	Q8VDS0	Q8VDS0	mus musculi
834	7	2.3	584	2	Q8VDS0	Q8VDS0	mus musculi

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835	7	2.3	586	2	06AW05	06aw05 caenorhabdi	908	7	2.3	719	2	06CSE9	06cse9 kluyveromyc
836	7	2.3	587	2	06Z132	06z132 oryza sativ	909	7	2.3	726	2	06RJUK	06rj1k streptomyce
837	7	2.3	586	2	07MH84	07mh84 vibrio vuln	910	7	2.3	727	1	05S21_HUMAN	05smu7 homo sapien
838	7	2.3	587	2	08DCJ4	08dcj4 vibrio vuln	911	7	2.3	727	2	08Z0N2	08z0n2 anabaena sp
839	7	2.3	588	2	09UYN4	09uyn4 pyrococcus	912	7	2.3	730	2	08KN10	08kn10 streptomyce
840	7	2.3	590	2	091VM4	091vm4 mus musculu	913	7	2.3	731	2	06MXX5	06mxx5 mycobacteri
841	7	2.3	591	2	0942N2	0942n2 oryza sativ	914	7	2.3	734	1	ZN42_HUMAN	PN2698 homo sapien
842	7	2.3	593	2	09D114	09d114 human immun	915	7	2.3	734	2	0872N8	0872n8 neurospora
843	7	2.3	594	2	09R1M6	09r1m6 arabidopsi	916	7	2.3	734	2	096171	096171 homo sapien
844	7	2.3	597	2	028610	028610 oryctolagus	917	7	2.3	738	1	SS21_RAT	096171 homo sapien
845	7	2.3	597	2	06R4Q5	06r4q5 bos taurus	918	7	2.3	741	1	08BG19	08bg19 rattus norv
846	7	2.3	598	2	06X244	06x244 bovine herp	919	7	2.3	742	2	06P9B2	06p9b2 homo sapien
847	7	2.3	599	2	06ZVU6	06zvuv6 homo sapien	920	7	2.3	742	2	023766	023766 chironomus
848	7	2.3	605	1	MUTL_RHIME	092tp4 rhizobium m	921	7	2.3	743	2	091Y12	091y12 ephydratia f
849	7	2.3	605	2	097M69	097m69 clostridium	922	7	2.3	745	2	06Z1Z5	06z1z5 oryza sativ
850	7	2.3	605	2	08AMX2	08amx2 streptomyce	923	7	2.3	746	1	PPK_STRCO	09zvz6 streptomyce
851	7	2.3	607	2	025379	025379 xenopus lae	924	7	2.3	748	2	044416	044416 chironomus
852	7	2.3	609	2	070Q63	070q63 xenopus lae	925	7	2.3	749	2	072SP6	072sp6 leptospira
853	7	2.3	611	2	098767	098767 oryza sativ	926	7	2.3	749	2	07TKK6	07tkw6 mycobacteri
854	7	2.3	612	2	088B55	088b55 oryza sativ	927	7	2.3	749	2	08F2V5	08f2v5 leptospira
855	7	2.3	612	2	07XRF5	07xrf5 oryza sativ	928	7	2.3	750	1	PRNG_MYCBO	PN5729 mycobacteri
856	7	2.3	616	2	09PCM5	09pcm5 xylella fas	929	7	2.3	750	1	PRNG_MYCTU	PN5728 mycobacteri
857	7	2.3	617	2	06GQH3	06gqh3 xenopus lae	930	7	2.3	754	2	0873B6	0873b6 neurospora
858	7	2.3	618	2	08B764	08b764 xanthomonas	931	7	2.3	761	1	VPA_BPP2	006419 bacterioph
859	7	2.3	619	2	081VM8	081vm8 homo sapien	932	7	2.3	761	2	07Y4B8	07y4b8 bacterioph
860	7	2.3	620	2	0919A7	0919a7 xenopus lae	933	7	2.3	761	2	0858T4	0858t4 bacterioph
861	7	2.3	621	2	067RMO	067rmo symbiobacte	934	7	2.3	763	2	092239	092239 mus musculu
862	7	2.3	621	2	08C4D2	08c4d2 mus musculu	935	7	2.3	769	2	08G6I8	08g6i8 blitidobacte
863	7	2.3	623	2	06Z707	06z707 oryza sativ	936	7	2.3	770	2	065Z19	065z19 chlamydomon
864	7	2.3	625	2	06CEM7	06cem7 yarrowia li	937	7	2.3	775	2	06K393	06k393 oryza sativ
865	7	2.3	626	2	06AN34	06an34 bacterioides	938	7	2.3	775	2	08VJ15	08vj15 mycobacteri
866	7	2.3	637	2	049524	049524 arabidopsi	939	7	2.3	780	2	070V27	070v27 giardia lam
867	7	2.3	642	2	0817S5	0817s5 arabidopsi	940	7	2.3	784	2	08ZG39	08zg39 streptomyce
868	7	2.3	642	2	088MH1	088mh1 bradyrhizob	941	7	2.3	786	2	06CJ37	06cj37 kluyveromyc
869	7	2.3	643	2	028603	028603 archaeoglob	942	7	2.3	790	2	06BXG7	06bxg7 debaryomyc
870	7	2.3	644	2	059116	059116 archaeoglob	943	7	2.3	792	2	07WJ82	07wj82 bordetella
871	7	2.3	645	2	06FMS2	06fms2 candida gla	944	7	2.3	792	2	0754U5	0754u5 ashyba goos
872	7	2.3	648	2	031644	031644 bacillus su	945	7	2.3	795	2	095U02	095u02 toxoplasma
873	7	2.3	650	2	091ZJ4	091zj4 arabidopsi	946	7	2.3	795	2	06EU01	06euq1 oryza sativ
874	7	2.3	651	2	06MTX4	06mtx4 mycoplasma	947	7	2.3	797	2	06QPH3	06qph3 simian aden
875	7	2.3	659	2	098R52	098r52 mycoplasma	948	7	2.3	800	2	07QAL5	07qal5 anopheles g
876	7	2.3	664	2	0885F7	0885f7 oryza sativ	949	7	2.3	800	2	06QPD7	06qpd7 simian aden
877	7	2.3	664	2	07XG58	07xg58 oryza sativ	950	7	2.3	801	2	06QPA1	06qpai simian aden
878	7	2.3	665	2	0757A0	0757a0 ashyba goos	951	7	2.3	802	2	08ZJVS	08zjvs salmonella
879	7	2.3	668	2	08B6N7	08b6n7 xanthomonas	952	7	2.3	803	2	06FV15	06fv15 candida gla
880	7	2.3	671	1	HMOC_DROME	P22810 dirosophila	953	7	2.3	803	2	09ULK9	09ulk9 homo sapien
881	7	2.3	673	1	0661J3	0661j3 xenopus tro	954	7	2.3	809	2	033339	033339 cryphonectr
882	7	2.3	674	2	091Z86	091z86 arabidopsi	955	7	2.3	810	2	08ZK60	08zk60 streptomyce
883	7	2.3	674	2	08BH21	08bh21 xanthomonas	956	7	2.3	812	2	08NOM6	08nom6 homo sapien
884	7	2.3	676	2	08BZ20	08bz20 mus musculu	957	7	2.3	813	1	AD33_HUMAN	09bz11 homo sapien
885	7	2.3	678	2	08YDT1	08ydt1 mus musculu	958	7	2.3	813	2	094LD6	094ld6 oryza sativ
886	7	2.3	680	2	08QLM5	08qlm5 mamestra co	959	7	2.3	813	2	08C9X6	08c9x6 mus musculu
887	7	2.3	680	2	071AK2	071ak2 mamestra co	960	7	2.3	818	2	093H51	093h51 streptomyce
888	7	2.3	681	2	08SQX1	08sqx1 encephalito	961	7	2.3	821	2	06AT74	06at74 oryza sativ
889	7	2.3	683	2	07XS06	07xs06 oryza sativ	962	7	2.3	823	2	067IU6	067iuv6 oryza sativ
890	7	2.3	685	2	08BGU9	08bgu9 m mus muscu	963	7	2.3	835	1	AXN1_BRABE	PN5094 brachydantio
891	7	2.3	685	2	08BZM1	08bz21 mus musculu	964	7	2.3	841	1	NEK4_HUMAN	PN1957 homo sapien
892	7	2.3	687	2	09KFP3	09kfp3 streptomyce	965	7	2.3	842	2	09C2C8	09c2c8 neurospora
893	7	2.3	690	2	09HG51	09hg51 aspergillus	966	7	2.3	844	2	082RNL	082rnl streptomyce
894	7	2.3	690	2	09UVX9	09uvx9 aspergillus	967	7	2.3	845	2	067IW8	067iw8 oryza sativ
895	7	2.3	691	2	09KZ87	09kz87 deinococcus	968	7	2.3	847	2	07R0E9	07r0e9 giardia lam
896	7	2.3	693	2	021649	021649 caenorhabdi	969	7	2.3	851	2	09Y4D4	09y4d4 homo sapien
897	7	2.3	694	2	07D724	07d724 mycobacteri	970	7	2.3	853	1	MUTS_VIBVU	08dc53 vibrio vuln
898	7	2.3	695	1	ZSM3_MOUSE	08cf18 mus musculu	971	7	2.3	853	1	MUTS_VIBVY	07mhr2 vibrio vuln
899	7	2.3	696	1	ZSW3_HUMAN	096mp5 homo sapien	972	7	2.3	855	2	P90549	PN90549 leishmania
900	7	2.3	697	2	061121	061121 citrildia f	973	7	2.3	856	2	07SHJ0	07shj0 neurospora
901	7	2.3	702	2	09ZPN6	09zpn6 zea mays (m	974	7	2.3	857	2	09TC08	09tc08 arabidopsi
902	7	2.3	702	2	097D01	097d01 clostridium	975	7	2.3	869	2	064CS4	064cs4 uncultured
903	7	2.3	706	2	07ZJS2	07zjs2 thermus the	976	7	2.3	869	2	08YNN3	08ynn3 anabaena sp
904	7	2.3	710	2	09XXU6	09xxu6 caenorhabdi	977	7	2.3	879	2	08KX11	08kx11 rhizobium e
905	7	2.3	712	2	06CZ84	06cz84 yarrowia.li	978	7	2.3	882	2	07SYD6	07syd6 brachydantio
906	7	2.3	713	2	081M21	081m21 oryza sativ	979	7	2.3	886	2	08PC19	08pc19 xanthomonas
907	7	2.3	716	2	081M77	081m77 oryza sativ	980	7	2.3	886	2	08PPC7	08ppc7 xanthomonas



CC -1- TISSUE SPECIFICITY: Expressed in most tissues. High levels were  
CC found in liver, kidney, heart, ovary, spleen, testes, skeletal  
CC muscle and peripheral blood leukocytes. Expression was absent or  
CC low in colon and small intestine. Expression is relatively high in  
CC the tumor cell lines chronic myelogenous leukemia K-562 and the  
CC colorectal adenocarcinoma SW480. Expression is moderate in the  
CC cervical carcinoma HeLa, the Burkitt's lymphoma Raji, the lung  
CC carcinoma A549, and the melanoma G361. In contrast, two leukemia  
CC cell lines, HL-60 (promyelocytic leukemia) and MOLT-4  
CC (lymphoblastic leukemia), show relatively low levels.  
CC -1- DOMAIN: Interacts with Casp8 and Casp10 are mediated by the DED  
CC domain.  
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.  
CC -1- CAUTION: Ref.5 (AAH13372) sequence differs from that shown due to  
CC a frameshift in position 186.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
CC EMBL; AF443591; AAL48220.1; -  
CC EMBL; AF457575; AAM10835.1; -  
CC EMBL; AY125448; AAM95240.1; -  
CC EMBL; AK075328; BAC11551.1; -  
CC EMBL; BC013372; AAH13372.2; ALT\_FRAME.  
CC EMBL; BC027930; AAH27930.1; -  
CC GeneW; HGNC:24450; DEDD2.  
CC H-invDB; HIX0015171; -  
CC InterPro; IPR011029; DEATH\_Like.  
CC InterPro; IPR001875; DED.  
CC Pfam; PF01335; DED; 1.  
CC SMART; SM00031; DED; 1.  
CC PROSITE; PS0168; DED; 1.  
CC Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;  
CC Transcription regulation.  
CC DOMAIN 25 104 DED.  
CC DOMAIN 104 109 Nuclear localization signal (Potential).  
CC DOMAIN 155 173 Bipartite nuclear localization signal  
CC (Potential).  
CC VARSPLIC 145 149 Missing (in isoform 2).  
CC FT CONFLICT 27 27 /FTid=VSP\_010312.  
CC FT CONFLICT 56 56 H -> N (in Ref. 2).  
CC FT CONFLICT 79 79 A -> G (in Ref. 2).  
CC FT CONFLICT 207 207 D -> G (in Ref. 2).  
CC FT CONFLICT 230 230 C -> R (in Ref. 4).  
CC FT CONFLICT 230 230 Missing (in Ref. 5; AAH13372).  
CC SEQUENCE 326 AA; 36178 MW; 3F7B0B307C870CD CRC64;  
Query Match 73.9%; Score 224; DB 1; Length 326;  
Best Local Similarity 100.0%; Pred. No. 7.8e-203;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
DED2\_MOUSE  
ID DED2\_MOUSE STANDARD; PRT; 330 AA.  
AC O8QZV0; O8QZV1;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE DNA-binding death effector domain-containing protein 2 (DED-containing  
DE protein FLAME-3).  
GN Name=DED2; Synonyms=Flame3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC STRAIN=C57BL/6J;  
RX MEDLINE=21961615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;  
RA Zhan Y., Hegde R., Srinivasula S.M., Fernandes-Alnemri T.,  
RA Alnemri E.S.,  
RT "Death effector domain-containing proteins DEDD and FLAME-3 form  
RT nuclear complexes with the Ffl1C102 subunit of human transcription  
RT factor IIIC".  
RL Cell Death Differ. 9:439-447(2002).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;  
RA Alciivar A., Hu S., Tang Y., Yang X.,  
RT "DED2 and DEDD2 associate with caspase-8/10 and signal cell death".  
RL Oncogene 22:291-297(2003).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Retina;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Narusina K., Farmer A.A., Ruidin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Watra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: May play a critical role in death receptor-induced  
CC apoptosis and may target Casp8 and Casp10 to the nucleus. May  
CC regulate degradation of intermediate filaments during apoptosis.  
CC May play a role in the general transcription machinery in the  
CC nucleus and might be an important regulator of the activity of  
CC GTP3C3.  
CC -1- SUBUNIT: Interacts with Casp8, Casp10 and GTP3C3. Homodimerizes  
CC and heterodimerizes with DEDD (by similarity).  
CC -1- SUBCELLULAR LOCATION: Nuclear, accumulated in subnuclear  
CC structures resembling nucleoli (by similarity).  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=O8QZV0-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=O8QZV0-2; Sequence=VSP\_010313, VSP\_010314;  
CC Note=No experimental confirmation available;  
CC -1- TISSUE SPECIFICITY: Expression is high in liver, heart, kidney,  
CC and testis but low in brain, spleen, lung, and skeletal muscle.



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CC -1- DOMAIN: Interactions with CASP8 and CASP10 are mediated by the DED
CC domain (By similarity).
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: AF457576; AAM10836.1; -
DR EMBL: AF543541; AAN3179.1; -
DR EMBL: BC037043; AAN37043.1; -
DR MGI: 1914629; 2410050E11R1K.
DR InterPro: IPR011029; DEATH_like.
DR Pfam: PF01335; DED.
DR SMART: SM00031; DED.1.
DR PROSITE: PS50166; DED.1.
KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 25 104 DED.
FT DOMAIN 104 109 Nuclear localization signal (Potential).
FT DOMAIN 156 174 Bipartite nuclear localization signal
FT VARSPIC 1 171 (Potential).
FT VARSPIC 1 171 Missing (in isoform 2).
FT VARSPIC 172 200 /FtId=VSP_010313.
FT VARSPIC 172 200 RRRAGLAASQOHOCHGRRSSRGKTC -> MGKAORG
FT VARSPIC 172 200 EVTCPRPRAVAMQSMDSLS (in isoform 2).
FT VARSPIC 172 200 /FtId=VSP_010314.
SQ SEQUENCE 330 AA; 36786 MW; 889BCAF5E01304B0 CRC64;
Query Match 38.6%; Score 117; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.le-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 RPSEGGKTCIDIRLRVRAVEGHPALBEGVARRPOLAROLVFGQATVLSRDGS 246
DB 191 RPSSBGGKTCIDIRLRVRAVEGHPALBEGVARRPOLAROLVFGQATVLSRDGS 250
QY 247 VVCIIKFESELYLDAFMGDYLSGALLQALRGVFTLEALREAVGREAVLLVSVDEAD 303
DB 251 VVCIIKFESELYLDAFMGDYLSGALLQALRGVFTLEALREAVGREAVLLVSVDEAD 307
RESULT 3
Q8BRM9 PRELIMINARY; PRT; 168 AA.
ID Q8BRM9 PRELIMINARY; PRT; 168 AA.
AC Q8BRM9.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone: A830049M19 product: similar to death effector domain-
DE containing and DNA-binding protein 2, full insert sequence.
GN Name=Dcd2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

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RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komano H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komano H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubara M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Fukuda J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai U., Kojima Y., Kondo S., Komano H., Koda M., Koya S.,
RA Kuyihira K., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
RA Nishii K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shitaki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Watanabe M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK043908; BAC31699.1; -
DR MGI: MGI:1914629; Dcd2.
DR GO: GO:0042981; P:regulation of apoptosis; TAS.
KW DNA-binding.
SQ SEQUENCE 168 AA; 17442 MW; F75D71DC48992425 CRC64;
Query Match 7.6%; Score 23; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 4.le-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 195 TCDIRLRVRAVEGHPALBEGV 217
DB 83 TCDIRLRVRAVEGHPALBEGV 105
RESULT 4
Q919M3 PRELIMINARY; PRT; 369 AA.
ID Q919M3 PRELIMINARY; PRT; 369 AA.
AC Q919M3.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dcd1.
GN Name=dcd1;

```

OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
NCBI\_TaxId=7955;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with homology to mammalian apoptosis regulators identified in  
zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL, AF232226; AAF66963.1; -  
DR ZFIN, ZDB-GENE-000616-2; dedd1.  
DR GO, GO:0005515; P:protein binding; IEA.  
DR GO, GO:0042981; P:regulation of apoptosis; IEA.  
DR InterPro, IPR01029; DEATH\_like.  
DR InterPro, IPR001875; DED.  
DR Pfam, PF01335; DED.1.  
DR PROSITE, PS50168; DED.1.  
SQ SEQUENCE 369 AA; 42244 MW; 73B09B9E17EC247 CRC64;  
Query Match 4.6%; Score 14; DB 2; Length 369;  
Best Local Similarity 100.0%; Pred. No. 0.00027;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 193 KYTCIDRLRVRAVY 206  
DB 235 KYTCIDRLRVRAVY 248  
RESULT 5  
DEDD HUMAN  
ID \_DEDD\_HUMAN STANDARD; PRT; 318 AA.  
AC 075618; 060737;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Death effector domain-containing protein (Death effector domain-  
containing testicular molecule) (DEDDProl) (FLEDD-1) (KE05).  
GN Name=DEDD; Synonyms=DEDDProl, DEFT;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN (1)  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=98447599; PubMed=9774341; DOI=10.1093/emboj/17.20.5974;  
RA Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhansel C.,  
Hofmann T.G., Grunert I., Kramer P.H., Peter M.E.;  
RT "DEDD, a novel death effector domain-containing protein, targeted to  
the nucleus."  
RL EMBL J. 17:5974-5986(1998).  
RN (2)  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.  
RC TISSUE=Testis;  
RX MEDLINE=96049260; PubMed=9832420; DOI=10.1210/en.139.12.4839;  
RA Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Hausen A.J.W.;  
RT "DEFT, a novel death effector domain-containing molecule predominantly  
expressed in testicular germ cells."  
RL Endocrinology 139:4839-4848(1998).  
RN (3)  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Pan G.;  
RT "FLEDD-1, a novel molecule with a DED-like domain."  
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
RN (4)  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RA Thome M., Tschopp J.;  
RT "DEDDProl, a novel DED-containing protein."  
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
RN (5)  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Dendritic cell;  
RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;  
RT "A novel gene from human dendritic cell."  
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.  
RN (6)  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Bone marrow, and Placenta;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Ueda T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dixon M.C.,  
RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN (7)  
RP FUNCTION, AND INTERACTIONS WITH KRT8; KRT18 AND CASP3.  
RX MEDLINE=22202288; PubMed=12235123; DOI=10.1083/jcb.200112124;  
RA Lee J.C., Schickling O., Stegh A.H., Oshima R.G., Dindale D.,  
RA Cohen G.M., Peter M.E.;  
RT "DEDD regulates degradation of intermediate filaments during  
apoptosis."  
RL J. Cell Biol. 158:1051-1066(2002).  
RN (8)  
RP INTERACTION WITH GTF3C3.  
RX MEDLINE=21961615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;  
RA Zhan Y., Hegde R., Srinivasula S.M., Fernandes-Alnemri T.,  
RA Alnemri E.S.;  
RT "Death effector domain-containing proteins DEDD and FLAME-3 form  
nuclear complexes with the TFRIC102 subunit of human transcription  
factor IIC."  
RL Cell Death Differ. 9:439-447(2002).  
RN (9)  
RP INTERACTIONS WITH CASP8 AND CASP10.  
RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;  
RA Alcivar A., Hu S., Tang J., Yang X.;  
RT "DEDD and DEDD2 associate with caspase-8/10 and signal cell death."  
RL Oncogene 22:291-297(2003).  
RN (10)  
RP FUNCTION: A scaffold protein that directs CASP3 to certain  
substrates and facilitates their ordered degradation during  
apoptosis. May also play a role in mediating CASP3 cleavage of  
KRT18. Regulates degradation of intermediate filaments during  
apoptosis. May play a role in the general transcription machinery  
in the nucleus and might be an important regulator of the activity  
of GTF3C3. Inhibits DNA transcription in vitro (By similarity).  
CC -1- SUBUNIT: Interacts with CASP8, CASP10, KRT8, KRT18, CASP3 and  
CC FADD. Homodimerizes and heterodimerizes with DEDD.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus  
CC during CD95-mediated apoptosis where it is localized in the  
CC nucleolus (By similarity). Following apoptosis induction, the mono  
CC and/or dimerization form increases and forms filamentous  
CC structures that colocalize with KRT8 and KRT18 intermediate  
CC filament network in simple epithelial cells.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=O75618-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=O75618-2; Sequence=VSP\_003846;  
CC Note=No experimental confirmation available;

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CC -1- TISSUE SPECIFICITY: widely expressed with highest levels in
CC testis.
CC -1- PFM: Exists predominantly in a mono- or dibiquitinated form.
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF083236; AAC33105.1; -
CC EMBL; AF100341; AAD16414.1; -
CC EMBL; AF043733; AAC80280.1; -
CC EMBL; AJ010973; CA09445.1; -
CC EMBL; AF064605; AAC17110.3; -
CC EMBL; BC013910; AAH13910.1; -
CC EMBL; BC013910; AAH13910.1; -
CC Genew; HGNC:2755; DEDD.
CC H-invdb; HIX0001231; -.
CC MIM; 606841; -.
CC DR GO; GO:0005737; C:cytoplasm; ISS.
CC DR GO; GO:0005730; C:nucleolus; ISS.
CC DR GO; GO:0003677; F:DNA binding; ISS.
CC DR GO; GO:0006917; P:induction of apoptosis; ISS.
CC DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; TMS.
CC DR GO; GO:0016481; P:negative regulation of transcription; ISS.
CC DR GO; GO:0007283; P:spermatogenesis; TMS.
CC InterPro; IPR011029; DEATH_like.
CC InterPro; IPR001875; DED.
CC Pfam; PF01335; DED; 1.
CC SMART; SM00031; DED; 1.
CC PROSITE; PS00168; DED; 1.
CC KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
CC Repressor; Transcription regulation.
CC FT DOMAIN 25 103 DED. GEEIQGQRMSRLGEYKELGHMVAIVIQ (in
CC VARSPLIC 194 194 isoform 2).
CC FT CONFLICT 13 13 /Ptm=VSP_003846.
CC FT SEQUENCE 318 AA; 36794 MW; FFD5F9B61FEBB6 CRC64;
CC SQ
CC Query Match 4.3%; Score 13; DB 1; Length 318;
CC Best Local Similarity 100.0%; Pred. NO. 0.0021;
CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 195 TCDFRLRAEYC 207
CC Db 192 TCDFRLRAEYC 204
CC
CC RESULT 6
CC DEDD_MOUSE STANDARD; PRT; 318 AA.
CC ID DEDD_MOUSE
CC AC Q9ZIL3; Q7QCH8; Q9R227;
CC DT 28-FEB-2003 (rel. 41, Created)
CC DT 28-FEB-2003 (rel. 41, Last sequence update)
CC DT 05-JUL-2004 (rel. 44, Last annotation update)
CC DE Death effector domain-containing protein (DEDDPro1).
CC GN Name=dedd;
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_Taxid=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
CC SPECIFICITY.
CC MEDLINE=98447599; PubMed=9774341; DOI=10.1093/emboj/17.20.5974;
CC RX Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhaensel C.,
CC RA Hofmann T.G., Grumet I., Kramer P.H., Peter M.E.;
CC "DEDD, a novel death effector domain containing protein, targeted to

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RT the nucleolus."
RL EMBL J. 17:5974-5986 (1998).
RN
RN SEQUENCE FROM N.A.
RA Thome M., Tschopp J.;
RA "DEDDPro1, a novel DED-containing protein."
RA submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshimaki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Snevchenko Y., Boulford G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
RA Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain
CC substrates and facilitates their ordered degradation during
CC apoptosis. May also play a role in mediating CASP3 cleavage of
CC KRT18. Regulates degradation of intermediate filaments during
CC apoptosis. May play a role in the general transcription machinery
CC in the nucleus and might be an important regulator of the activity
CC of GTF3C3 (By similarity). Inhibits DNA transcription in vitro.
CC -1- SUBUNIT: Interacts with CASP8, CASP10, KRT8, KRT18, CASP3 and
CC FADD. Homodimerizes and heterodimerizes with DEDD2 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus
CC during CP95-mediated apoptosis where it is localized in the
CC nucleoli. Following apoptosis induction, the mono and/or
CC dibiquitination form increases and forms filamentous structures
CC that colocalize with KRT8 and KRT18 intermediate filament network
CC in simple epithelial cells (By similarity).
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -1- PFM: Exists predominantly in a mono- or dibiquitinated form.
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ011386; CA09604.1; -
CC EMBL; AF100342; AAD16415.1; -
CC DR EMBL; BC023668; AAH23668.1; -
CC DR EMBL; BC054445; AAH54445.1; -
CC MGD; MGI:133874; Dedd.
CC DR GO; GO:0005737; C:cytoplasm; IDA.
CC DR GO; GO:0005730; C:nucleolus; IDA.
CC DR GO; GO:0003677; F:DNA binding; IDA.
CC DR GO; GO:0006917; P:induction of apoptosis; IDA.
CC DR GO; GO:0016481; P:negative regulation of transcription; IDA.
CC InterPro; IPR011029; DEATH_like.
CC InterPro; IPR001875; DED.
CC Pfam; PF01335; DED; 1.
CC SMART; SM00031; DED; 1.

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DR PROSITE; PSS0168; DED; 1.  
 KM Apoptosis; DNA-binding; Nuclear protein; Repressor;  
 KW Transcription regulation.  
 FT DOMAIN 25 103 DED.  
 FT CONFLICT 237 237 K -> N (in Ref. 2).  
 FT CONFLICT 316 316 A -> V (in Ref. 3; AAHS4445).  
 SQ SEQUENCE 318 AA; 36805 MW; C9A1DFC4C0E57CA CRC64;  
 Query Match 4.3%; Score 13; DB 1; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 0.0021;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 TCDIRLRVRAEYC 207  
 Db 192 TCDIRLRVRAEYC 204

RESULT 7  
 ID DEDD\_RAT STANDARD; PRT; 318 AA.  
 AC 0922X0;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Death effector domain-containing protein (Death effector domain-  
 containing testicular molecule).  
 GN Name=Ded; Synonyms=Defc;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.  
 RC TISSUE-Testis;  
 RX MEDLINE=99049260; PubMed=9832420; DOI=10.1210/en.139.12.4839;  
 RA Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Hansen A.U.W.;  
 RT "DEFT, a novel death effector domain-containing molecule predominantly  
 expressed in testicular germ cells.";  
 RL Endocrinology 139:4839-4848(1998).  
 CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain  
 substrates and facilitates their ordered degradation during  
 apoptosis. May also play a role in mediating CASP3 cleavage of  
 KR18. Regulates degradation of intermediate filaments during  
 apoptosis. May play a role in the general transcription machinery  
 in the nucleus and might be an important regulator of the activity  
 of GTP3C3. Inhibits DNA transcription in vitro (By similarity).  
 CC -1- SUBUNIT: Interacts with CASP8, CASP10, KR18, KR19, CASP3 and  
 FADD. Homodimerizes and heterodimerizes with DEDD2 (By  
 similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus  
 during CD95-mediated apoptosis where it is localized in the  
 nucleoli. Following apoptosis induction, the mono and/or  
 dimerization form increases and forms filamentous structures  
 that colocalize with KR18 and KR19 intermediate filament network  
 in simple epithelial cells (By similarity).  
 CC TISSUE SPECIFICITY: Widely expressed with highest levels in  
 testis. Within the testis, highly expressed in germ cells but not  
 expressed in Sertoli cells.  
 CC -1- DEVELOPMENTAL STAGE: First detected in 20-day-old animals. Reaches  
 a peak at 30 days.  
 CC -1- PTM: Exists predominantly in a mono- or dimerized form.  
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.  
 CC -----  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; AF053362; AAC80287.1; -;  
 DR GO; GO:0005737; C:cytoplasm; ISS.

DR GO; GO:0005730; C:nucleus; ISS.  
 DR GO; GO:0003677; F:DNA binding; ISS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:0016481; P:negative regulation of transcription; ISS.  
 DR InterPro; IPR011029; DEATH-like.  
 DR InterPro; IPR01875; DED.  
 DR Pfam; PF01335; DED; 1.  
 DR SMART; SM00031; DED; 1.  
 DR PROSITE; PSS0168; DED; 1.  
 KW Apoptosis; DNA-binding; Nuclear protein; Repressor;  
 KW Transcription regulation.  
 FT DOMAIN 25 103 DED.  
 SQ SEQUENCE 318 AA; 36847 MW; B8751791F66A03DE CRC64;  
 Query Match 4.3%; Score 13; DB 1; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 0.0021;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 TCDIRLRVRAEYC 207  
 Db 192 TCDIRLRVRAEYC 204

RESULT 8  
 ID 06DHN2 PRELIMINARY; PRT; 404 AA.  
 AC 06DHN2;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Zgc:92202.  
 GN Name=zgc:92202;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxId=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-whole;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stachek M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzanski M.I., Sklaska U., Smalios D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Mair M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-whole;  
 RA Strusberg R.;  
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC075935; AAH75935.1; -;  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR011029; DEATH-like.  
 DR InterPro; IPR01875; DED.  
 DR Pfam; PF01335; DED; 1.  
 DR SMART; SM00031; DED; 1.

DR PROSITE; PSS0168; DED; 1.  
SQ SEQUENCE 404 AA; 44888 MW; 3C949DB3B07B81A CRC64;

Query Match 4.3%; Score 13; DB 2; Length 404;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
Db 267 TCDIRLRVRAEYC 279

RESULT 9  
ID Q6GNZ8 PRELIMINARY; PRT; 243 AA.  
AC Q6GNZ8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DB MGC80767 protein.  
GN Name=MGC80767;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OC NCBI\_TaxID=8335;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=SpLent;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner U., Sherman C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein W.J., Ueda T.B., Toshiyuki S., Carlini P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
RA Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=SpLent;  
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RT Dev. Dyn. 225:384-391(2002).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP TISSUE=SpLent;  
RC Klein S., Gerhard D.S.;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073351; AAH73351.1; -;  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0042881; F:regulation of apoptosis; IEA.  
DR InterPro; IPR011029; DEATH\_Like.  
DR InterPro; IPR011875; DEATH\_Like.  
DR Pfam; PF01335; DED; 1.  
DR PROSITE; PSS0168; DED; 1.  
SQ SEQUENCE 243 AA; 27767 MW; 57A2E89CFBD3E0BC CRC64;

Query Match 3.6%; Score 11; DB 2; Length 243;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 YYGMLSLHRMF 30  
Db 21 YYGMLSLHRMF 31

RESULT 10  
ID Q9IWI3 PRELIMINARY; PRT; 218 AA.  
AC Q9IWI3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Interleukin 18 binding protein.  
GN Name=054L;  
OS Molluscum contagiosum virus subtype 1 (MCV1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Molluscipoxvirus.  
OC NCBI\_TaxID=10280;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=20231932; PubMed=10769064;  
RX Smith V.P., Bryant N.A., Alcamí A.;  
RA "Ectromelia, vaccinia and cowpox viruses encode secreted interleukin  
RT 18 binding proteins";  
RL J. Gen. Virol. 81:1223-1230(2000).  
DR EMBL; AJ271163; CAB89814.1; -;  
SQ SEQUENCE 218 AA; 23853 MW; 3FPA9C240DD24E75 CRC64;

Query Match 3.3%; Score 10; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRRGAP 176  
Db 160 GARRRRRGAP 169

RESULT 11  
ID Q98222 PRELIMINARY; PRT; 235 AA.  
AC Q98222;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MCO54L.  
GN Name=MCO54L;  
OS Molluscum contagiosum virus subtype 1 (MCV1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Molluscipoxvirus.  
OC NCBI\_TaxID=10280;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=96325459; PubMed=8670425;  
RX Senkevich T.G., Bugert J.J., Sieler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RT "Genome sequence of a human tumorigenic poxvirus: prediction of  
RT specific host response-evasion genes";  
RT Science 273:813-816(1996).  
DR EMBL; U60315; AAC55182.1; -;  
DR FIR; T30656; T30656.  
SQ SEQUENCE 235 AA; 25209 MW; BA47745C68608889 CRC64;

Query Match 3.3%; Score 10; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRRGAP 176  
Db 156 GARRRRRGAP 165

## RESULT 12

```

O6DHV2
ID O6DHV2 PRELIMINARY; PRT; 244 AA.
AC O6DHV2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dedd1 protein.
GN Name=Dedd1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC075865; AAH75865.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR011875; DED.
DR Pfam; PF01335; DED. 1.
DR PROSITE; PS50168; DED; 1.
SQ SEQUENCE 244 AA; 28051 MW; 043225AEASD79527 CRC64;

```

Query Match 3.3%; Score 10; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 ELLLELERRG 76  
 |||||  
 Db 113 ELLLELERRG 122

## RESULT 13

```

O9Y9Y9
ID O9Y9Y9 PRELIMINARY; PRT; 127 AA.
AC O9Y9Y9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Hypothetical protein APE2150.
DE OrderedLocustNames=APE2150;
GN Aeropyrum pernix.
OS

```

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;  
 OC Desulfurococcaceae; Aeropyrum.  
 OX NCBI\_Taxid=56636;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatakeyama Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anai A., Koyagi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kusida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Res. 6:83-101(1999).  
 DR EMBL; AP000063; BAA81161.1; -.  
 DR PIR; A72522; A72522.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 127 AA; 13517 MW; 1C28D0E67B34434C CRC64;

Query Match 3.0%; Score 9; DB 2; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 SYGTSSSSK 124  
 |||||  
 Db 95 SYGTSSSSK 103

## RESULT 14

```

O67IV3
ID O67IV3 PRELIMINARY; PRT; 222 AA.
AC O67IV3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBA0048L03.36.
GN Name=OSUNBA0048L03.36;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  

OC Ehrhartoideae; Oryzeae; Oryza.  

OX NCBI_Taxid=39947;  

RN (1)  

RP SEQUENCE FROM N.A.  

RA Sasaki T., Matsumoto T., Fujisawa M.;  

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC  

RT clone:OSUNBA0048L03.36";  

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  

DR EMBL; AP007205; BAD38588.1; -.  

KW Hypothetical protein.  

SQ SEQUENCE 222 AA; 24596 MW; 95C5B33F65534936 CRC64;

```

Query Match 3.0%; Score 9; DB 2; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 9.1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 GGARRRRRG 174  
 |||||  
 Db 85 GGARRRRRG 93

## RESULT 15

```

O7O6G3
ID O7O6G3 PRELIMINARY; PRT; 227 AA.
AC O7O6G3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP6626 (Fragment).
GN Name=agCG48835; ORFName=ENSANGCG00000015017;
OS Anopheles gambiae str. PE8T.

```

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 OX NCBI\_TaxID=180454;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PEST;  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.  
 CC -! CAUTION: The sequence shown here is derived from an  
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AAAB01008960; EAL1634.1; -  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR008958; Transglut\_C.  
 DR InterPro; IPR008856; TRAP\_beta.  
 DR Pfam; PF05753; TRAP\_beta; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 227 AA; 24921 MW; 2ADF4D013495ED59 CRC64;

Query Match 3.0%; Score 9; DB 2; Length 227;  
 Best Local Similarity 100.0%; Pred.No. 9.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 FEVVGQOLT 38  
 |||||  
 DB 109 FEVVGQOLT 117

Search completed: February 12, 2005, 16:39:14  
 Job time : 126 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:34:11 ; Search time 20 Seconds  
(without alignments)  
1457.684 Million cell updates/sec

Title: US-10-030-271-2  
Perfect score: 303  
Sequence: 1 MALSGSTPAPCWEDECLDY.....LREAVGRAVRLVSVDEAD 303

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	3.3	235	2 T30656	hypothetical prote
2	9	3.0	127	2 A72522	hypothetical prote
3	8	2.6	75	2 AE2664	ATP synthase C cha
4	8	2.6	75	2 D97446	ATP synthase chain
5	8	2.6	170	2 C84492	hypothetical prote
6	7	2.6	197	2 C70601	hypothetical prote
7	8	2.6	224	2 B87197	hypothetical prote
8	8	2.6	224	2 E70790	probable transcrip
9	8	2.6	279	2 B70328	hypothetical prote
10	8	2.6	282	2 S46793	vacuolar protein s
11	8	2.6	339	2 S20880	homeotic protein H
12	8	2.6	342	2 S18649	homeotic protein H
13	8	2.6	363	2 T34931	hypothetical prote
14	8	2.6	417	2 E86858	cell division prot
15	8	2.6	475	2 A83340	66k glycoprotein p
16	8	2.6	528	2 AC3236	hypothetical prote
17	8	2.6	786	2 S20458	pgqr protein - Kle
18	8	2.6	828	2 S22155	oncogene 1 (tre-2
19	8	2.6	914	2 T33481	hypothetical prote
20	8	2.6	928	2 T00757	probable ubiquitin
21	8	2.6	928	2 T04192	hypothetical prote
22	8	2.6	937	2 T04194	hypothetical prote
23	8	2.6	963	2 T09478	ubiquitin thioleat
24	8	2.6	1089	2 S22158	transforming prote
25	8	2.6	1095	2 B83471	probable nuclear a
26	8	2.6	1733	1 B45344	hypothetical prote
27	8	2.6	1958	2 B40505	hypothetical prote
28	7	2.3	47	2 T2970	hypothetical prote
29	7	2.3	66	2 T15539	hypothetical prote

30	7	2.3	92	2 T37077	hypothetical prote
31	7	2.3	115	2 S28937	prolamine 2 precu
32	7	2.3	116	2 AH3150	hypothetical prote
33	7	2.3	118	2 G02438	D-dopachrome cauto
34	7	2.3	118	2 J80162	dopachrome isomera
35	7	2.3	118	2 T16216	hypothetical prote
36	7	2.3	152	2 A43627	hypothetical 17.1K
37	7	2.3	152	2 AB2011	two-component resp
38	7	2.3	153	2 G72476	hypothetical prote
39	7	2.3	155	2 G72580	hypothetical prote
40	7	2.3	157	2 T27697	VPS29-like phospho
41	7	2.3	184	2 G70321	GTP cyclonhydrolase
42	7	2.3	186	2 T06911	H+-transporting tw
43	7	2.3	187	2 E71464	interferon RNA meth
44	7	2.3	195	1 IYB011	interferon alpha-I
45	7	2.3	195	2 A61403	interferon alpha-I
46	7	2.3	195	2 I47070	interferon omega -
47	7	2.3	195	2 I46397	interferon alpha -
48	7	2.3	195	2 A12678	hypothetical prote
49	7	2.3	197	2 B85923	probable decarboxy
50	7	2.3	197	2 A91078	probable phenylact
51	7	2.3	197	2 T44998	phenylacrylic acid
52	7	2.3	200	2 S21148	hypothetical prote
53	7	2.3	206	2 G75396	hypothetical prote
54	7	2.3	212	2 E69522	hypothetical prote
55	7	2.3	213	2 J64928	histone H1x - huma
56	7	2.3	215	2 A71541	hypothetical prote
57	7	2.3	225	2 D95183	conserved hypotet
58	7	2.3	225	2 H98050	conserved hypotet
59	7	2.3	242	2 A43904	homeotic protein G
60	7	2.3	246	2 G75570	conserved hypotet
61	7	2.3	255	2 J67264	CCAAT-enhancer bin
62	7	2.3	256	2 T48787	hypothetical prote
63	7	2.3	259	2 S76585	hypothetical prote
64	7	2.3	267	1 TVHUF5	fibroblast growth
65	7	2.3	273	2 B89884	hypothetical prote
66	7	2.3	277	2 T49543	hypothetical prote
67	7	2.3	278	2 T06026	homeobox protein H
68	7	2.3	279	2 T34848	probable transcrip
69	7	2.3	281	2 AC2789	conserved hypotet
70	7	2.3	281	2 D97568	hypothetical prote
71	7	2.3	291	2 T43139	hypothetical prote
72	7	2.3	296	2 H81726	UDP-N-acetylglucy
73	7	2.3	296	2 AC2698	DNA polymerase IIm
74	7	2.3	296	2 C97480	hypothetical prote
75	7	2.3	297	2 T27525	hypothetical prote
76	7	2.3	299	1 RDSS2R	ribonucleoside-dip
77	7	2.3	314	2 T07898	myrosinase-aseocia
78	7	2.3	318	1 F70536	3',5'-cyclic-nucle
79	7	2.3	323	2 T51621	myb-like protein (
80	7	2.3	323	2 T51645	myb-related trans
81	7	2.3	326	2 A84277	hypothetical prote
82	7	2.3	329	2 AE2128	transcription regu
83	7	2.3	336	2 T21565	hypothetical prote
84	7	2.3	337	2 E95871	probable oxidoredu
85	7	2.3	346	2 T26097	hypothetical prote
86	7	2.3	346	2 T21552	hypothetical prote
87	7	2.3	347	2 F75319	conserved hypotet
88	7	2.3	366	2 H81010	D-amino acid oxida
89	7	2.3	366	2 F82032	myrosinase-aseocia
90	7	2.3	371	2 T07896	hypothetical prote
91	7	2.3	375	2 S76663	hypothetical prote
92	7	2.3	382	2 A83171	probable aminotran
93	7	2.3	383	2 S61195	hypothetical prote
94	7	2.3	384	2 S24585	ribonucleoside-dip
95	7	2.3	384	2 S73429	glycerol-3-phosphat
96	7	2.3	396	2 G71044	probable molybdopt
97	7	2.3	401	2 T36882	hypothetical prote
98	7	2.3	402	2 A95924	probable glycosylt
99	7	2.3	412	2 T16480	hypothetical prote
100	7	2.3	414	2 S24154	alanine-glyoxylate
101	7	2.3	414	2 T15086	hypothetical prote
102	7	2.3	416	1 A41267	transcription fact

103	2.3	418	2	A39567	thyroxine-binding
104	2.3	421	2	T35205	citrate synthase-1
105	2.3	423	2	A99924	fmbb protein limpo
106	2.3	432	2	G83595	noncatalytic dihyd
107	2.3	432	2	T24072	hypothetical prote
108	2.3	432	2	A82799	HyD family secret
109	2.3	433	2	B82537	probable phosphodi
110	2.3	435	2	T15737	hypothetical prote
111	2.3	437	2	G97578	probable periplasm
112	2.3	438	2	T35789	probable secreted
113	2.3	446	2	T34782	probable signal pe
114	2.3	447	2	T35519	hypothetical prote
115	2.3	449	2	B87639	hypothetical prote
116	2.3	450	2	B71909	hypothetical prote
117	2.3	454	2	T26296	hypothetical prote
118	2.3	458	2	T49480	alpha-2-adrenergic
119	2.3	458	2	A37869	alpha-2b-adrenergic
120	2.3	458	2	A40392	alpha-2-adrenergic
121	2.3	464	2	A56600	intermediate filam
122	2.3	465	2	T40697	probable tata bind
123	2.3	468	2	C82449	conserved hypotet
124	2.3	469	2	D81017	chloride channel p
125	2.3	469	2	I37451	HBF-G2 (HFK-2) pro
126	2.3	474	2	H95322	hypothetical prote
127	2.3	485	2	A40751	finger protein MZF
128	2.3	490	2	B70645	probable regulator
129	2.3	497	2	B87721	ribonuclease G XPI
130	2.3	514	2	T41648	C2 domain family p
131	2.3	517	2	T18636	hypothetical prote
132	2.3	522	2	A82558	glutamine amidotra
133	2.3	527	2	B86432	T518.15 protein -
134	2.3	527	2	T36729	probable serine/th
135	2.3	576	2	H95370	probable transpor
136	2.3	584	2	E75060	hydrogenase-4 comp
137	2.3	603	2	T16655	hypothetical prote
138	2.3	605	2	C96940	sporulation specif
139	2.3	607	2	D64603	hypothetical prote
140	2.3	616	2	C82641	hypothetical prote
141	2.3	637	2	T04552	hypothetical prote
142	2.3	643	2	B69458	adenyl-1-sulfate r
143	2.3	648	2	F69848	transcription anti
144	2.3	650	2	T48060	beta-D-glucan exoh
145	2.3	659	2	F90531	lipoprotein limpor
146	2.3	671	2	A35912	homeotic protein o
147	2.3	674	2	T48261	hypothetical prote
148	2.3	691	2	B75622	hypothetical prote
149	2.3	694	2	F70868	membrane-associate
150	2.3	702	2	F97352	hypothetical prote
151	2.3	727	2	AC1814	hypothetical glyci
152	2.3	731	2	C70974	hypothetical glyci
153	2.3	750	2	H70628	probable phnc prot
154	2.3	776	2	T51911	related to protein
155	2.3	823	2	A58788	procollagen C-endo
156	2.3	826	2	E81706	conserved hypotet
157	2.3	841	1	I78885	serine/threonine-s
158	2.3	851	2	T00374	hypothetical prote
159	2.3	857	2	T04208	probable anthranil
160	2.3	869	2	AD2418	SMI/SNF family hel
161	2.3	904	2	G64840	protein-histidine
162	2.3	904	2	D90772	sensor protein tor
163	2.3	904	2	H85634	probable DNA damag
164	2.3	935	2	T39389	probable tetrahydr
165	2.3	969	2	T40147	probable RND efflu
166	2.3	1029	2	D83120	probable cation effl
167	2.3	1054	2	S77008	cation efflux syst
168	2.3	1058	2	AG2541	hypothetical prote
169	2.3	1065	2	T49827	nonsense-mediated
170	2.3	1069	2	T43280	serine-rich protei
171	2.3	1077	2	A44067	ubiquitin-specific
172	2.3	1083	2	E70726	probable polyketid
173	2.3	1168	2	E70726	proline dehydrogen
174	2.3	1224	2	T43218	hypothetical prote
175	2.3	1288	2	T09908	
176	2.3	1293	2	S42402	xeroderma pigmento
177	2.3	1378	1	T48751	protein-tyrosine k
178	2.3	1400	1	T38185	protein-tyrosine k
179	2.3	1404	1	A48186	protein-tyrosine k
180	2.3	1429	2	T41699	C2-domain family p
181	2.3	2108	2	H70819	probable polyketid
182	2.3	2424	2	T46480	calcium channel Bi
183	2.3	2559	2	T09144	probable guanine n
184	2.3	7576	2	T17478	FS506 polyketide s
185	2.0	11	2	EC2372	58k heat shock pro
186	2.0	20	2	PC4387	GroEL protein homo
187	2.0	21	2	PT0089	4-hydroxybenzoate
188	2.0	27	1	SRAPAS	proteinase A - stei
189	2.0	27	1	SRAPC	proteinase B - Russ
190	2.0	30	1	IRTR78	proteinase CIII, mi
191	2.0	30	1	IRTRC2	proteinase Ia - rai
192	2.0	30	1	IRTRC3	proteinase CIII, ma
193	2.0	31	2	I51349	proteinase - rainbo
194	2.0	31	2	B20883	variant surface gl
195	2.0	32	1	IRTR2	proteinase II - rai
196	2.0	32	1	SIOMN1	proteinase Ai - chu
197	2.0	32	1	VZPK1	proteinase I - nort
198	2.0	32	2	B02669	proteinase (belaine
199	2.0	32	2	F24970	proteinase 3a - rai
200	2.0	32	2	I51089	proteinase - Japane
201	2.0	33	1	IRTR1A	proteinase IA - rai
202	2.0	33	1	IRTR1B	proteinase IB - rai
203	2.0	33	1	IRTR42	proteinase 2c - rai
204	2.0	33	1	IRTR59	proteinase CII - ra
205	2.0	33	2	D21211	proteinase TP17 - r
206	2.0	33	2	S00710	proteinase CII - ch
207	2.0	33	2	A21211	proteinase TP14 - r
208	2.0	33	2	E21211	proteinase TP21 - r
209	2.0	33	2	C21211	proteinase TP16 - r
210	2.0	33	2	T01070	proteinase - rainbo
211	2.0	34	1	TYTUZ2	proteinase Z2 - blu
212	2.0	34	1	TYTUZ2	proteinase Y2 - blu
213	2.0	34	1	TYTUZ1	proteinase Z1 - blu
214	2.0	34	2	JX0204	proteinase Z1 - str
215	2.0	34	2	JX0203	variant surface gl
216	2.0	34	2	A44806	proteinase Z3 - sma
217	2.0	37	2	S29829	proteinase - green
218	2.0	41	2	A58213	proteinase I - biac
219	2.0	41	2	G58208	proteinase I - Am
220	2.0	43	2	D58213	proteinase I - Am
221	2.0	45	2	D58208	proteinase II-2 - p
222	2.0	45	2	D58208	proteinase II-3 - p
223	2.0	45	2	B58208	proteinase II-1 - p
224	2.0	47	2	F58208	proteinase II-5 - p
225	2.0	48	2	E58208	proteinase II-4 - p
226	2.0	48	2	C60505	hemoglobin A1-3 be
227	2.0	53	2	H84319	hypothetical prote
228	2.0	55	2	VRBO	vasoactive intesti
229	2.0	55	1	VRBR	vasoactive intesti
230	2.0	55	1	VRGP	vasoactive intesti
231	2.0	55	1	VRSH	vasoactive intesti
232	2.0	56	2	C58213	proteinase II - Ame
233	2.0	57	2	H95296	hypothetical prote
234	2.0	58	1	VRPG	vasoactive intesti
235	2.0	58	2	S34045	proteinase - North
236	2.0	58	2	A58208	proteinase I-1 - pa
237	2.0	60	2	D82277	hypothetical prote
238	2.0	60	2	B37290	homeotic protein G
239	2.0	61	1	H82779	DNA-binding protei
240	2.0	61	2	AE2370	hypothetical prote
241	2.0	65	2	AE2370	hypothetical prote
242	2.0	66	2	DNVBP	DNA-binding gene-re
243	2.0	72	2	I37232	calcitonin gene-re
244	2.0	72	2	B89853	hypothetical prote
245	2.0	74	2	AC9722	hypothetical prote
246	2.0	74	1	DNVPAS	DNA-binding protei
247	2.0	75	2	AC3445	H+-transporting tw
248	2.0	77	2	C82988	hypothetical prote

249	6	2.0	78	2	T29828	hypotheical prote	322	6	2.0	129	2	S37670	trab protein - Bsc
250	6	2.0	80	2	AH1057	Relb protein (impo	323	6	2.0	130	2	T47751	ribosomal protein
251	6	2.0	81	2	B91000	hypotheical prote	324	6	2.0	130	2	C70971	hypotheical prote
252	6	2.0	83	2	E71267	hypotheical prote	325	6	2.0	130	2	S34493	cellulase (Ec 3.2.
253	6	2.0	85	2	I39718	hypotheical prote	326	6	2.0	131	2	T29498	hypotheical prote
254	6	2.0	85	2	H87164	hypotheical prote	327	6	2.0	131	2	D72855	AcOof-44 protein -
255	6	2.0	86	2	G84527	hypotheical prote	328	6	2.0	131	2	T41790	AcMPV orf44 - Bom
256	6	2.0	86	2	F86294	hypotheical prote	329	6	2.0	132	2	H83048	hypotheical transcrip
257	6	2.0	87	2	AD3436	hypotheical prote	330	6	2.0	132	2	B69889	hypotheical prote
258	6	2.0	88	2	T36458	hypotheical prote	331	6	2.0	132	2	S10305	protamine - boll w
259	6	2.0	91	2	A59493	protamine p2 - Sty	332	6	2.0	132	2	I39004	cyclin-dependent k
260	6	2.0	92	2	S13132	protamine 2 precu	333	6	2.0	133	2	E72603	trans-regulatory s
261	6	2.0	94	2	E84902	probable MYB fami1	334	6	2.0	133	1	VKLJCE	hypotheical prote
262	6	2.0	95	2	AH0905	probable sigma(54)	335	6	2.0	133	2	T26755	hypotheical prote
263	6	2.0	95	2	E85984	probable sigma-54	336	6	2.0	133	2	D87593	hypotheical prote
264	6	2.0	95	2	B91139	probable sigma-54	337	6	2.0	133	2	D86697	hypotheical prote
265	6	2.0	95	2	I76719	hypotheical prote	338	6	2.0	134	1	WMVA16	B2IR 16k protein -
266	6	2.0	95	2	B41026	hypotheical prote	339	6	2.0	135	1	B64664	hypotheical prote
267	6	2.0	96	2	T26651	phosphoglyceromuta	340	6	2.0	135	2	F71852	MAP3g family prote
268	6	2.0	97	2	AC2927	hypotheical prote	341	6	2.0	135	2	F87264	hypotheical prote
269	6	2.0	97	2	D98355	hypotheical prote	342	6	2.0	136	2	D75009	hypotheical prote
270	6	2.0	97	2	C70828	hypotheical prote	343	6	2.0	136	2	E90440	hypotheical prote
271	6	2.0	99	2	T30451	probable DNA-bind1	344	6	2.0	136	2	C95291	hypotheical prote
272	6	2.0	99	2	E83235	hypotheical prote	345	6	2.0	137	2	AF2435	ATP synthase epsil
273	6	2.0	101	2	F71059	hypotheical prote	346	6	2.0	137	2	G69461	small multidrug ex
274	6	2.0	101	2	F90470	hypotheical prote	347	6	2.0	138	2	AG2914	conserved hypotet
275	6	2.0	102	2	S33336	protamine p2 - rbe	348	6	2.0	138	2	B97689	hypotheical prote
276	6	2.0	103	2	S33337	protamine p2 - pig	349	6	2.0	138	2	T10309	hypotheical prote
277	6	2.0	103	2	T28354	hypotheical prote	350	6	2.0	138	2	S30092	hypotheical prote
278	6	2.0	104	2	S53118	protamine p2 - com	351	6	2.0	138	2	A84482	hypotheical prote
279	6	2.0	104	2	S57666	protamine 2 - rat	352	6	2.0	139	2	E85845	unknown protei en
280	6	2.0	104	2	AG0706	probable membrane	353	6	2.0	140	2	D72680	hypotheical prote
281	6	2.0	105	2	E87149	conserved hypotet	354	6	2.0	141	2	AE1255	transcription regu
282	6	2.0	106	1	L4HUKN	Ig lambda chain V-	355	6	2.0	141	2	T46654	transcription regu
283	6	2.0	106	1	G1EPR	tegument protein -	356	6	2.0	141	2	AB1618	transcription regu
284	6	2.0	107	2	A29995	protamine p2 precu	357	6	2.0	141	2	H85217	hypotheical prote
285	6	2.0	107	2	B72716	hypotheical prote	358	6	2.0	141	2	AH2725	hypotheical prote
286	6	2.0	108	2	A85844	unknown protei en	359	6	2.0	141	2	E84522	hypotheical prote
287	6	2.0	108	2	H90875	hypotheical prote	360	6	2.0	141	2	C83768	hypotheical prote
288	6	2.0	108	2	F85691	unknown protei en	361	6	2.0	142	2	D90269	conserved hypotet
289	6	2.0	108	2	A99822	hypotheical prote	362	6	2.0	142	2	S34257	hypotheical prote
290	6	2.0	108	2	G90909	hypotheical prote	363	6	2.0	143	2	D75617	response regulator
291	6	2.0	108	2	G85629	hypotheical prote	364	6	2.0	143	2	E72504	hypotheical prote
292	6	2.0	108	2	D90853	hypotheical prote	365	6	2.0	143	2	B86857	conserved hypotet
293	6	2.0	108	2	C83528	hypotheical prote	366	6	2.0	143	2	AC1730	hypotheical prote
294	6	2.0	108	2	F72653	hypotheical prote	367	6	2.0	144	2	G83342	hypotheical prote
295	6	2.0	109	2	D81996	hypotheical prote	368	6	2.0	144	2	S60456	cysteine proteins
296	6	2.0	110	2	D84378	hypotheical prote	369	6	2.0	145	2	D82315	probable ribonucle
297	6	2.0	112	2	JQ1063	glycine-rich prote	370	6	2.0	146	2	T14667	hypotheical prote
298	6	2.0	113	2	A99915	hypotheical prote	371	6	2.0	146	2	T49867	hemoglobin beta ch
299	6	2.0	113	2	F85763	hypotheical prote	372	6	2.0	147	1	H8CY	hemoglobin beta ch
300	6	2.0	113	2	G75581	hypotheical prote	373	6	2.0	147	1	H8TR4	hemoglobin IV beta
301	6	2.0	113	2	B71088	hypotheical prote	374	6	2.0	147	2	S03400	conserved hypotet
302	6	2.0	113	4	A31199	beta-galactosidase	375	6	2.0	148	2	A70077	receptor activity-
303	6	2.0	114	2	AB3583	sulfide dehydrogen	376	6	2.0	148	2	JC7261	hemoglobin beta ch
304	6	2.0	115	2	I37901	histone H2A relate	377	6	2.0	148	2	JC7235	hemoglobin beta ch
305	6	2.0	115	2	B90742	hypotheical prote	378	6	2.0	148	2	S41625	hemoglobin beta ch
306	6	2.0	115	2	E85592	hypotheical prote	379	6	2.0	149	1	G70400	phosphatidylatidyl p
307	6	2.0	118	2	A75108	hypotheical prote	380	6	2.0	149	2	C75598	response regulator
308	6	2.0	118	2	E71026	hypotheical prote	381	6	2.0	149	2	S02164	regulatory protein
309	6	2.0	119	2	G69106	transcription regu	382	6	2.0	149	2	F75327	hypotheical prote
310	6	2.0	121	2	A71344	conserved hypotet	383	6	2.0	150	2	B70519	hypotheical prote
311	6	2.0	121	2	S42590	hypotheical 14.1K	384	6	2.0	150	2	S09872	probable furu prot
312	6	2.0	123	2	A71312	probable anti-sigm	385	6	2.0	151	2	T14948	hypotheical prote
313	6	2.0	123	2	E72680	hypotheical prote	386	6	2.0	152	2	D75367	hypotheical prote
314	6	2.0	125	2	S76216	hypotheical prote	387	6	2.0	152	2	S46272	hypotheical prote
315	6	2.0	125	2	AH2235	hypotheical prote	388	6	2.0	153	2	F72667	hypotheical prote
316	6	2.0	126	2	AD3508	transcription regu	389	6	2.0	153	2	AC2653	hypotheical prote
317	6	2.0	127	2	A86155	hypotheical prote	390	6	2.0	153	2	A70855	hypotheical prote
318	6	2.0	127	2	F95976	hypotheical prote	391	6	2.0	153	2	AC1710	hypotheical prote
319	6	2.0	127	2	AH2680	conserved hypotet	392	6	2.0	153	2	F97462	hypotheical prote
320	6	2.0	128	2	C84515	hypotheical prote	393	6	2.0	154	2	AE0445	hypotheical prote
321	6	2.0	129	2	T08527	trab protein - Ent	394	6	2.0	154	2	B75358	hypotheical prote

395	6	2.0	155	1	IGRO2	insulin-like growt
396	6	2.0	155	2	T28945	hypothetical prote
397	6	2.0	155	3	C95002	hypothetical prote
398	6	2.0	155	2	F97874	conserved hypotet
399	6	2.0	155	2	F90740	probable toxin [im
400	6	2.0	155	2	F87696	hypothetical prote
401	6	2.0	155	2	A85591	probable toxin Z10
402	6	2.0	155	2	A64810	hypothetical prote
403	6	2.0	156	2	H82496	ribose ABC transpo
404	6	2.0	157	2	G64459	hypothetical prote
405	6	2.0	157	2	G82214	hypothetical prote
406	6	2.0	157	2	A10601	transcription regu
407	6	2.0	157	2	E75530	hypothetical prote
408	6	2.0	158	2	G83847	hypothetical prote
409	6	2.0	159	2	F86541	C1102 hypothetical
410	6	2.0	159	2	G72082	conserved hypotet
411	6	2.0	160	2	E72631	hypothetical prote
412	6	2.0	161	2	JC4275	pleiotrophic facto
413	6	2.0	161	2	J00141	hypothetical 17.6K
414	6	2.0	162	2	T10928	3C3.19c protein -
415	6	2.0	162	2	A84217	hypothetical prote
416	6	2.0	162	2	E87685	hypothetical prote
417	6	2.0	163	1	WWVWM	18K protein - Abel
418	6	2.0	163	2	B39662	18K protein - mou
419	6	2.0	163	2	D87293	Fur family protein
420	6	2.0	164	2	S31480	hypothetical prote
421	6	2.0	165	2	S43302	single-stranded DN
422	6	2.0	165	2	E83417	hypothetical prote
423	6	2.0	165	2	A59492	prolamine P1 - Sty
424	6	2.0	166	1	S35973	regulatory protein
425	6	2.0	166	2	T08208	nonstructural prote
426	6	2.0	166	2	C72641	hypothetical prote
427	6	2.0	168	1	P6BPP6	Pe protein - phase
428	6	2.0	168	2	B72635	hypothetical prote
429	6	2.0	168	2	T35737	probable integral
430	6	2.0	169	2	C95394	protein [imported
431	6	2.0	170	2	B69587	adenine phosphorib
432	6	2.0	170	2	A83135	4-hydroxyphenylac
433	6	2.0	170	2	S74997	hypothetical prote
434	6	2.0	171	2	D75174	hypothetical prote
435	6	2.0	171	2	B36162	hypothetical prote
436	6	2.0	172	2	H83634	conserved hypotet
437	6	2.0	173	2	H75553	hypothetical prote
438	6	2.0	173	2	G96549	hypothetical prote
439	6	2.0	174	2	F87632	conserved hypotet
440	6	2.0	175	1	Q14D22	early B1B 21K prot
441	6	2.0	176	2	T45308	hypothetical prote
442	6	2.0	177	2	D69062	imidazoleglycerol-
443	6	2.0	177	2	T12717	hypothetical prote
444	6	2.0	177	2	T49802	hypothetical prote
445	6	2.0	177	2	B83271	hypothetical prote
446	6	2.0	179	2	S04858	insulin-like growt
447	6	2.0	179	2	C86853	hypothetical prote
448	6	2.0	180	2	E84260	hypothetical prote
449	6	2.0	180	2	A75579	ankyrin-related pr
450	6	2.0	180	2	AD3499	ribosomal -protein-
451	6	2.0	181	2	AP2468	50S ribosomal prot
452	6	2.0	181	2	A11222	Salmonella enteric
453	6	2.0	181	2	AD1576	Salmonella enteric
454	6	2.0	182	2	AG0040	single-strand bind
455	6	2.0	183	2	B75152	adenyllyl cyclase r
456	6	2.0	183	2	B81089	hypothetical prote
457	6	2.0	183	2	H81853	hypothetical prote
458	6	2.0	183	2	B86374	protein T23E23.20
459	6	2.0	183	2	AB3181	hypothetical prote
460	6	2.0	184	2	C71193	hypothetical prote
461	6	2.0	184	2	JC2429	activin-A protein
462	6	2.0	184	2	AG0115	probable membrane
463	6	2.0	184	2	S63441	hypothetical prote
464	6	2.0	184	2	T29373	hypothetical prote
465	6	2.0	185	2	F91020	acid phosphatase r
466	6	2.0	185	2	C75169	molymbdenum cofacto
467	6	2.0	186	2	F87250	
468	6	2.0	186	2	G82110	Tip repressor-bind
469	6	2.0	187	2	A82746	conserved hypotet
470	6	2.0	187	2	S09806	hypothetical prote
471	6	2.0	188	2	AB2761	thymidylate kinase
472	6	2.0	188	2	DB1149	deoxycytidine triph
473	6	2.0	190	2	G82624	glutathione peroxi
474	6	2.0	191	2	G82765	deoxycytidine triph
475	6	2.0	191	2	S57642	interferon precurs
476	6	2.0	191	2	S75503	hypothetical prote
477	6	2.0	192	1	G64746	phosphoprotease 180
478	6	2.0	192	2	AD0542	phosphoprotease 180
479	6	2.0	192	2	A90660	phosphoprotease 180
480	6	2.0	192	2	G85510	phosphoprotease 180
481	6	2.0	192	2	S56309	probable membrane
482	6	2.0	192	2	AA3220	transcription regu
483	6	2.0	195	2	D96817	hypothetical prote
484	6	2.0	196	1	BRECAU	transcription regu
485	6	2.0	196	2	AD0963	two-component syst
486	6	2.0	196	2	H86050	hypothetical prote
487	6	2.0	196	2	F91204	transcription regu
488	6	2.0	196	2	A41853	hexose phosphate t
489	6	2.0	196	2	F83625	conserved hypotet
490	6	2.0	197	2	AD0835	probable decarboxy
491	6	2.0	198	2	T06261	probable imidazole
492	6	2.0	199	2	S16063	acp-22 protein - y
493	6	2.0	199	2	S32224	acp-22 protein - y
494	6	2.0	200	2	E72303	transcription regu
495	6	2.0	200	2	AD3633	hypothetical prote
496	6	2.0	200	2	S61025	anhydrin-like prote
497	6	2.0	201	1	VCVQGB	coat protein - bee
498	6	2.0	201	2	DB3288	acyl-CoA thioester
499	6	2.0	201	2	P95270	hypothetical prote
500	6	2.0	201	2	AD1191	conserved hypotet
501	6	2.0	202	1	VCVQPL	coat protein - bee
502	6	2.0	202	2	B81371	hypothetical prote
503	6	2.0	203	2	T39877	spindle assembly c
504	6	2.0	204	2	B83279	hypothetical prote
505	6	2.0	205	2	AH3407	hypothetical cytos
506	6	2.0	205	2	F87660	hydrolase, haloact
507	6	2.0	205	2	T35707	hypothetical prote
508	6	2.0	206	2	B18821	hypothetical prote
509	6	2.0	206	2	E83047	hypothetical prote
510	6	2.0	207	2	AC3381	hypothetical prote
511	6	2.0	208	1	VCVQL2	coat protein - pot
512	6	2.0	208	1	S24593	coat protein - pot
513	6	2.0	208	2	S41878	coat protein - pot
514	6	2.0	208	2	S41878	coat protein - pot
515	6	2.0	208	2	S41874	hypothetical prote
516	6	2.0	208	2	AE2378	hypothetical prote
517	6	2.0	208	2	D71313	response regulator
518	6	2.0	209	2	T28656	response regulator
519	6	2.0	209	2	T30899	ribosomal protein
520	6	2.0	210	2	S41335	hypothetical phage
521	6	2.0	210	2	AC0259	collagen - nematod
522	6	2.0	210	2	B44984	hypothetical prote
523	6	2.0	210	2	T41982	amidoxanferase l
524	6	2.0	211	2	AB1977	fixd protein - Azo
525	6	2.0	211	2	S15167	hypothetical prote
526	6	2.0	211	2	A05123	hypothetical prote
527	6	2.0	211	2	T08764	thymidylate kinase
528	6	2.0	212	2	S66058	hypothetical prote
529	6	2.0	212	2	AH0195	dymp kinase (EC 2.
530	6	2.0	212	2	F82581	ribonuclease III X
531	6	2.0	212	2	T10883	probable response
532	6	2.0	212	2	A84359	hypothetical prote
533	6	2.0	213	2	T36076	tms-like protein
534	6	2.0	213	2	C83243	acyl carrier prote
535	6	2.0	213	2	C49918	hypothetical prote
536	6	2.0	213	2	F70080	hypothetical prote
537	6	2.0	214	2	E75521	DNA-binding respon
538	6	2.0	214	2	E75613	hypothetical prote
539	6	2.0	214	2	A70846	hypothetical prote
540	6	2.0	215	1	WMBE21	UL14 protein - hum

541	6	2.0	215	2	A41681	S-crystallin 1 - g	614	6	2.0	235	2	F86598	pseudouridine synt
542	6	2.0	215	2	JC5114	glutathione transf	615	6	2.0	235	2	G81515	ribosomal large ch
543	6	2.0	215	2	E72736	probable DNA polym	616	6	2.0	235	2	G64915	detribiotin synth
544	6	2.0	215	2	H87602	flagellin modifica	617	6	2.0	235	2	H85764	detribiotin synth
545	6	2.0	216	2	C83879	transcription regu	618	6	2.0	235	2	C90916	detribiotin synth
546	6	2.0	216	2	AF2905	esterase [imported	619	6	2.0	235	2	A75413	hypothetical prote
547	6	2.0	216	2	T46688	hypothetical prote	620	6	2.0	236	2	T07260	sulfate transport
548	6	2.0	217	2	T47175	hypothetical prote	621	6	2.0	236	2	A84319	DNA repair protei
549	6	2.0	218	2	E85021	hypothetical prote	622	6	2.0	236	2	D97128	probable pseudouri
550	6	2.0	218	2	B72116	hypothetical prote	623	6	2.0	236	2	S51332	ubiquitin thiole
551	6	2.0	218	2	H82758	hypothetical prote	624	6	2.0	236	2	AG0589	probable polyacch
552	6	2.0	219	2	S62804	ribosomal protein	625	6	2.0	237	2	A64153	dtpw kinase (BC 2.
553	6	2.0	219	2	I52911	cytoskeletal prote	626	6	2.0	237	2	C64637	amino acid ABC tra
554	6	2.0	219	2	C84280	ABC-type transport	627	6	2.0	237	2	D71877	probable amino aci
555	6	2.0	220	2	A97953	multidrug efflux p	628	6	2.0	237	2	A88640	protein C3H4.4 f1
556	6	2.0	220	2	AC1109	hypothetical prote	629	6	2.0	237	2	A64352	hypothetical prote
557	6	2.0	221	2	G83604	conserved hypotet	630	6	2.0	237	2	T13649	hypothetical prote
558	6	2.0	221	2	E71477	hypothetical prote	631	6	2.0	237	2	JC7217	paternally imprint
559	6	2.0	221	2	F84148	hypothetical prote	632	6	2.0	238	1	S72623	ribulose-5-phospha
560	6	2.0	222	2	AE0276	detribiotin synth	633	6	2.0	238	1	WZBE2	gene 2 protein - h
561	6	2.0	222	2	S07280	para protein - Agr	634	6	2.0	238	2	T05962	1,3-beta-glucanase
562	6	2.0	222	2	B49599	polymerase-associa	635	6	2.0	238	2	T05959	1,3-beta-glucanase
563	6	2.0	222	2	F86758	DNA replication pr	636	6	2.0	238	2	T05957	probable membrane
564	6	2.0	222	2	A36730	hutg protein - Kle	637	6	2.0	238	2	T35088	hypothetical prote
565	6	2.0	222	2	S19931	glycine-rich prote	638	6	2.0	238	2	H72646	hypothetical prote
566	6	2.0	223	2	E87654	hypothetical prote	639	6	2.0	239	2	AB3143	conserved hypotet
567	6	2.0	223	2	T08672	hypothetical prote	640	6	2.0	239	2	AC0987	gntr family regula
568	6	2.0	224	2	H97541	thymidylate kinase	641	6	2.0	239	2	AB3193	conserved hypotet
569	6	2.0	224	2	T43331	clathrin light cha	642	6	2.0	240	1	VCWGN4	coat protein - nar
570	6	2.0	224	2	G97680	arylesterase VCA07	643	6	2.0	240	2	A95219	hypothetical prote
571	6	2.0	224	2	S61386	lcmy protein - Leg	644	6	2.0	241	2	G98082	hypothetical prote
572	6	2.0	224	2	D95335	hypothetical prote	645	6	2.0	241	2	E81741	ribosomal large ch
573	6	2.0	225	2	G83244	probable two-compo	646	6	2.0	241	2	F71478	probable pseudouri
574	6	2.0	225	2	G84310	cobalamin adenosyl	647	6	2.0	242	2	S35060	croptomycin - hydr
575	6	2.0	225	2	T08780	hypothetical prote	648	6	2.0	242	2	A11238	uridylylate kinases
576	6	2.0	226	2	G83336	probable two-compo	649	6	2.0	242	2	AB1601	ABC transporter, A
577	6	2.0	226	2	F83406	hypothetical prote	650	6	2.0	242	2	F95256	hypothetical prote
578	6	2.0	226	2	G95247	hypothetical prote	651	6	2.0	242	2	G98121	hypothetical prote
579	6	2.0	226	2	PC6047	probable ABC-type	652	6	2.0	244	2	B81690	probable sodium-tr
580	6	2.0	227	2	D75522	oxidoreductase, sh	653	6	2.0	244	2	H75107	hypothetical prote
581	6	2.0	227	2	A35514	[D-Ala(2)] deltorp	654	6	2.0	244	2	E70905	hypothetical prote
582	6	2.0	227	2	G83110	hypothetical prote	655	6	2.0	244	2	T02511	DREB-like AP2 doma
583	6	2.0	227	2	T37134	hypothetical prote	656	6	2.0	245	2	C95314	myb-related protei
584	6	2.0	228	2	S46965	microfilariar shea	657	6	2.0	245	2	D95334	dhfrdipicolinat
585	6	2.0	228	2	S19132	rab25 protein - ri	658	6	2.0	245	2	F81223	conserved hypotet
586	6	2.0	228	2	C70884	probable transcrip	659	6	2.0	245	2	E84169	hypothetical prote
587	6	2.0	228	2	T49891	glycine-rich prote	660	6	2.0	245	2	E32057	hypothetical prote
588	6	2.0	229	2	S66342	ribonuclease II (E	661	6	2.0	246	1	S71283	myb-related protei
589	6	2.0	229	2	T40789	clathrin light cha	662	6	2.0	246	2	C81679	dihydridipicolinat
590	6	2.0	229	2	D82426	conserved hypotet	663	6	2.0	246	2	A33692	cytotoxic T-lympho
591	6	2.0	229	2	H83980	ABC transporter (A	664	6	2.0	246	2	D86197	hypothetical prote
592	6	2.0	230	2	AC2281	cob(I)alamin adeno	665	6	2.0	246	2	B48350	infected-cell prote
593	6	2.0	231	2	B81215	thiol-disulfide in	666	6	2.0	246	2	E95085	transcription regu
594	6	2.0	231	2	AG0681	detribiotin synth	667	6	2.0	246	2	F72766	hypothetical prote
595	6	2.0	231	2	C97552	hypothetical prote	668	6	2.0	246	2	D83476	probable sigma-70
596	6	2.0	231	2	AD2772	hypothetical prote	669	6	2.0	246	2	S74408	lipopeptide antibi
597	6	2.0	231	2	F83032	hypothetical prote	670	6	2.0	246	2	D98112	hypothetical prote
598	6	2.0	231	2	AH2872	hypothetical prote	671	6	2.0	246	2	AH3072	transcription regu
599	6	2.0	231	2	B97649	probable ATP-bindi	672	6	2.0	246	2	AD2084	transcription regu
600	6	2.0	232	2	G69080	conserved hypotet	673	6	2.0	247	2	S06035	type II site-speci
601	6	2.0	232	2	T04354	hypothetical prote	674	6	2.0	247	2	A55717	myelin/oligodendro
602	6	2.0	232	2	H75422	hypothetical prote	675	6	2.0	248	2	T35870	hypothetical prote
603	6	2.0	232	2	B46265	photosystem I-like	676	6	2.0	248	2	G98224	serine dehydrogena
604	6	2.0	233	2	S33946	hexon-associated p	677	6	2.0	249	2	AH3061	conserved hypotet
605	6	2.0	233	2	T35594	hypothetical prote	678	6	2.0	249	2	B70427	hypothetical prote
606	6	2.0	233	2	C64412	hypothetical prote	679	6	2.0	249	2	E64404	hypothetical prote
607	6	2.0	233	2	A83862	initiation of chro	680	6	2.0	249	2	E72646	probable molybdopt
608	6	2.0	233	2	G70776	hypothetical prote	681	6	2.0	249	2	JC7857	NADP+-dependent se
609	6	2.0	234	2	T26560	hypothetical prote	682	6	2.0	250	2	D69470	conserved hypotet
610	6	2.0	234	2	A87337	conserved hypotet	683	6	2.0	251	2	D96010	hypothetical expor
611	6	2.0	235	2	T42096	ATP-dependent Clp	684	6	2.0	251	2	G95361	probable ABC trans
612	6	2.0	235	2	H75539	branched-chain ami	685	6	2.0	252	2	H82956	probable short-cha
613	6	2.0	235	2	H72025	probable pseudouri	686	6	2.0	252	2	AB1030	probable membrane

687	6	2.0	252	2	E83570	hypothetical prote	760	6	2.0	268	2	A49303	homeotic protein C
688	2.0	253	2	T04642	hypothetical prote	761	6	2.0	269	2	H82616	hypothetical prote	
689	2.0	253	2	D71975	hypothetical prote	762	6	2.0	269	2	G98144	hypothetical prote	
690	2.0	253	2	E64532	hypothetical prote	763	6	2.0	269	2	AH0838	probable exported	
691	2.0	253	2	T31021	hypothetical prote	764	6	2.0	269	2	T36910	hypothetical prote	
692	2.0	254	2	A82625	endonuclease V (de	765	6	2.0	270	2	G75412	spermidine/putresc	
693	2.0	254	2	T26793	hypothetical prote	766	6	2.0	270	2	T41759	LEF-1 orf14 - Bomb	
694	2.0	254	2	T35366	probable membrane	767	6	2.0	270	2	T35721	hypothetical prote	
695	2.0	255	2	C75594	phosphoadenosine P	768	6	2.0	271	2	F81381	2-dehydro-3-deoxy-	
696	2.0	255	2	A27122	cathepsin G (EC 3.	769	6	2.0	272	2	T48567	ABA-responsive pro	
697	2.0	255	2	E95931	probable amino aci	770	6	2.0	272	2	A11098	PuRr, transcriptio	
698	2.0	255	2	T35217	hypothetical prote	771	6	2.0	272	2	AH1461	PuRr, transcriptio	
699	2.0	255	2	A39195	DA82 protein - Ye	772	6	2.0	272	2	H83269	hypothetical prote	
700	2.0	255	2	B84179	hypothetical prote	773	6	2.0	272	2	H83004	hypothetical prote	
701	2.0	255	2	T46350	hypothetical prote	774	6	2.0	272	2	S52977	hypothetical prote	
702	2.0	256	2	A11119	transcription regu	775	6	2.0	272	2	C75548	hypothetical prote	
703	2.0	256	2	AD1480	transcription regu	776	6	2.0	272	2	AC0140	probable membrane	
704	2.0	256	2	T47020	hypothetical prote	777	6	2.0	273	1	X1ECRO	rRNA (adenine-N6,N	
705	2.0	256	2	AEO236	probable deor-fam1	778	6	2.0	273	2	C75562	probable shikimate	
706	2.0	256	2	H72078	probable sodium-tr	779	6	2.0	273	2	AF0513	dimethyladenosine	
707	2.0	256	2	D66544	NADH (ubiquinone)	780	6	2.0	273	2	H85486	dimethyladenosine	
708	2.0	256	2	A96027	probable ABC trans	781	6	2.0	273	2	H90635	chlorophyll a/b-pi	
709	2.0	257	2	AF0396	probable amino aci	782	6	2.0	273	2	J50172	transposase - Bac	
710	2.0	257	2	C86784	pseudouridine synt	783	6	2.0	273	2	S12637	hypothetical prote	
711	2.0	257	2	G72648	hypothetical prote	784	6	2.0	273	2	B83318	hypothetical prote	
712	2.0	257	2	A81412	SMF family protein	785	6	2.0	273	2	T33619	hypothetical prote	
713	2.0	257	2	B97726	hypothetical prote	786	6	2.0	274	2	AF0493	probable formate d	
714	2.0	258	2	T32939	hypothetical prote	787	6	2.0	274	2	T36680	probable oxidoredu	
715	2.0	259	2	A83294	probable permease	788	6	2.0	274	2	A55335	myelin regulatory	
716	2.0	259	2	T34536	hypothetical prote	789	6	2.0	274	2	H83525	conserved hypothet	
717	2.0	259	2	T29459	hypothetical prote	790	6	2.0	274	2	F83601	hypothetical prote	
718	2.0	259	2	S32898	hypothetical prote	791	6	2.0	275	1	WJ2FX2	homeotic protein H	
719	2.0	259	2	A86409	hypothetical prote	792	6	2.0	275	1	H83325	hypothetical prote	
720	2.0	259	2	G81714	ABC transporter, A	793	6	2.0	275	2	T36573	probable partition	
721	2.0	259	2	F71561	probable rRNA meth	794	6	2.0	275	2	T16312	hypothetical prote	
722	2.0	260	2	G75169	abc transporter AT	795	6	2.0	275	2	B55224	hypothetical prote	
723	2.0	260	2	E71045	probable ABC trans	796	6	2.0	276	2	D75302	ABC transporter, p	
724	2.0	261	2	A95930	probable enoyl-CoA	797	6	2.0	276	2	H86922	probable ABC trans	
725	2.0	261	2	JC4110	triacylglycerol 1i	798	6	2.0	276	2	G75358	hypothetical prote	
726	2.0	261	2	A99965	flagellar biosynth	799	6	2.0	277	1	S68421	endopeptidase Clp	
727	2.0	261	2	A85813	flagellar biosynth	800	6	2.0	277	2	H87045	short chain alcoh	
728	2.0	261	2	C64959	probable export pr	801	6	2.0	277	2	G83473	probable short-cha	
729	2.0	261	2	E72735	hypothetical prote	802	6	2.0	277	2	T51975	proteasome endopep	
730	2.0	261	2	AC0332	probable Ompa fam1	803	6	2.0	277	2	AB3185	conserved hypothet	
731	2.0	261	2	G72470	probable ABC trans	804	6	2.0	278	1	A47404	alpha-tocopherol t	
732	2.0	261	2	S63604	homeobox protein G	805	6	2.0	278	2	B83152	probable short-cha	
733	2.0	263	2	D90231	conserved hypothet	806	6	2.0	278	2	H75259	epoxide hydrolase-	
734	2.0	264	2	B95231	pyruvate formate-I	807	6	2.0	278	2	S54352	alpha-tocopherol t	
735	2.0	264	2	E96095	formate acetyltran	808	6	2.0	278	2	C43670	integral membrane	
736	2.0	264	2	T09449	allergen V - velve	809	6	2.0	278	2	S44796	probable ATP-bind1	
737	2.0	264	2	AF0753	flagellar biosynth	810	6	2.0	278	2	B83354	quinolinate phosph	
738	2.0	264	2	B86432	protein T518.12 1i	811	6	2.0	279	2	A69112	thioesterase - Str	
739	2.0	265	2	T36396	probable short cha	812	6	2.0	280	2	T34920	probable pseudour	
740	2.0	265	2	AH0775	hydroxyethylthiazo	813	6	2.0	280	2	H71276	allergen Phl p Vb	
741	2.0	265	2	B96322	phosphomethylpyrim	814	6	2.0	280	2	S38584	Tomb protein NMA19	
742	2.0	265	2	AD2961	phosphomethylpyrim	815	6	2.0	280	2	F81827	Tomb protein NMA17	
743	2.0	265	2	A33513	hypothetical prote	816	6	2.0	280	2	A81049	granzyme B (EC 3.4	
744	2.0	265	2	T17386	vr1g protein - Dic	817	6	2.0	281	1	A61021	aldo/keto reductas	
745	2.0	265	2	T48410	hypothetical prote	818	6	2.0	281	2	A97604	probable imidazole	
746	2.0	265	2	B61188	SCI protein - mous	819	6	2.0	281	2	AB2826	hypothetical prote	
747	2.0	265	2	H72574	hypothetical prote	820	6	2.0	281	2	T06530	hypothetical prote	
748	2.0	266	2	F70595	hypothetical prote	821	6	2.0	281	2	T34282	hypothetical prote	
749	2.0	266	2	F72851	late expression fa	822	6	2.0	281	2	T26795	hypothetical prote	
750	2.0	266	2	T20142	hypothetical prote	823	6	2.0	281	2	F86355	probable rRNA meth	
751	2.0	266	2	T02807	arsenate reductase	824	6	2.0	282	2	T36832	hypothetical prote	
752	2.0	266	2	S54440	hemin-specific ATP	825	6	2.0	282	2	A17081	phosphoprotein pho	
753	2.0	267	2	T08283	hypothetical prote	826	6	2.0	282	2	H75537	hypothetical prote	
754	2.0	267	2	E83232	probable ATP-bind1	827	6	2.0	283	2	H95194	hypothetical prote	
755	2.0	267	2	AB2933	hypothetical prote	828	6	2.0	283	2	E82979	conserved hypothet	
756	2.0	267	2	E98349	hypothetical prote	829	6	2.0	283	2	E98061	transcription regu	
757	2.0	268	2	E75607	2-oxo-hepta-3-ene-	830	6	2.0	283	2	A11027	lyser-type transect	
758	2.0	268	2	T51066	hypothetical prote	831	6	2.0	283	2	B98257	deoxyribonuclease	
759	2.0	268	2	B30819	interferon-regulat	832	6	2.0	284	1	S13676		

833	6	2.0	284	2	T28018	hypothetical prote
834	6	2.0	284	2	T13621	hypothetical prote
835	6	2.0	284	2	E69113	hypothetical prote
836	6	2.0	284	2	S18957	fix3-5 protein -
837	6	2.0	284	2	S04278	hypoxanthine phosph
838	6	2.0	284	2	B41224	homeotic protein p
839	6	2.0	285	1	NDBC4	deoxyribonuclease
840	6	2.0	285	1	E85854	endonuclease IV (l
841	6	2.0	285	2	AC0783	endonuclease IV (l
842	6	2.0	285	2	C91010	endonuclease IV (l
843	6	2.0	285	2	S66076	transcription repr
844	6	2.0	285	2	A82609	hypothetical prote
845	6	2.0	285	2	C84170	ribosomal protein
846	6	2.0	285	2	A40657	hypothetical prote
847	6	2.0	285	2	S09614	hypoxanthine phosph
848	6	2.0	286	2	B70833	carbon-monoxide de
849	6	2.0	286	2	B64536	hypothetical prote
850	6	2.0	286	2	B84537	hypothetical prote
851	6	2.0	288	2	S62175	transport vesicle
852	6	2.0	288	2	D82781	conserved hypothet
853	6	2.0	289	2	H95929	probable hydroxyme
854	6	2.0	289	2	G95963	probable transcrip
855	6	2.0	289	2	H85434	hypothetical prote
856	6	2.0	289	2	F87110	probable signal pep
857	6	2.0	289	2	C69349	conserved hypothet
858	6	2.0	290	2	I39522	3-dehydroquinate d
859	6	2.0	290	2	T03552	malose transport
860	6	2.0	290	2	H98336	malose transport
861	6	2.0	290	2	A82946	hypothetical prote
862	6	2.0	290	2	A11014	4-hydroxybenzoate
863	6	2.0	291	2	S64825	hypothetical prote
864	6	2.0	291	2	AC3299	glutamate-tRNA lig
865	6	2.0	292	2	H82113	dihydrodipicolinat
866	6	2.0	292	2	G75288	hypothetical prote
867	6	2.0	292	2	C95147	11c protein (impo
868	6	2.0	293	2	D90978	hypothetical prote
869	6	2.0	293	2	D95381	probable LysR-fam1
870	6	2.0	294	2	H84023	phosphate ABC tran
871	6	2.0	295	2	AE0993	glycerol-3-phospha
872	6	2.0	295	2	H98222	hypothetical prote
873	6	2.0	295	2	AH3063	hypothetical prote
874	6	2.0	295	2	AD3552	high-affinity bran
875	6	2.0	295	2	B83433	translocator prote
876	6	2.0	295	2	E82659	peptidyl-prolyl ci
877	6	2.0	295	2	T22833	hypothetical prote
878	6	2.0	296	2	F87411	hypothetical prote
879	6	2.0	296	2	A98015	hypothetical prote
880	6	2.0	297	2	A83049	hypothetical prote
881	6	2.0	297	2	B89473	hypothetical prote
882	6	2.0	297	2	T13317	protein F52D2.3 (l
883	6	2.0	297	2	H95323	hypothetical prote
884	6	2.0	298	2	AG3165	hypothetical prote
885	6	2.0	298	2	H82953	conserved hypothet
886	6	2.0	299	2	A95878	hypothetical prote
887	6	2.0	299	2	S32874	probable N-acetylin
888	6	2.0	299	2	T35765	hyb protein - Rhl
889	6	2.0	299	2	S55472	hypothetical prote
890	6	2.0	300	2	T06569	pectin lyase (EC 4
891	6	2.0	300	2	F63793	farneesyltransferas
892	6	2.0	300	2	H86358	site-specific reco
893	6	2.0	300	2	G82975	zinc finger protei
894	6	2.0	301	1	RGEGR	probable two-compo
895	6	2.0	301	2	E85902	GTP-binding protei
896	6	2.0	301	2	A80829	GTP-binding protei
897	6	2.0	301	2	H91057	GTP-binding protei
898	6	2.0	301	2	E97972	conserved hypothet
899	6	2.0	301	2	T36520	hypothetical prote
900	6	2.0	301	2	B84533	hypothetical prote
901	6	2.0	301	2	A98214	hypothetical prote
902	6	2.0	303	2	T36826	probable 3-hydroxy
903	6	2.0	303	2	S73051	tropinesterase hom
904	6	2.0	303	2	F83791	hydroxymethylgluta
905	6	2.0	303	2	S23440	hypothetical prote
906	6	2.0	303	2	A43708	gamma-interferon-1
907	6	2.0	303	2	H83108	hypothetical prote
908	6	2.0	303	2	T02588	hypothetical prote
909	6	2.0	304	2	T22602	hypothetical prote
910	6	2.0	305	2	F83548	GTP-binding protei
911	6	2.0	305	2	UN0647	hydrogenase expres
912	6	2.0	305	2	T20470	hypothetical prote
913	6	2.0	305	2	T36261	hypothetical prote
914	6	2.0	305	2	I57039	genomic screen hom
915	6	2.0	306	2	F98183	malose transport
916	6	2.0	306	2	A90966	probable transmemb
917	6	2.0	306	2	JS0266	membrane protein y
918	6	2.0	306	2	G70481	thiamin monophosph
919	6	2.0	306	2	T21220	hypothetical prote
920	6	2.0	306	2	A85814	hypothetical prote
921	6	2.0	306	2	E72598	probable transmemb
922	6	2.0	307	2	D86194	probable ABC-trans
923	6	2.0	307	2	T27609	hypothetical prote
924	6	2.0	307	2	G69505	hypothetical prote
925	6	2.0	307	2	B96745	unknown protein T9
926	6	2.0	307	2	A45581	Distal-less homeob
927	6	2.0	308	2	S77938	EBNA-LP protein -
928	6	2.0	308	2	F72704	probable iron (III
929	6	2.0	308	2	A70761	hypothetical prote
930	6	2.0	308	2	H87095	conserved hypothet
931	6	2.0	308	2	A12993	hypothetical prote
932	6	2.0	309	2	F70394	3-oxoacyl-l-acyl-ca
933	6	2.0	309	2	A24849	ADP-ATP carrier pr
934	6	2.0	309	2	AE1904	hypothetical prote
935	6	2.0	309	2	B96032	probable two-compo
936	6	2.0	310	2	A83353	probable binding-P
937	6	2.0	310	2	G95395	probable LysR-fam1
938	6	2.0	310	2	G87624	integral membrane
939	6	2.0	310	2	AC2035	phytoene synthase
940	6	2.0	310	2	D70745	hypothetical prote
941	6	2.0	310	2	A70620	probable PB protei
942	6	2.0	311	2	F75366	hypothetical prote
943	6	2.0	311	2	T23438	hypothetical prote
944	6	2.0	311	2	A24400	nodulation protei
945	6	2.0	312	2	E69045	8-oxoguanine DNA g
946	6	2.0	312	2	D95891	probable glycine-b
947	6	2.0	312	2	AP2772	lipid A biosynthes
948	6	2.0	312	2	D97552	lipid A biosynthes
949	6	2.0	313	1	XYNHCL	site-specific DNA-
950	6	2.0	313	2	AC0603	asparaginase (EC 3
951	6	2.0	313	2	F72575	hypothetical prote
952	6	2.0	313	2	AH0966	conserved hypothet
953	6	2.0	313	2	C75288	conserved hypothet
954	6	2.0	313	2	G71550	probable phospholi
955	6	2.0	313	2	AB0596	formimidoylglutama
956	6	2.0	313	2	F64069	survival protein 8
957	6	2.0	314	2	F96574	hypothetical prote
958	6	2.0	314	2	B83559	probable peptidyl-
959	6	2.0	314	2	S70101	hypothetical prote
960	6	2.0	314	2	JC5273	paired type homeob
961	6	2.0	314	2	T03775	DNA-binding homeob
962	6	2.0	315	2	B84403	dipeptide ABC tran
963	6	2.0	316	2	G64762	acetaldehyde dehyd
964	6	2.0	316	2	B85530	acetaldehyde dehyd
965	6	2.0	316	2	F90679	acetaldehyde dehyd
966	6	2.0	316	2	T44749	hypothetical prote
967	6	2.0	316	2	G81045	piilin gene inverti
968	6	2.0	316	2	B70571	hypothetical prote
969	6	2.0	316	2	T10436	probable transposa
970	6	2.0	317	1	E87185	3',5'-cyclic-nucle
971	6	2.0	317	2	T35981	probable peptide t
972	6	2.0	317	2	A55884	retinol dehydrogen
973	6	2.0	317	2	I55462	hypothetical prote
974	6	2.0	317	2	PA6901	hypothetical prote
975	6	2.0	318	2	A82319	hypothetical prote
976	6	2.0	318	2	AG0829	glutathione synth
977	6	2.0	318	2	I63298	sigma-B factor reg
978	6	2.0	318	2	C85903	regulates activity



```

979 6 2.0 318 2 B91058 sigma-E factor reg
980 6 2.0 318 2 T02998 sigma-E factor reg
981 6 2.0 318 2 C83209 probable oxidoredu
982 6 2.0 319 2 T35538 cytochrome-c oxida
983 6 2.0 319 2 G83888 transmembrane 1ipo
984 6 2.0 319 2 G82694 ABC transporter su
985 6 2.0 319 2 P75420 hypothetical prote
986 6 2.0 320 2 E98176 hypothetical prote
987 6 2.0 320 2 AG3110 dehydrogenase Atu4
988 6 2.0 320 2 AD0563 ferredoxin-like (fm
989 6 2.0 320 2 A12305 hypothetical prote
990 6 2.0 321 2 D64820 probable asparagin
991 6 2.0 322 2 T27308 hypothetical prote
992 6 2.0 322 2 T04595 conserved hypotnet
993 6 2.0 322 2 E70306 F15K3_4 protein -
994 6 2.0 322 2 C86165 chlorodoxin reduct
995 6 2.0 323 2 D90413 hypothetical prote
996 6 2.0 323 2 H70765 porphobilinogen sy
997 6 2.0 324 1 C42728 probable class II
998 6 2.0 324 2 E75522 delta-aminolevulin
999 6 2.0 324 2 AB1269 delta-aminolevulin
1000 6 2.0 324 2 AD1631

```

## ALIGNMENTS

```

RESULT 1
T30656
hypothetical protein 54L - Molluscum contagiosum virus 1
N:Alternate names: MC054L
C:Species: Molluscum contagiosum virus 1
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T30656
R:Senkevich, T.G.; Buger, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A:Reference number: 220876; MUID:9652559; PMID:8670425
A:Accession: T30656
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <SEN>
A:Cross-references: UNIPROT:Q98222; EMBL:U60315; PIDN:AA055182.1
C:Genetics:
A:Note: MC054L

Query Match 3.3%; Score 10; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRGAP 176
Db 156 GARRRRGAP 165

RESULT 2
A72522
hypothetical protein APE2150 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72522
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
dna, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <KAW>
A:Cross-references: UNIPROT:Q9Y9Y9; DDBJ:AP000063; NID:G5105654; PIDN:BA081161.1; PID:dl
A:Experimental source: strain K1
C:Genetics:

```

```

A:Gene: APE2150
C:Superfamily: Aeropyrum pernix hypothetical protein APE2150

```

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Query Match 3.0%; Score 9; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 116 SYGRSSSSK 124
Db 95 SYGRSSSSK 103

```

```

RESULT 3
AE2664
ATP synthase C chain atpC [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE2664
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepsan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE2664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: UNIPROT:Q8UH97; GB:AE008688; PIDN:AAL41731.1; PID:gl7739081; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: atpC
A:Map position: circular chromosome
A:Superfamily: H+-transporting ATP synthase lipid-binding protein

```

```

Query Match 2.6%; Score 8; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 264 GDYISGAL 271
Db 30 GDYISGAL 37

```

```

RESULT 4
D97446
ATP synthase chain C (AF054609) [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: D97446
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurollo, B.; Goldman,
A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: D97446
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: UNIPROT:Q8UH97; GB:AE007869; PIDN:AAK86525.1; PID:g15155683; GSPDB:G
C:Genetics:
A:Gene: AGR_C 1297
A:Map position: circular chromosome
C:Superfamily: H+-transporting ATP synthase lipid-binding protein

Query Match 2.6%; Score 8; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 GDYISGAL 271

```

Db 30 GDYLSGAL 37

# RESULT 5

C84492 hypothetical protein At2g10550 [imported] - Arabidopsis thaliana

CISpecies: Arabidopsis thaliana (mouse-ear cress)

CDate: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

CISpecies: C84492

RLin: X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon, L.

enes, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:1061197

A:Accession: C84492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-170 <STO>

A:Cross-references: UNIPROT:Q9S187; GB:AE002093; NID:g4733994; PIDN:AAD28673.1; GSPDB:GN

C:Genetics:

A:Gene: At2g10550

A:Map position: 2

Query Match 2.6%; Score 8; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 240 RSRDLSV 247  
|||||  
Db 37 RSRDLSV 44

# RESULT 6

C70601 hypothetical protein RV0992c - Mycobacterium tuberculosis (strain H37RV)

CISpecies: Mycobacterium tuberculosis

CDate: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

CISpecies: C70601

R: Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70601

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <COL>

A:Cross-references: UNIPROT:O05575; GB:Z94752; GB:AL123456; NID:g3261731; PIDN:CAB08152.

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV0992c

C:Superfamily: human 5-formyltetrahydrofolate cyclo-ligase

Query Match 2.6%; Score 8; DB 2; Length 197;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 AGGLARAR 63  
|||||  
Db 95 AGGLARAR 102

# RESULT 7

B87197 hypothetical protein ML2302 [imported] - Mycobacterium leprae

CISpecies: Mycobacterium leprae

CDate: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

CISpecies: B87197

R: Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc

A>Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: B87197

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-224 <STO>

A:Cross-references: UNIPROT:Q9CB91; GB:AL450380; NID:g13093927; PIDN:CAC31818.1; GSPDB:G

C:Genetics:

A:Gene: ML2302

C:Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding c

Query Match 2.6%; Score 8; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 QLLRVLAR 95  
|||||  
Db 122 QLLRVLAR 129

# RESULT 8

E70790 probable transcription regulator RV3676 - Mycobacterium tuberculosis (strain H37RV)

CISpecies: Mycobacterium tuberculosis

CDate: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

CISpecies: E70790

R: Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: E70790

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-224 <COL>

A:Cross-references: UNIPROT:O69644; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA1799

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV3676

C:Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding d

Query Match 2.6%; Score 8; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 QLLRVLAR 95  
|||||  
Db 122 QLLRVLAR 129

# RESULT 9

B70328 hypothetical protein ag\_313 - Aquifex aeolicus

CISpecies: Aquifex aeolicus

CDate: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

CISpecies: B70328

R: Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V.

Nature 392, 353-358, 1998

A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: B70328

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-279 <AGP>

A:Cross-references: UNIPROT:O66554; GB:AE000683; NID:g2982996; PIDN:AAC06617.1; PID:g298

A:Experimental source: strain VPS

C:Genetics:

A:Gene: sq\_313  
 C:Superfamily: hypothetical protein HP0152

Query Match 2.6%; Score 8; DB 2; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 GREAVRL 296  
 DB 248 GREAVRL 255

RESULT 10  
 S46793  
 N:Alternate names: protein PEP1; protein VPS29; protein YHR012w  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
 C:Accession: S46793

R:Du. Z.  
 Submitted to the EMBL Data Library, June 1994  
 A:Description: The sequence of S. cerevisiae cosmid L2825.  
 A:Reference number: S46774  
 A:Accession: S46793  
 A:Molecule type: DNA  
 A:Residues: 1-282 <DUB>  
 A:Cross-references: UNIPROT:P38759; EMBL:U10400; NID:G500701; PID:G500712; GSPDB:GN00008  
 C:Genetic8:  
 A:Gene: VPS29; MIPS:YHR012w  
 A:Cross-references: MIPS:YHR012w; SGD:S0001054  
 A:Map position: 8R  
 A:Introns: 16/3  
 C:Superfamily: VPS29-like phosphoesterase-related protein

Query Match 2.6%; Score 8; DB 2; Length 282;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ALAROLDV 231  
 DB 120 ALAROLDV 127

RESULT 11  
 S20880  
 homeotic protein Hox 4.5 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-2004  
 C:Accession: S20880; S09569; S09398  
 R:Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte, J.C.; Buerki, K.; Duboule, EMO J. 11, 1459-1468, 1992  
 A>Title: Comparison of mouse and human HOX-4 complexes defines conserved sequences invol  
 A:Reference number: S20879; MUID:92224884; PMID:1348690  
 A:Accession: S20880  
 A:Molecule type: DNA  
 A:Residues: 1-339 <RNA>  
 A:Cross-references: UNIPROT:P28357; EMBL:X62669; NID:G51414; PIDN:CAA44542.1; PID:G51416  
 R:Duboule, D.; Dolle, P.  
 EMO J. 8, 1497-1505, 1989  
 A>Title: The structural and functional organization of the murine HOX gene family resemb  
 A:Reference number: S09569; MUID:89356621; PMID:2569969  
 A:Accession: S09569  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 272-331 <DUB>  
 A:Cross-references: EMBL:X14714; NID:G51427; PIDN:CAB57813.1; PID:G6015583  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989  
 R:Dolle, P.; Duboule, D.  
 EMO J. 8, 1507-1515, 1989  
 A>Title: Two gene members of the murine HOX-5 complex show regional and cell-type specific  
 A:Reference number: S09398; MUID:89356622; PMID:2569970  
 A:Accession: S09398  
 A:Molecule type: DNA

A:Residues: 272-331 <DOL>  
 A:Cross-references: GB:X14714; GB:W21040; NID:G51427; PIDN:CAB57813.1; PID:G6015583  
 C:Genetic8:  
 A:Gene: Hox-4.5  
 A:Introns: 260/1  
 C:Superfamily: homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:273-329/Domain: homeobox homology <HOX>

Query Match 2.6%; Score 8; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 SSSSKRTE 127  
 DB 173 SSSSKRTE 180

RESULT 12  
 S18649  
 homeotic protein HOX D9 - human  
 N:Alternate names: homeotic protein Hox 4C; homeotic protein Hox 5.2  
 C:Species: Homo sapiens (man)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Aug-2004  
 C:Accession: S18649; S05958; S14935; A32830  
 R:Zappavigna, V.; Renucci, A.; Izpisua-Belmonte, J.C.; Uribe, G.; Peschle, C.; Duboule, EMO J. 10, 4177-4187, 1991  
 A>Title: HOX4 gene encode transcription factors with potential auto- and cross-regulatio  
 A:Reference number: S18649; MUID:92097538; PMID:1756725  
 A:Accession: S18649  
 A:Molecule type: mRNA  
 A:Residues: 1-342 <ZAP>  
 A:Cross-references: UNIPROT:P28356; EMBL:X59372; NID:G32390; PIDN:CAA42016.1; PID:G32391  
 A>Note: intron position was determined by sequencing of genomic DNA  
 R:Oliver, G.; Sidell, N.; Fiske, W.; Heinemann, C.; Mohandes, T.; Sparkes, R.S.; De Robe  
 Genes Dev. 3, 641-650, 1989  
 A>Title: Complementary homeo protein gradients in developing limb buds.  
 A:Reference number: A32830; MUID:89306602; PMID:2568311  
 A:Accession: S05958  
 A:Molecule type: DNA  
 A:Residues: 264-265, 'A', 267-342 <OLI>  
 A:Cross-references: EMBL:X15506; NID:G32397; PIDN:CAA33528.1; PID:G32398  
 R:Acampora, D.; d'Esposito, M.; Falletta, A.; Pannese, M.; Migliaccio, E.; Morelli, F.; S  
 Nucleic Acids Res. 17, 10385-10402, 1989  
 A>Title: The human HOX gene family.  
 A:Reference number: S07541; MUID:90098876; PMID:2574852  
 A:Accession: S14935  
 A:Molecule type: DNA  
 A:Residues: 275-340 <ACA>  
 C:Genetic8:  
 A:Gene: GDB:HOXD9  
 A:Cross-references: GDB:120678; OMIM:142982  
 A:Map position: 2q31-2q31  
 A:Introns: 263/1  
 C:Superfamily: homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:276-332/Domain: homeobox homology <HOX>

Query Match 2.6%; Score 8; DB 2; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 SSSSKRTE 127  
 DB 175 SSSSKRTE 182

RESULT 13  
 T34931  
 hypothetical protein SC3F9.09 SC3F9.09 - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
 C:Accession: T34931

R,Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, June 1998  
 A:Reference number: Z21562  
 A:Accession: T34931  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-363 <SEE>  
 A:Cross-references: UNIPROT:O69949; EMBL:AL023862; PIDD:CAA19632.1; GSPDB:GN00070; SCOPED  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCOPDB:SC3F9.09

Query Match 2.6%; Score 8; DB 2; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LSGSTPAP 10  
 |||||  
 Db 269 LSGSTPAP 276

RESULT 14  
 E86858  
 cell division protein FtsZ [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #ext\_change 09-Jul-2004  
 C:Accession: E86858  
 R:Botolin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich  
 Genome Res. 11, 731-753, 2001  
 A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
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 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: ftsZ  
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 J. Biol. Chem. 265, 21232-21236, 1990  
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OM protein - protein search, using sw model

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#### SUMMARIES

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236	7	2.3	123	16	US-10-437-963-107619	Sequence 107619,	309	7	2.3	173	15	US-10-108-260A-3431	Sequence 3431, Ap
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244	7	2.3	131	15	US-10-424-559-143113	Sequence 143113,	317	7	2.3	178	15	US-10-277-216-339	Sequence 339, App
245	7	2.3	132	15	US-10-437-963-191332	Sequence 191332,	318	7	2.3	178	15	US-10-126-022-339	Sequence 339, App
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393	2.3	233	US-10-437-963-159155	Sequence 159155,	466	2.3	267	US-10-932-284-7	Sequence 7, Appl
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399	2.3	236	US-10-437-963-147375	Sequence 147375,	472	2.3	268	US-10-081-347-33	Sequence 33, Appl
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435	2.3	253	US-10-425-114-65145	Sequence 62468, A	508	2.3	281	US-10-287-971-166	Sequence 166, App
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438	2.3	253	US-10-461-194-98	Sequence 98, Appl	511	2.3	281	US-10-287-971-172	Sequence 172, App
439	2.3	254	US-10-425-114-41468	Sequence 41468, A	512	2.3	281	US-10-287-971-174	Sequence 174, App
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698	7	2.3	366	15	US-10-243-552-443	Sequence 443, App	771	7	2.3	396	15	US-10-310-154-648	Sequence 648, App
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## ALIGNMENTS

## RESULT 1

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US-10-013-477-11
; Sequence 11, Application US/10013477
; Publication No. US20030049732A1
; GENERAL INFORMATION:
; APPLICANT: N1 et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO002P1
; CURRENT APPLICATION NUMBER: US/10/013,477
; PRIOR FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/669,445
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US00/06642
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/126,018
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/139,638
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/149,449
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-477-11

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 Best Local Similarity 100.0%; Pred. No. 5.4e-189;

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## RESULT 2

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US-10-001-254-18
; Sequence 18, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stemmer-Liawen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-18

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## RESULT 3

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US-10-296-539-1
; Sequence 1, Application US/10296539
; Publication No. US20030165933A1
; GENERAL INFORMATION:

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APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: AZIMZAI, Yalda
APPLICANT: YUE, Henry
APPLICANT: BURFORD, Neil
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: PATTERSON, Chandra
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: REGULATORS OF APOPTOSIS
FILE REFERENCE: PI-0307 PCT
CURRENT APPLICATION NUMBER: US/10/296,539
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
PRIOR FILING DATE: 2000-06-01; 2000-11-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: incyte ID No. US20030165933A1 3102521CD1
US-10-296-539-1
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RESULT 4
US-10-106-698-4626
/ Sequence 4626, Application US/10106698
/ Publication No. US20030109690A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
/ FILE REFERENCE: PA005PI
/ CURRENT APPLICATION NUMBER: US/10/106,698
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26524
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: US 60/157,137
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: US 60/163,280
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 8564
/ SOFTWARE: Patentin Ver. 3.0
/ SEQ ID NO 4626
/ LENGTH: 366
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-106-698-4626
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Query Match      73.9%; Score 224; DB 14; Length 366;
Best Local Similarity 100.0%; Pred. No. 6.3e-189;
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Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      80 ESNLRLLGQLRLVLAHDLPLHLARKRRPVSPERYSYGTSSSKRTGSCRRRQSSSS 139
DB     120 ESNLRLLGQLRLVLAHDLPLHLARKRRPVSPERYSYGTSSSKRTGSCRRRQSSSS 179
QY     140 ANSOGQWETGSPPTKRQRRSGRPSGARRRRRGAAPAPQOQSEPARPSSEKVTCDIR 199
DB     180 ANSOGQWETGSPPTKRQRRSGRPSGARRRRRGAAPAPQOQSEPARPSSEKVTCDIR 239
QY     200 LKVRAYEYCHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 259
DB     240 LKVRAYEYCHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 299
QY     260 DAFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
DB     300 DAFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 343
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RESULT 5
US-09-925-302-758
/ Sequence 758, Application US/09925302
/ Patent No. US20020044941A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1998-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 758
/ LENGTH: 319
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-925-302-758
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Query Match      64.0%; Score 194; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 1.6e-162;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      80 ESNLRLLGQLRLVLAHDLPLHLARKRRPVSPERYSYGTSSSKRTGSCRRRQSSSS 139
DB     120 ESNLRLLGQLRLVLAHDLPLHLARKRRPVSPERYSYGTSSSKRTGSCRRRQSSSS 179
QY     140 ANSOGQWETGSPPTKRQRRSGRPSGARRRRRGAAPAPQOQSEPARPSSEKVTCDIR 199
DB     180 ANSOGQWETGSPPTKRQRRSGRPSGARRRRRGAAPAPQOQSEPARPSSEKVTCDIR 239
QY     200 LKVRAYEYCHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 259
DB     240 LKVRAYEYCHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 299
QY     260 DAFMGDYLSGALLQ 273
DB     300 DAFMGDYLSGALLQ 313
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RESULT 6
US-09-925-302-758
/ Sequence 758, Application US/09925302
/ Publication No. US20030064072A9
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ CURRENT FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
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;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR APPLICATION NUMBER: 60/124,270  
;; PRIOR FILING DATE: 1999-03-12  
;; NUMBER OF SEQ ID NOS: 896  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO: 758  
;; LENGTH: 319  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-925-302-758

Query Match 64.0%; Score 194; DB 10; Length 319;  
Best Local Similarity 100.0%; Pred. No. 1.6e-162;  
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ESNRLGQLRVLRARHLLPHLARKRRPVSPERYSGTSSSKRTGSCRRRQSSSS 139  
DB 120 ESNRLGQLRVLRARHLLPHLARKRRPVSPERYSGTSSSKRTGSCRRRQSSSS 179  
QY 140 ANSOGQWETSPPTKRRRRSGRRSGARRRRRGAPAPQOQSEPARPSRGKTCIDR 199  
DB 180 ANSOGQWETSPPTKRRRRSGRRSGARRRRRGAPAPQOQSEPARPSRGKTCIDR 239  
QY 200 LRVRAVEYCEHGPALGQVARRRPPQALARDVFGQATVLRSRDLGVSVCIDIKFSELSTL 259  
DB 240 LRVRAVEYCEHGPALGQVARRRPPQALARDVFGQATVLRSRDLGVSVCIDIKFSELSTL 299  
QY 260 DAFMGDYLSGALLQ 273  
DB 300 DAFMGDYLSGALLQ 313

RESULT 7  
US-10-296-115-1220  
; Sequence 1220; Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO: 1220  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-296-115-1220

Query Match 44.2%; Score 134; DB 15; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1e-109;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 170 RRRRGAPAPQOQSEPARPSRGKTCIDRLRVRAVEYCEHGPALGQVARRRPPQALARDL 229  
DB 86 RRRRGAPAPQOQSEPARPSRGKTCIDRLRVRAVEYCEHGPALGQVARRRPPQALARDL 145  
QY 230 DVEGQATVLRSRDLGVSVCIDIKFSELSTYLDAFMGDYLSGALLQALRGVFLTEALREAVG 289  
DB 146 DVEGQATVLRSRDLGVSVCIDIKFSELSTYLDAFMGDYLSGALLQALRGVFLTEALREAVG 205  
QY 290 REAVRLVSVDEAD 303  
DB 206 REAVRLVSVDEAD 219

RESULT 8  
US-09-799-777-26  
; Sequence 26; Application US/09799777

;; Patent No. US20020091244A1  
;; GENERAL INFORMATION:  
;; APPLICANT: IAL, Preeti  
;; Hillman, Jennifer L.  
;; Corley, Neil C.  
;; Guegler, Karl J.  
;; Baugh, Mariah  
;; Sather, Susan  
;; Shah, Purvi  
;; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS  
;; NUMBER OF SEQUENCES: 154  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
;; STREET: 3174 PORTER DRIVE  
;; CITY: PALO ALTO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/799,777  
;; FILING DATE: 06-Mar-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/002,485  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BILLINGS, LUCY J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0459 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650) 855-0555  
;; TELEFAX: (650) 845-4166  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 217 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: UTRSN0T06  
;; CLONE: 1638407  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 26 :  
US-09-799-777-26

Query Match 35.3%; Score 107; DB 9; Length 217;  
Best Local Similarity 100.0%; Pred. No. 5.8e-86;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 DIRLRVRAVEYCEHGPALGQVARRRPPQALARDVFGQATVLRSRDLGVSVCIDIKFSEL 256  
DB 88 DIRLRVRAVEYCEHGPALGQVARRRPPQALARDVFGQATVLRSRDLGVSVCIDIKFSEL 147  
QY 257 SYLDAFMGDYLSGALLQALRGVFLTEALREAVRRLVSVDEAD 303  
DB 148 SYLDAFMGDYLSGALLQALRGVFLTEALREAVRRLVSVDEAD 194

RESULT 9  
US-10-001-254-8  
; Sequence 8; Application US/10001254  
; Publication No. US20030049702A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Pawloweki, Krzysztof  
; APPLICANT: Fiorentino, Loredana  
; APPLICANT: Lee, Sung Hyung  
; APPLICANT: Roth, Wilfred

```
/ APPLICANT: Stenner-Liewen, Frank
/ TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
/ FILE REFERENCE: P-LJ 5037
/ CURRENT APPLICATION NUMBER: US10/001,254
/ PRIOR FILING DATE: 2001-11-15
/ PRIOR APPLICATION NUMBER: 60/301,889
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: 09/715,893
/ PRIOR FILING DATE: 2000-11-17
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: faaSeq for windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 101
/ TYPE: PRF
/ ORGANISM: Homo sapien
US-10-001-254-8

Query Match          22.1%; Score 67; DB 14; Length 101;
Best Local Similarity 100.0%; Pred. No. 5,6e-51;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 WEDECLDYGMLSLRMEVVGSGUTGCELELALFLDBAPAGGLARASGLLELLR 71
    |||||
Db 1 WEDECLDYGMLSLRMEVVGSGUTGCELELALFLDBAPAGGLARASGLLELLR 60
    |||||

QY 72 LRRGQC 78
    |||||
Db 61 LRRGQC 67

RESULT 10
US-09-733-167-6
/ Sequence 6, Application US/09733167
/ Patent No. US20020099009A1
/ GENERAL INFORMATION:
/ APPLICANT: Peter, Marcus
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Protein for Regulation of Apoptosis
/ FILE REFERENCE: 4121-120
/ CURRENT APPLICATION NUMBER: US/09/733,167
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: PCT/DE99/01712
/ PRIOR FILING DATE: 1999-06-08
/ PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
/ PRIOR FILING DATE: 1998-06-08
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 210
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising amino
/ OTHER INFORMATION: acids 109-318 of the naturally occurring human DEDD.
US-09-733-167-6

Query Match          4.3%; Score 13; DB 9; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
    |||||
Db 84 TCDIRLRVRAEYC 96

RESULT 11
US-09-935-223-4
/ Sequence 4, Application US/09935223
/ Patent No. US20020086983A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
/ TITLE OF INVENTION: Compositions For And Methods Of Making The Same
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/ FILE REFERENCE: TJU2499
/ CURRENT APPLICATION NUMBER: US/09/935,223
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 09/723,450
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/276,993
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 08/859,167
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 318
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Novel Sequence
US-09-935-223-4

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
    |||||
Db 192 TCDIRLRVRAEYC 204

RESULT 12
US-09-935-223-6
/ Sequence 6, Application US/09935223
/ Patent No. US20020086983A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
/ TITLE OF INVENTION: Compositions For And Methods Of Making The Same
/ FILE REFERENCE: TJU2499
/ CURRENT APPLICATION NUMBER: US/09/935,223
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 09/723,450
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/276,993
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 08/859,167
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 318
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Novel Sequence
US-09-935-223-6

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
    |||||
Db 192 TCDIRLRVRAEYC 204

RESULT 13
US-09-733-167-1
/ Sequence 1, Application US/09733167
/ Patent No. US20020099009A1
/ GENERAL INFORMATION:
/ APPLICANT: Peter, Marcus
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Protein for Regulation of Apoptosis
/ FILE REFERENCE: 4121-120
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; CURRENT APPLICATION NUMBER: US/09/733,167
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/DE99/01712
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
; PRIOR FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-167-1

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
Db      192 TCDIRLRVRAEYC 204

RESULT 14
US-09-733-167-3
; Sequence 3, Application US/09733167
; Patent No. US20020099009A1
; GENERAL INFORMATION:
; APPLICANT: Peter, Marcus
; TITLE OF INVENTION: Protein for Regulation of Apoptosis
; FILE REFERENCE: 4121-120
; CURRENT APPLICATION NUMBER: US/09/733,167
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/DE99/01712
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
; PRIOR FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-733-167-3

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
Db      192 TCDIRLRVRAEYC 204

RESULT 15
US-10-437-963-166242
; Sequence 166242, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166242
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64970C.1.pep
US-10-437-963-166242

Query Match          3.6%; Score 11; DB 16; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      169 RRRRGAPAP 179
Db      51 RRRRGAPAP 61

Search completed: February 12, 2005, 16:44:29
Job time : 76 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:34:36 ; Search time 25 Seconds  
(without alignments)  
904.747 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 303  
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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0  
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Post-processing: Listing first 1000 summaries

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5: /cgn2\_6/prodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	4.3	210	US-09-733-167A-6	Sequence 6, Appl1
2	13	4.3	318	US-08-859-167-4	Sequence 4, Appl1
3	13	4.3	318	US-08-859-167-6	Sequence 6, Appl1
4	13	4.3	318	US-09-109-273-4	Sequence 4, Appl1
5	13	4.3	318	US-09-109-273-6	Sequence 6, Appl1
6	13	4.3	318	US-09-276-993-4	Sequence 4, Appl1
7	13	4.3	318	US-09-276-993-6	Sequence 6, Appl1
8	13	4.3	318	US-09-723-450-4	Sequence 4, Appl1
9	13	4.3	318	US-09-723-450-6	Sequence 6, Appl1
10	13	4.3	318	US-09-733-167A-1	Sequence 1, Appl1
11	13	4.3	318	US-09-733-167A-3	Sequence 3, Appl1
12	9	3.0	91	US-09-252-991A-30543	Sequence 30543, A
13	9	3.0	336	US-09-602-777A-230	Sequence 230, App
14	9	3.0	350	US-09-252-991A-18973	Sequence 18973, A
15	9	3.0	350	US-09-252-991A-25124	Sequence 25124, A
16	9	3.0	504	US-09-252-991A-23374	Sequence 23374, A
17	9	3.0	657	US-09-252-991A-28601	Sequence 28601, A
18	8	2.6	52	US-08-726-306A-143	Sequence 143, App
19	8	2.6	67	US-08-159-340A-6	Sequence 6, Appl1
20	8	2.6	131	US-09-252-991A-17914	Sequence 17914, A
21	8	2.6	179	US-09-252-991A-24966	Sequence 24966, A
22	8	2.6	192	US-09-252-991A-28554	Sequence 28554, A
23	8	2.6	266	US-09-252-991A-25310	Sequence 25310, A
24	8	2.6	223	US-09-252-991A-17835	Sequence 17835, A
25	8	2.6	300	US-09-261-599B-6	Sequence 6, Appl1
26	8	2.6	300	US-09-261-599B-7	Sequence 7, Appl1
27	8	2.6	338	US-09-252-991A-31633	Sequence 31633, A

28	8	2.6	354	US-09-949-016-11550	Sequence 11550, A
29	8	2.6	361	US-09-261-599B-1	Sequence 1, Appl1
30	8	2.6	361	US-09-261-599B-4	Sequence 4, Appl1
31	8	2.6	361	US-09-456-455A-1	Sequence 1, Appl1
32	8	2.6	361	US-09-456-455A-4	Sequence 4, Appl1
33	8	2.6	452	US-09-252-991A-24195	Sequence 24195, A
34	8	2.6	462	US-09-166-350-18	Sequence 18, Appl1
35	8	2.6	493	US-09-252-991A-32463	Sequence 32463, A
36	8	2.6	679	US-09-252-991A-25400	Sequence 25400, A
37	8	2.6	679	US-09-252-991A-28950	Sequence 28950, A
38	8	2.6	690	US-09-252-991A-33250	Sequence 32350, A
39	8	2.6	810	US-09-489-039A-9748	Sequence 9748, Ap
40	8	2.6	989	US-09-252-991A-17435	Sequence 17435, A
41	8	2.6	1116	US-09-252-991A-24374	Sequence 24374, A
42	8	2.6	1958	US-07-945-283-2	Sequence 2, Appl1
43	7	2.3	31	US-09-227-357-653	Sequence 653, App
44	7	2.3	37	US-08-438-753B-35	Sequence 35, Appl1
45	7	2.3	37	US-08-443-883A-35	Sequence 35, Appl1
46	7	2.3	37	US-08-631-328-35	Sequence 35, Appl1
47	7	2.3	37	US-08-455-524B-35	Sequence 35, Appl1
48	7	2.3	37	US-08-455-021B-35	Sequence 35, Appl1
49	7	2.3	37	US-09-045-467-35	Sequence 35, Appl1
50	7	2.3	87	US-09-270-767-38674	Sequence 38674, A
51	7	2.3	87	US-09-270-767-53891	Sequence 53891, A
52	7	2.3	91	US-09-270-767-62183	Sequence 62183, A
53	7	2.3	103	US-09-513-999C-4915	Sequence 4915, Ap
54	7	2.3	115	US-09-134-000C-3468	Sequence 3468, Ap
55	7	2.3	118	US-08-460-528-2	Sequence 2, Appl1
56	7	2.3	118	US-08-303-224-2	Sequence 2, Appl1
57	7	2.3	122	US-09-902-540-10858	Sequence 10858, A
58	7	2.3	123	US-08-822-573-2	Sequence 2, Appl1
59	7	2.3	127	US-09-949-016-10809	Sequence 10809, A
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61	7	2.3	134	US-09-252-991A-13062	Sequence 19062, A
62	7	2.3	134	US-09-252-991A-26070	Sequence 26070, A
63	7	2.3	136	US-09-252-991A-24532	Sequence 24532, A
64	7	2.3	142	US-09-252-991A-20257	Sequence 20257, A
65	7	2.3	147	US-09-640-211A-682	Sequence 682, App
66	7	2.3	160	US-09-252-991A-20458	Sequence 20458, A
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68	7	2.3	164	US-09-902-540-14156	Sequence 14156, A
69	7	2.3	171	US-09-902-540-15953	Sequence 15953, A
70	7	2.3	171	US-09-302-540-13213	Sequence 13213, A
71	7	2.3	172	US-08-438-753B-34	Sequence 34, Appl1
72	7	2.3	172	US-08-443-883A-34	Sequence 34, Appl1
73	7	2.3	172	US-08-631-328-34	Sequence 34, Appl1
74	7	2.3	172	US-08-455-524B-34	Sequence 34, Appl1
75	7	2.3	172	US-08-455-021B-34	Sequence 34, Appl1
76	7	2.3	172	US-09-045-467-34	Sequence 34, Appl1
77	7	2.3	172	US-08-616-904-6	Sequence 6, Appl1
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79	7	2.3	173	US-09-543-681A-5934	Sequence 5934, Ap
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81	7	2.3	179	US-09-252-991A-30404	Sequence 30404, A
82	7	2.3	186	US-09-252-991A-32250	Sequence 32250, A
83	7	2.3	184	US-09-252-991A-32085	Sequence 32085, A
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85	7	2.3	185	US-08-443-883A-32	Sequence 32, Appl1
86	7	2.3	185	US-08-631-328-32	Sequence 32, Appl1
87	7	2.3	185	US-08-455-524B-32	Sequence 32, Appl1
88	7	2.3	195	US-08-455-021B-32	Sequence 32, Appl1
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97	7	2.3	225	US-09-583-110-3301	Sequence 3301, Ap
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103	7	2.3	255	US-09-489-039A-9075	Sequence 9075, Ap	176	7	2.3	385	US-09-252-991A-22010	Sequence 22010, A
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110	7	2.3	266	5175383-5	Patent No. 5175383	183	7	2.3	413	US-10-237-551-196	Sequence 196, App
111	7	2.3	267	US-08-462-169B-13	Sequence 13, App1	184	7	2.3	416	US-09-710-279-2402	Sequence 2402, Ap
112	7	2.3	267	US-09-103-079-13	Sequence 13, App1	185	7	2.3	417	US-09-134-001C-5006	Sequence 5006, Ap
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116	7	2.3	268	US-08-464-590A-17	Sequence 17, App1	189	7	2.3	432	US-09-328-355-4955	Sequence 4955, Ap
117	7	2.3	268	US-08-207-412B-12	Sequence 12, App1	190	7	2.3	440	US-09-252-991A-32913	Sequence 22913, A
118	7	2.3	268	US-08-867-471-12	Sequence 12, App1	191	7	2.3	440	US-09-252-991A-30167	Sequence 30167, A
119	7	2.3	268	US-08-438-439C-8	Sequence 8, App11	192	7	2.3	444	US-09-107-533A-3952	Sequence 3952, Ap
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121	7	2.3	268	US-08-705-245-14	Sequence 14, App1	194	7	2.3	450	US-09-252-991A-32284	Sequence 32284, A
122	7	2.3	268	US-08-718-904-14	Sequence 14, App1	195	7	2.3	455	US-08-635-130A-2	Sequence 2, App11
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129	7	2.3	268	US-09-329-947-33	Sequence 33, App1	202	7	2.3	482	US-09-252-991A-31492	Sequence 31492, A
130	7	2.3	268	US-09-248-998-15	Sequence 15, App1	203	7	2.3	484	US-09-252-991A-24249	Sequence 24249, A
131	7	2.3	268	US-09-572-406B-11	Sequence 11, App1	204	7	2.3	486	US-09-252-991A-31404	Sequence 31404, A
132	7	2.3	268	US-09-490-714-14	Sequence 14, App1	205	7	2.3	490	US-09-252-991A-31404	Sequence 22715, A
133	7	2.3	268	US-09-610-651-15	Sequence 15, App1	206	7	2.3	493	US-09-270-767-44663	Sequence 44663, A
134	7	2.3	268	US-09-949-016-7942	Sequence 7942, Ap	207	7	2.3	496	US-09-252-991A-26668	Sequence 26668, A
135	7	2.3	269	US-08-438-439C-18	Sequence 18, App1	208	7	2.3	499	US-09-252-991A-19621	Sequence 19621, A
136	7	2.3	269	US-09-252-991A-28651	Sequence 28651, A	209	7	2.3	501	US-09-252-991A-16795	Sequence 16795, A
137	7	2.3	273	US-08-928-213B-9	Sequence 9, App11	210	7	2.3	501	US-09-252-991A-17730	Sequence 17730, A
138	7	2.3	273	US-09-252-991A-16693	Sequence 16693, A	211	7	2.3	501	US-09-252-991A-31885	Sequence 31885, A
139	7	2.3	279	US-09-252-991A-31733	Sequence 31733, A	212	7	2.3	506	US-09-252-991A-18390	Sequence 18390, A
140	7	2.3	281	US-09-252-991A-30528	Sequence 30528, A	213	7	2.3	508	US-09-252-991A-18390	Sequence 17468, A
141	7	2.3	281	US-09-252-991A-17748	Sequence 17748, A	214	7	2.3	527	US-08-928-213B-8	Sequence 8, App11
142	7	2.3	281	US-09-252-991A-24898	Sequence 24898, A	215	7	2.3	553	US-09-252-991A-17429	Sequence 17429, A
143	7	2.3	284	US-09-352-991A-27572	Sequence 27572, A	216	7	2.3	560	US-09-252-991A-26107	Sequence 26107, A
144	7	2.3	285	US-09-270-767-46359	Sequence 46359, A	217	7	2.3	561	US-09-922-36A-1	Sequence 1, App11
145	7	2.3	297	US-09-252-991A-18932	Sequence 18932, A	218	7	2.3	561	US-09-254-599-1	Sequence 1, App11
146	7	2.3	300	US-09-302-540-14290	Sequence 14290, A	219	7	2.3	561	US-09-949-016-6197	Sequence 6197, Ap
147	7	2.3	304	US-09-949-016-6824	Sequence 6824, Ap	220	7	2.3	561	US-10-115-415-1	Sequence 1, App11
148	7	2.3	312	US-09-949-016-7149	Sequence 7149, Ap	221	7	2.3	561	US-10-115-263-1	Sequence 1, App11
149	7	2.3	313	US-09-252-991A-21867	Sequence 21867, A	222	7	2.3	561	US-10-115-671-1	Sequence 1, App11
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151	7	2.3	318	US-09-252-991A-23557	Sequence 23557, A	224	7	2.3	571	US-09-248-796A-22498	Sequence 22498, A
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153	7	2.3	325	US-09-252-991A-28166	Sequence 28166, A	226	7	2.3	576	US-09-134-001C-3955	Sequence 3955, Ap
154	7	2.3	330	US-09-252-991A-18573	Sequence 18573, A	227	7	2.3	587	US-09-252-991A-18280	Sequence 18280, A
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156	7	2.3	340	US-09-214-631-3	Sequence 3, App11	229	7	2.3	590	US-09-252-991A-19127	Sequence 19127, A
157	7	2.3	340	US-09-051-994-4	Sequence 2, App11	230	7	2.3	590	US-09-443-067-22	Sequence 22, App1
158	7	2.3	340	US-08-635-130A-4	Sequence 4, App11	231	7	2.3	593	US-09-252-991A-32340	Sequence 32340, A
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163	7	2.3	348	US-09-710-279-1702	Sequence 1702, Ap	236	7	2.3	635	US-09-252-991A-31646	Sequence 31646, A
164	7	2.3	351	US-09-710-279-338	Sequence 338, App	237	7	2.3	655	US-09-252-991A-17112	Sequence 17112, A
165	7	2.3	355	US-09-902-540-15046	Sequence 15046, A	238	7	2.3	658	US-09-252-991A-30495	Sequence 20495, A
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167	7	2.3	368	US-09-489-039A-17553	Sequence 17553, A	240	7	2.3	659	US-09-270-767-43969	Sequence 43969, A
168	7	2.3	368	US-09-668-097A-10	Sequence 10, App1	241	7	2.3	672	US-09-252-991A-22407	Sequence 22407, A
169	7	2.3	372	US-09-252-991A-27359	Sequence 27359, A	242	7	2.3	684	US-09-252-991A-32342	Sequence 32342, A
170	7	2.3	374	US-09-252-991A-22425	Sequence 22425, A	243	7	2.3	690	US-10-262-083-2	Sequence 2, App11
171	7	2.3	375	US-09-134-000C-5852	Sequence 5852, Ap	244	7	2.3	702	US-09-252-991A-31609	Sequence 31609, A
172	7	2.3	375	US-09-818-780-23	Sequence 23, App1	245	7	2.3	702	US-09-252-991A-32740	Sequence 32740, A
173	7	2.3	376	US-09-056-556-202	Sequence 202, App	246	7	2.3	715		

247	7	2.3	722	4	US-09-252-991A-18481	Sequence 18481, A	320	6	2.0	12	5	PCT-US91-08328-28	Sequence 28, Appl
248	7	2.3	724	4	US-09-252-991A-31715	Sequence 31715, A	321	6	2.0	13	1	US-08-469-582-2	Sequence 2, Appl
249	7	2.3	731	4	US-09-902-540-13763	Sequence 13763, A	322	6	2.0	13	2	US-08-753-8321-24	Sequence 24, Appl
250	7	2.3	746	4	US-09-548-7978-4	Sequence 4, Appl	323	6	2.0	13	5	PCT-US91-08328-27	Sequence 27, Appl
251	7	2.3	767	4	US-09-548-7978-5	Sequence 5, Appl	324	6	2.0	14	1	US-08-469-582-3	Sequence 3, Appl
252	7	2.3	802	4	US-09-632-098-2	Sequence 2, Appl	325	6	2.0	14	1	US-08-469-582-12	Sequence 12, Appl
253	7	2.3	802	4	US-10-177-098-2	Sequence 2, Appl	326	6	2.0	14	1	US-08-473-025-8	Sequence 8, Appl
254	7	2.3	812	4	US-09-632-098-4	Sequence 4, Appl	327	6	2.0	14	2	US-09-428-0828-557	Sequence 557, App
255	7	2.3	812	4	US-10-177-308-4	Sequence 4, Appl	328	6	2.0	14	5	PCT-US91-08328-36	Sequence 36, Appl
256	7	2.3	830	4	US-09-252-991A-28961	Sequence 28961, A	329	6	2.0	15	1	US-08-439-905-5	Sequence 5, Appl
257	7	2.3	841	4	US-09-538-092-1183	Sequence 1183, A	330	6	2.0	15	1	US-08-469-582-13	Sequence 13, Appl
258	7	2.3	849	4	US-09-548-7978-6	Sequence 6, Appl	331	6	2.0	15	2	US-08-335-8321-13	Sequence 13, Appl
259	7	2.3	855	4	US-09-949-016-7263	Sequence 7263, Ap	332	6	2.0	15	2	US-08-902-367-6	Sequence 6, Appl
260	7	2.3	863	4	US-09-252-991A-20821	Sequence 20821, A	333	6	2.0	20	1	US-08-440-861-13	Sequence 13, Appl
261	7	2.3	869	4	US-09-252-991A-22748	Sequence 22748, A	334	6	2.0	20	1	US-08-440-861-14	Sequence 14, Appl
262	7	2.3	883	4	US-09-489-039A-13542	Sequence 13542, A	335	6	2.0	15	3	US-09-100-537-5	Sequence 5, Appl
263	7	2.3	885	4	US-09-252-991A-26129	Sequence 26129, A	336	6	2.0	15	3	US-08-535-170-14	Sequence 14, Appl
264	7	2.3	889	4	US-09-949-016-6036	Sequence 6036, Ap	337	6	2.0	16	2	US-09-141-127-7	Sequence 7, Appl
265	7	2.3	910	4	US-09-949-016-7055	Sequence 7055, Ap	338	6	2.0	16	2	US-08-753-781-6	Sequence 6, Appl
266	7	2.3	922	4	US-09-252-991A-31682	Sequence 31682, A	339	6	2.0	20	1	US-08-440-861-13	Sequence 13, Appl
267	7	2.3	951	4	US-09-252-991A-26766	Sequence 26766, A	340	6	2.0	23	2	US-08-847-176-2	Sequence 2, Appl
268	7	2.3	977	4	US-09-252-991A-16655	Sequence 16655, A	341	6	2.0	23	2	US-08-847-176-15	Sequence 15, Appl
269	7	2.3	1033	4	US-09-252-991A-20611	Sequence 20611, A	342	6	2.0	23	2	US-08-847-176-19	Sequence 19, Appl
270	7	2.3	1037	4	US-09-902-540-9845	Sequence 9845, Ap	343	6	2.0	26	2	US-08-847-176-6	Sequence 6, Appl
271	7	2.3	1046	4	US-09-252-991A-27508	Sequence 27508, A	344	6	2.0	26	2	US-08-847-176-7	Sequence 7, Appl
272	7	2.3	1186	2	US-08-861-464-8	Sequence 8, Appl	345	6	2.0	26	2	US-08-847-176-8	Sequence 8, Appl
273	7	2.3	1186	2	US-08-396-001-8	Sequence 8, Appl	346	6	2.0	26	2	US-08-847-176-21	Sequence 21, Appl
274	7	2.3	1186	3	US-09-323-433A-8	Sequence 8, Appl	347	6	2.0	26	2	US-08-847-176-22	Sequence 22, Appl
275	7	2.3	1186	4	US-09-826-752-8	Sequence 8, Appl	348	6	2.0	26	2	US-09-462-917A-125	Sequence 125, App
276	7	2.3	1195	4	US-09-540-236-3165	Sequence 3165, Ap	349	6	2.0	27	1	US-07-776-272-27	Sequence 27, Appl
277	7	2.3	1364	4	US-09-252-991A-26880	Sequence 26880, A	350	6	2.0	27	3	US-09-260-846-17	Sequence 17, Appl
278	7	2.3	1404	4	US-09-345-473E-24	Sequence 24, Appl	351	6	2.0	27	4	US-08-469-260A-481	Sequence 481, App
279	7	2.3	1466	4	US-09-252-991A-30085	Sequence 30085, A	352	6	2.0	27	4	US-08-488-446-481	Sequence 481, App
280	7	2.3	2353	3	US-08-984-709A-50	Sequence 50, Appl	353	6	2.0	27	4	US-08-467-344A-481	Sequence 481, App
281	7	2.3	3724	2	US-08-804-227C-10	Sequence 10, Appl	354	6	2.0	27	4	US-08-424-508A-481	Sequence 481, App
282	7	2.3	3724	2	US-08-804-198-4	Sequence 4, Appl	355	6	2.0	27	4	US-10-014-269-51	Sequence 51, Appl
283	7	2.0	8	2	US-08-473-025-11	Sequence 11, Appl	356	6	2.0	28	4	US-10-014-269-17	Sequence 17, Appl
284	6	2.0	9	1	US-08-178-570-36	Sequence 36, Appl	357	6	2.0	31	4	US-09-152-841-37	Sequence 37, Appl
285	6	2.0	9	3	US-08-369-643-36	Sequence 36, Appl	358	6	2.0	32	1	US-09-152-841-39	Sequence 39, Appl
286	6	2.0	9	5	PCT-US91-08328-31	Sequence 31, Appl	359	6	2.0	32	1	US-08-303-025-9	Sequence 9, Appl
287	6	2.0	9	5	PCT-US91-08328-31	Sequence 31, Appl	360	6	2.0	32	2	US-08-677-304-9	Sequence 9, Appl
288	6	2.0	10	1	US-08-469-582-16	Sequence 16, Appl	361	6	2.0	32	2	US-08-436-703B-14	Sequence 14, Appl
289	6	2.0	10	4	US-09-648-400A-7	Sequence 7, Appl	362	6	2.0	33	3	US-09-122-144-4	Sequence 4, Appl
290	6	2.0	10	4	US-09-792-480-7	Sequence 7, Appl	363	6	2.0	33	3	US-09-172-841-37	Sequence 37, Appl
291	6	2.0	10	5	US-10-209-421-7	Sequence 7, Appl	364	6	2.0	38	3	US-09-172-841-39	Sequence 39, Appl
292	6	2.0	10	5	PCT-US91-08328-30	Sequence 30, Appl	365	6	2.0	38	4	US-08-951-621-37	Sequence 37, Appl
293	6	2.0	11	1	US-08-462-880-13	Sequence 13, Appl	366	6	2.0	38	4	US-08-951-621-39	Sequence 39, Appl
294	6	2.0	11	2	US-08-273-274-13	Sequence 13, Appl	367	6	2.0	40	4	US-09-270-767-37180	Sequence 37180, A
295	6	2.0	11	2	US-08-475-041-13	Sequence 13, Appl	368	6	2.0	40	4	US-09-270-767-52397	Sequence 52397, A
296	6	2.0	11	2	US-08-484-773-13	Sequence 13, Appl	369	6	2.0	40	4	US-09-385-219A-67	Sequence 67, Appl
297	6	2.0	11	2	US-08-361-864-17	Sequence 17, Appl	370	6	2.0	42	3	US-09-172-841-1	Sequence 1, Appl
298	6	2.0	11	3	US-09-208-966-7	Sequence 7, Appl	371	6	2.0	42	4	US-08-951-621-1	Sequence 1, Appl
299	6	2.0	11	3	US-09-208-966-8	Sequence 8, Appl	372	6	2.0	43	4	US-09-007-905-57	Sequence 57, Appl
300	6	2.0	11	3	US-09-083-259-20	Sequence 20, Appl	373	6	2.0	43	4	US-09-232-074-57	Sequence 57, Appl
301	6	2.0	11	4	US-09-396-195-20	Sequence 20, Appl	374	6	2.0	43	4	US-09-385-219A-15	Sequence 15, Appl
302	6	2.0	11	4	US-09-775-052A-7	Sequence 7, Appl	375	6	2.0	44	4	US-09-823-266-17	Sequence 17, Appl
303	6	2.0	11	4	US-09-775-052A-8	Sequence 8, Appl	376	6	2.0	46	3	US-08-483-533-30	Sequence 30, Appl
304	6	2.0	11	5	PCT-US91-08328-29	Sequence 29, Appl	377	6	2.0	46	3	US-09-283-471A-30	Sequence 30, Appl
305	6	2.0	12	1	US-08-177-351-52	Sequence 52, Appl	378	6	2.0	46	3	US-08-861-476C-7	Sequence 7, Appl
306	6	2.0	12	1	US-08-480-367B-52	Sequence 52, Appl	379	6	2.0	46	4	US-09-372-210-258	Sequence 258, App
307	6	2.0	12	1	US-08-487-221A-52	Sequence 52, Appl	380	6	2.0	48	3	US-09-314-268-166	Sequence 166, App
308	6	2.0	12	1	US-08-480-370-52	Sequence 52, Appl	381	6	2.0	48	4	US-09-369-247-117	Sequence 117, App
309	6	2.0	12	1	US-08-299-636-32	Sequence 32, Appl	382	6	2.0	50	4	US-09-902-540-10534	Sequence 10534, A
310	6	2.0	12	1	US-08-279-155-32	Sequence 32, Appl	383	6	2.0	53	4	US-09-513-999C-7165	Sequence 7165, Ap
311	6	2.0	12	1	US-08-475-745-124	Sequence 124, App	384	6	2.0	55	2	US-08-459-568-80	Sequence 80, Appl
312	6	2.0	12	1	US-08-464-456-30	Sequence 30, Appl	385	6	2.0	55	2	US-08-599-411-80	Sequence 80, Appl
313	6	2.0	12	1	US-08-703-988A-32	Sequence 32, Appl	386	6	2.0	55	3	US-08-516-859A-80	Sequence 80, Appl
314	6	2.0	12	1	US-08-463-052-30	Sequence 30, Appl	387	6	2.0	55	3	US-09-586-472-80	Sequence 80, Appl
315	6	2.0	12	2	US-08-480-551-30	Sequence 30, Appl	388	6	2.0	56	4	US-09-528-706-80	Sequence 80, Appl
316	6	2.0	12	2	US-08-378-709-31	Sequence 31, Appl	389	6	2.0	57	4	US-09-370-767-59181	Sequence 59181, A
317	6	2.0	12	2	US-08-612-842-32	Sequence 32, Appl	390	6	2.0	57	4	US-09-513-999C-6181	Sequence 6181, Ap
318	6	2.0	12	4	US-08-445-638-124	Sequence 124, App	391	6	2.0	61	4	US-09-072-634-10	Sequence 10, Appl
319	6	2.0	12	4	US-09-428-0828-550	Sequence 550, App	392	6	2.0	61	4		

393	6	2.0	61	4	US-09-621-976-4027	Sequence 4027, Ap
394	6	2.0	63	4	US-09-270-767-58468	Sequence 58468, A
395	6	2.0	64	4	US-09-252-991A-25121	Sequence 25121, A
396	6	2.0	64	4	US-09-270-767-37216	Sequence 37216, A
397	6	2.0	64	4	US-09-270-767-39939	Sequence 39939, A
398	6	2.0	64	4	US-09-270-767-52433	Sequence 52433, A
399	6	2.0	64	4	US-09-270-767-55156	Sequence 55156, A
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401	6	2.0	65	4	US-09-621-976-7130	Sequence 7130, Ap
402	6	2.0	67	4	US-09-513-999C-7084	Sequence 7084, Ap
403	6	2.0	68	3	US-09-007-905-50	Sequence 50, Appl
404	6	2.0	68	4	US-09-232-074-50	Sequence 50, Appl
405	6	2.0	70	4	US-09-252-991A-27697	Sequence 27697, A
406	6	2.0	71	4	US-09-621-976-4052	Sequence 4052, Ap
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408	6	2.0	72	4	US-09-248-796A-23475	Sequence 23475, A
409	6	2.0	73	4	US-08-311-731A-296	Sequence 296, App
410	6	2.0	74	4	US-09-248-796A-24240	Sequence 24240, A
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412	6	2.0	76	4	US-09-248-796A-24505	Sequence 24505, A
413	6	2.0	77	4	US-09-270-767-57875	Sequence 57875, A
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415	6	2.0	80	4	US-09-134-000C-3717	Sequence 3717, Ap
416	6	2.0	80	4	US-09-621-976-5556	Sequence 5556, Ap
417	6	2.0	81	4	US-09-502-540-15595	Sequence 15595, A
418	6	2.0	83	4	US-09-489-039A-11690	Sequence 11690, A
419	6	2.0	83	4	US-09-248-796A-25628	Sequence 25628, A
420	6	2.0	83	4	US-09-302-540-11751	Sequence 11751, A
421	6	2.0	84	4	US-09-902-540-13717	Sequence 13717, A
422	6	2.0	85	4	US-08-311-731A-100	Sequence 100, App
423	6	2.0	85	4	US-09-841-879B-8	Sequence 8, Appl
424	6	2.0	86	4	US-09-513-999C-7021	Sequence 7021, Ap
425	6	2.0	87	4	US-09-489-039A-10564	Sequence 10564, A
426	6	2.0	87	4	US-09-302-540-13177	Sequence 13177, A
427	6	2.0	88	4	US-09-540-236-1943	Sequence 1943, Ap
428	6	2.0	89	4	US-09-599-360B-122	Sequence 122, App
429	6	2.0	89	4	US-09-540-236-2401	Sequence 2401, Ap
430	6	2.0	90	4	US-09-252-991A-21131	Sequence 21131, A
431	6	2.0	91	4	US-09-252-991A-23967	Sequence 23967, A
432	6	2.0	91	4	US-09-489-039A-11092	Sequence 11092, A
433	6	2.0	91	4	US-09-489-039A-11802	Sequence 11802, A
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435	6	2.0	92	4	US-09-134-000C-4655	Sequence 4655, Ap
436	6	2.0	93	4	US-09-489-039A-7356	Sequence 7356, Ap
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438	6	2.0	95	4	US-09-252-991A-19357	Sequence 19357, A
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441	6	2.0	97	2	US-08-726-306A-128	Sequence 128, App
442	6	2.0	97	4	US-08-311-731A-37	Sequence 37, Appl
443	6	2.0	97	4	US-09-489-039A-8775	Sequence 8775, Ap
444	6	2.0	98	4	US-09-615-192A-382	Sequence 382, App
445	6	2.0	100	4	US-09-621-976-5449	Sequence 5449, Ap
446	6	2.0	101	3	US-09-199-637A-77	Sequence 77, Appl
447	6	2.0	101	3	US-09-199-637A-289	Sequence 289, App
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455	6	2.0	106	3	US-09-083-351-15	Sequence 15, Appl
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457	6	2.0	106	3	US-09-083-352-15	Sequence 15, Appl
458	6	2.0	106	4	US-09-198-452A-253	Sequence 253, App
459	6	2.0	106	4	US-09-270-767-58597	Sequence 58597, A
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462	6	2.0	106	4	US-09-612-809B-14	Sequence 14, Appl
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467	6	2.0	108	4	US-09-535-852-40	Sequence 40, Appl
468	6	2.0	108	4	US-09-902-540-16230	Sequence 16230, A
469	6	2.0	112	4	US-09-489-039A-7344	Sequence 7344, Ap
470	6	2.0	112	4	US-09-673-399A-237	Sequence 237, App
471	6	2.0	112	4	US-09-621-976-6045	Sequence 6045, Ap
472	6	2.0	113	4	US-09-106-568E-157	Sequence 157, App
473	6	2.0	113	4	US-09-248-796A-20113	Sequence 20113, A
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475	6	2.0	114	4	US-09-733-167A-5	Sequence 5, Appl
476	6	2.0	114	4	US-09-270-767-57487	Sequence 57487, A
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479	6	2.0	117	4	US-09-489-039A-13048	Sequence 13048, A
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481	6	2.0	117	4	US-09-513-999C-6709	Sequence 6709, Ap
482	6	2.0	117	4	US-09-949-01E-88965	Sequence 88965, Ap
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484	6	2.0	119	4	US-09-270-767-43255	Sequence 43255, A
485	6	2.0	120	4	US-09-252-991A-21271	Sequence 21271, A
486	6	2.0	120	4	US-08-311-731A-411	Sequence 411, App
487	6	2.0	120	4	US-09-489-039A-7641	Sequence 7641, Ap
488	6	2.0	121	1	US-08-481-377-21	Sequence 21, Appl
489	6	2.0	121	2	US-08-491-835-19	Sequence 19, Appl
490	6	2.0	121	3	US-09-153-733A-21	Sequence 21, Appl
491	6	2.0	121	3	US-08-946-093A-19	Sequence 19, Appl
492	6	2.0	121	3	US-09-172-062-19	Sequence 19, Appl
493	6	2.0	121	3	US-08-624-633-19	Sequence 19, Appl
494	6	2.0	121	3	US-09-301-520D-19	Sequence 19, Appl
495	6	2.0	121	3	US-09-489-705-21	Sequence 21, Appl
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499	6	2.0	121	5	PCT-US94-00665-19	Sequence 19, Appl
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501	6	2.0	122	1	US-08-455-555-23	Sequence 23, Appl
502	6	2.0	122	2	US-08-525-596B-27	Sequence 27, Appl
503	6	2.0	122	2	US-08-581-528A-17	Sequence 17, Appl
504	6	2.0	122	3	US-09-097-616-17	Sequence 17, Appl
505	6	2.0	122	3	US-09-177-860A-27	Sequence 27, Appl
506	6	2.0	122	3	US-09-145-0067-23	Sequence 23, Appl
507	6	2.0	122	4	US-09-378-238-37	Sequence 37, Appl
508	6	2.0	122	4	US-09-629-933-27	Sequence 27, Appl
509	6	2.0	122	4	US-09-686-344-45	Sequence 45, Appl
510	6	2.0	122	4	US-09-412-791D-17	Sequence 17, Appl
511	6	2.0	122	4	US-09-619-061-17	Sequence 17, Appl
512	6	2.0	122	5	PCT-US94-00657-23	Sequence 23, Appl
513	6	2.0	122	5	PCT-US94-07782-17	Sequence 17, Appl
514	6	2.0	122	5	PCT-US94-07799-17	Sequence 17, Appl
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518	6	2.0	123	4	US-09-270-767-55402	Sequence 55402, A
519	6	2.0	124	4	US-09-270-767-40657	Sequence 40657, A
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521	6	2.0	124	4	US-09-902-540-12036	Sequence 12036, A
522	6	2.0	125	3	US-09-199-637A-317	Sequence 317, App
523	6	2.0	125	3	US-09-252-991A-33028	Sequence 33028, A
524	6	2.0	127	4	US-09-134-000C-4940	Sequence 4940, Ap
525	6	2.0	128	4	US-09-252-991A-23567	Sequence 23567, A
526	6	2.0	128	4	US-09-640-211A-720	Sequence 720, App
527	6	2.0	129	4	US-09-252-991A-76731	Sequence 76731, A
528	6	2.0	129	4	US-09-640-211A-825	Sequence 825, App
529	6	2.0	130	1	US-08-455-550-9	Sequence 9, Appl
530	6	2.0	131	4	US-09-252-991A-21357	Sequence 21357, A
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532	6	2.0	131	4	US-09-270-767-61319	Sequence 61319, A
533	6	2.0	132	1	US-08-534-975-4	Sequence 4, Appl
534	6	2.0	132	2	US-08-954-470-4	Sequence 4, Appl
535	6	2.0	132	3	US-09-129-885A-4	Sequence 4, Appl
536	6	2.0	132	3	US-09-247-154-4	Sequence 4, Appl
537	6	2.0	132	3	US-09-480-718-4	Sequence 4, Appl
538	6	2.0	132	4	US-09-610-833-4	Sequence 4, Appl



539	6	2.0	132	4	US-09-129-855A-4	Sequence 4, Appli	612	6	2.0	149	4	US-09-270-767-49997	Sequence 49997, A
540	6	2.0	133	4	US-09-252-991A-18533	Sequence 18533, A	613	6	2.0	150	4	US-09-252-991A-21785	Sequence 21785, A
541	6	2.0	133	4	US-09-252-991A-31987	Sequence 31987, A	614	6	2.0	151	4	US-09-252-991A-24676	Sequence 24676, A
542	6	2.0	133	4	US-09-134-000C-4871	Sequence 4871, Ap	615	6	2.0	151	4	US-09-621-976-5158	Sequence 5158, Ap
543	6	2.0	134	4	US-09-252-991A-19660	Sequence 19660, A	616	6	2.0	151	4	US-09-270-767-38747	Sequence 38747, A
544	6	2.0	134	4	US-09-252-991A-26710	Sequence 26710, A	617	6	2.0	151	4	US-09-270-767-53964	Sequence 53964, A
545	6	2.0	134	4	US-09-248-796A-25493	Sequence 25493, A	618	6	2.0	151	4	US-09-302-540-11681	Sequence 11681, A
546	6	2.0	135	4	US-09-252-991A-29308	Sequence 29308, A	619	6	2.0	151	4	US-09-302-540-13473	Sequence 13473, A
547	6	2.0	135	4	US-09-252-991A-31675	Sequence 31675, A	620	6	2.0	152	4	US-09-270-767-50345	Sequence 50345, A
548	6	2.0	136	4	US-09-252-991A-21384	Sequence 21384, A	621	6	2.0	152	4	US-09-370-767-55128	Sequence 55128, A
549	6	2.0	136	4	US-09-252-991A-31120	Sequence 31120, A	622	6	2.0	153	3	US-08-943-173-1	Sequence 1, Appli
550	6	2.0	136	4	US-09-270-767-57789	Sequence 57789, A	623	6	2.0	153	4	US-09-252-991A-24783	Sequence 24783, A
551	6	2.0	137	4	US-09-252-991A-17770	Sequence 17770, A	624	6	2.0	153	4	US-09-252-991A-30178	Sequence 30178, A
552	6	2.0	137	4	US-09-252-991A-24808	Sequence 24808, A	625	6	2.0	153	4	US-09-134-000C-51073	Sequence 5107, Ap
553	6	2.0	137	4	US-09-252-991A-26220	Sequence 26220, A	626	6	2.0	153	4	US-09-270-767-42492	Sequence 42492, A
554	6	2.0	138	1	US-08-698-551-4	Sequence 4, Appli	627	6	2.0	153	4	US-09-302-540-12154	Sequence 12154, A
555	6	2.0	138	2	US-08-602-228-4	Sequence 4, Appli	628	6	2.0	154	3	US-08-866-928B-5	Sequence 5, Appli
556	6	2.0	138	2	US-08-649-341A-4	Sequence 4, Appli	629	6	2.0	154	3	US-08-866-928B-6	Sequence 6, Appli
557	6	2.0	138	2	US-08-494-440B-4	Sequence 4, Appli	630	6	2.0	154	3	US-08-866-928B-7	Sequence 7, Appli
558	6	2.0	138	2	US-08-533-901B-4	Sequence 4, Appli	631	6	2.0	154	3	US-09-685-836-5	Sequence 5, Appli
559	6	2.0	138	2	US-08-839-032A-4	Sequence 4, Appli	632	6	2.0	154	4	US-09-685-836-6	Sequence 6, Appli
560	6	2.0	138	3	US-09-185-258C-4	Sequence 4, Appli	633	6	2.0	154	4	US-09-685-836-7	Sequence 7, Appli
561	6	2.0	138	3	US-09-252-991A-20026	Sequence 20026, A	634	6	2.0	154	4	US-09-252-991A-25607	Sequence 25607, A
562	6	2.0	138	4	US-09-252-991A-20131	Sequence 20131, A	635	6	2.0	154	4	US-09-252-991A-30329	Sequence 30329, A
563	6	2.0	138	4	US-09-252-991A-20131	Sequence 20131, A	636	6	2.0	154	4	US-09-252-991A-17892	Sequence 17892, A
564	6	2.0	138	4	US-09-902-540-14536	Sequence 14536, A	637	6	2.0	154	4	US-09-252-991A-25518	Sequence 25518, A
565	6	2.0	138	4	US-09-902-540-15833	Sequence 15833, A	638	6	2.0	156	4	US-09-489-039A-12749	Sequence 12749, A
566	6	2.0	138	5	PCT-US95-12724-40	Sequence 4, Appli	639	6	2.0	156	4	US-09-489-039A-12832	Sequence 12832, A
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568	6	2.0	139	3	US-09-085-761A-40	Sequence 40, Appli	641	6	2.0	157	4	US-09-252-991A-30836	Sequence 30836, A
569	6	2.0	139	4	US-09-252-991A-19685	Sequence 19685, A	642	6	2.0	157	4	US-09-252-991A-31576	Sequence 31576, A
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571	6	2.0	139	4	US-09-252-991A-23661	Sequence 23661, A	644	6	2.0	157	4	US-09-489-039A-9364	Sequence 9364, A
572	6	2.0	139	4	US-09-252-991A-28981	Sequence 28981, A	645	6	2.0	157	4	US-09-270-767-39506	Sequence 39506, A
573	6	2.0	139	4	US-09-252-991A-31179	Sequence 31179, A	646	6	2.0	157	4	US-09-270-767-54723	Sequence 54723, A
574	6	2.0	139	4	US-09-248-796A-15962	Sequence 15962, A	647	6	2.0	158	3	US-08-946-329A-66	Sequence 66, Appli
575	6	2.0	140	4	US-09-252-991A-23242	Sequence 23242, A	648	6	2.0	158	4	US-09-252-991A-26763	Sequence 26763, A
576	6	2.0	140	4	US-09-489-039A-13900	Sequence 13900, A	649	6	2.0	158	4	US-09-489-039A-10898	Sequence 10898, A
577	6	2.0	140	4	US-09-248-796A-25300	Sequence 25300, A	650	6	2.0	159	4	US-09-489-039A-8927	Sequence 8927, Ap
578	6	2.0	141	4	US-09-252-991A-21853	Sequence 21853, A	651	6	2.0	159	4	US-09-489-039A-9662	Sequence 9662, Ap
579	6	2.0	141	4	US-09-252-991A-23895	Sequence 23895, A	652	6	2.0	159	4	US-09-902-540-10781	Sequence 10781, A
580	6	2.0	141	4	US-09-270-767-31706	Sequence 31706, A	653	6	2.0	159	4	US-09-252-991A-17039	Sequence 17039, A
581	6	2.0	141	4	US-09-270-767-46923	Sequence 46923, A	654	6	2.0	160	4	US-09-252-991A-18043	Sequence 18043, A
582	6	2.0	141	4	US-09-513-999C-4215	Sequence 4215, Ap	655	6	2.0	160	4	US-09-252-991A-23375	Sequence 23375, A
583	6	2.0	142	4	US-09-252-991A-25603	Sequence 25603, A	656	6	2.0	160	4	US-09-270-767-33721	Sequence 33721, A
584	6	2.0	142	4	US-09-252-991A-28784	Sequence 28784, A	657	6	2.0	160	4	US-09-270-767-48938	Sequence 48938, A
585	6	2.0	142	4	US-09-270-767-45160	Sequence 45160, A	658	6	2.0	160	4	US-09-902-540-12994	Sequence 12994, A
586	6	2.0	142	4	US-09-107-433-4175	Sequence 4175, Ap	659	6	2.0	160	4	US-09-902-540-15069	Sequence 15069, A
587	6	2.0	143	4	US-09-252-991A-21012	Sequence 21012, A	660	6	2.0	161	4	US-09-252-991A-18142	Sequence 18142, A
588	6	2.0	143	4	US-09-252-991A-21367	Sequence 21367, A	661	6	2.0	161	4	US-09-252-991A-23452	Sequence 23452, A
589	6	2.0	143	4	US-09-252-991A-27046	Sequence 27046, A	662	6	2.0	161	4	US-09-252-991A-30023	Sequence 30023, A
590	6	2.0	143	4	US-09-252-991A-28392	Sequence 28392, A	663	6	2.0	161	4	US-09-198-452A-319	Sequence 319, App
591	6	2.0	143	4	US-09-252-991A-32985	Sequence 32985, A	664	6	2.0	161	4	US-09-489-039A-9917	Sequence 9917, Ap
592	6	2.0	144	4	US-09-252-991A-17046	Sequence 17046, A	665	6	2.0	161	4	US-09-513-999C-5070	Sequence 5070, Ap
593	6	2.0	144	4	US-09-252-991A-19305	Sequence 19305, A	666	6	2.0	162	4	US-09-252-991A-32101	Sequence 32101, A
594	6	2.0	144	4	US-09-270-767-48156	Sequence 48156, A	667	6	2.0	163	4	US-09-252-991A-17451	Sequence 17451, A
595	6	2.0	145	3	US-08-946-329A-55	Sequence 55, Appli	668	6	2.0	163	4	US-09-252-991A-22533	Sequence 22533, A
596	6	2.0	145	4	US-09-252-991A-21532	Sequence 21532, A	669	6	2.0	163	4	US-09-252-991A-22703	Sequence 22703, A
597	6	2.0	145	4	US-09-252-991A-25175	Sequence 25175, A	670	6	2.0	163	4	US-09-489-039A-9968	Sequence 9968, Ap
598	6	2.0	145	4	US-09-252-991A-31281	Sequence 31281, A	671	6	2.0	163	4	US-09-134-000C-3710	Sequence 3710, Ap
599	6	2.0	145	4	US-09-489-039A-10021	Sequence 10021, A	672	6	2.0	164	4	US-09-252-991A-16730	Sequence 16730, A
600	6	2.0	146	4	US-09-252-991A-23040	Sequence 23040, A	673	6	2.0	164	4	US-09-198-452A-427	Sequence 427, App
601	6	2.0	146	4	US-09-489-039A-7946	Sequence 7946, Ap	674	6	2.0	164	4	US-09-328-352-4685	Sequence 4685, Ap
602	6	2.0	147	3	US-08-065-844A-7	Sequence 7, Appli	675	6	2.0	164	4	US-09-270-767-59203	Sequence 59203, A
603	6	2.0	147	4	US-09-252-991A-28936	Sequence 28936, A	676	6	2.0	164	4	US-09-438-185A-410	Sequence 410, App
604	6	2.0	147	4	US-09-252-991A-29687	Sequence 29687, A	677	6	2.0	165	4	US-09-252-991A-24384	Sequence 24384, A
605	6	2.0	147	4	US-09-270-767-31829	Sequence 31829, A	678	6	2.0	165	4	US-09-248-796A-23180	Sequence 23180, A
606	6	2.0	147	4	US-09-270-767-47046	Sequence 47046, A	679	6	2.0	166	4	US-09-252-991A-27562	Sequence 27562, A
607	6	2.0	148	4	US-09-252-991A-26957	Sequence 26957, A	680	6	2.0	166	4	US-09-252-991A-3439	Sequence 3439, Ap
608	6	2.0	148	4	US-09-134-000C-3771	Sequence 3771, Ap	681	6	2.0	166	4	US-09-270-767-43161	Sequence 43161, A
609	6	2.0	149	4	US-09-252-991A-20244	Sequence 20244, A	682	6	2.0	166	4	US-09-270-767-45796	Sequence 45796, A
610	6	2.0	149	4	US-09-252-991A-22850	Sequence 22850, A	683	6	2.0	167	4	US-09-270-767-61415	Sequence 61415, A
611	6	2.0	149	4	US-09-270-767-34780	Sequence 34780, A	684	6	2.0	167	4	US-09-252-991A-17526	Sequence 17526, A

685	6	2.0	168	2	US-08-408-095-13	Sequence 13, Appl	758	6	2.0	189	4	US-09-252-991A-19775	Sequence 19775, A
686	6	2.0	168	4	US-09-252-991A-21273	Sequence 21273, A	759	6	2.0	190	4	US-09-252-991A-17851	Sequence 17851, A
687	6	2.0	168	4	US-09-252-991A-23198	Sequence 23198, A	760	6	2.0	190	4	US-09-252-991A-22679	Sequence 22679, A
688	6	2.0	168	4	US-09-252-991A-24947	Sequence 24947, A	761	6	2.0	190	4	US-09-252-991A-24624	Sequence 24624, A
689	6	2.0	168	4	US-09-252-991A-28064	Sequence 28064, A	762	6	2.0	190	4	US-09-270-767-31332	Sequence 31332, A
690	6	2.0	168	4	US-09-248-796A-20339	Sequence 20339, A	763	6	2.0	190	4	US-09-270-767-48549	Sequence 48549, A
691	6	2.0	168	4	US-09-902-540-12003	Sequence 12003, A	764	6	2.0	190	4	US-09-270-767-61626	Sequence 61626, A
692	6	2.0	168	4	US-09-252-991A-22544	Sequence 22544, A	765	6	2.0	190	4	US-09-107-433-4319	Sequence 4319, Ap
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694	6	2.0	170	4	US-09-252-991A-19980	Sequence 19980, A	767	6	2.0	191	4	US-09-252-991A-19742	Sequence 19742, A
695	6	2.0	170	4	US-09-252-991A-29047	Sequence 29047, A	768	6	2.0	191	4	US-09-252-991A-24515	Sequence 24515, A
696	6	2.0	171	4	US-09-489-039A-8235	Sequence 8235, Ap	769	6	2.0	191	4	US-09-248-796A-24047	Sequence 24047, A
697	6	2.0	172	4	US-09-328-352-7411	Sequence 7411, Ap	770	6	2.0	192	4	US-09-540-236-3681	Sequence 3681, Ap
698	6	2.0	173	4	US-09-252-991A-18184	Sequence 18184, A	771	6	2.0	193	4	US-09-252-991A-23470	Sequence 23470, A
699	6	2.0	173	4	US-09-252-991A-22700	Sequence 22700, A	772	6	2.0	194	4	US-09-270-767-39426	Sequence 39426, A
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702	6	2.0	173	4	US-09-328-352-7665	Sequence 7665, Ap	775	6	2.0	195	1	US-08-236-427-4	Sequence 4, Appl1
703	6	2.0	174	4	US-09-489-039A-8647	Sequence 8647, Ap	776	6	2.0	195	4	US-09-340-620A-49	Sequence 49, Appl
704	6	2.0	175	2	US-08-408-095-8	Sequence 8, Appl1	777	6	2.0	195	4	US-09-252-991A-30009	Sequence 30009, A
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706	6	2.0	175	2	US-08-408-095-10	Sequence 10, Appl	779	6	2.0	195	4	US-09-270-767-41580	Sequence 41580, A
707	6	2.0	175	2	US-08-408-095-11	Sequence 11, Appl	780	6	2.0	195	4	US-09-841-879B-5	Sequence 5, Appl1
708	6	2.0	175	2	US-08-408-095-12	Sequence 12, Appl	781	6	2.0	196	4	US-09-252-991A-26457	Sequence 26457, A
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711	6	2.0	175	4	US-09-270-767-62407	Sequence 62407, A	784	6	2.0	197	4	US-09-252-991A-30392	Sequence 30392, A
712	6	2.0	175	4	US-09-710-279-1336	Sequence 1336, Ap	785	6	2.0	197	4	US-09-252-991A-33294	Sequence 33294, A
713	6	2.0	175	4	US-09-484-577A-54	Sequence 54, Appl	786	6	2.0	199	4	US-09-252-991A-13323	Sequence 13323, A
714	6	2.0	176	4	US-08-469-360A-51	Sequence 51, Appl	787	6	2.0	199	4	US-09-252-991A-22308	Sequence 22308, A
715	6	2.0	176	4	US-08-468-446-51	Sequence 51, Appl	788	6	2.0	199	4	US-09-252-991A-30363	Sequence 30363, A
716	6	2.0	176	4	US-08-467-344A-51	Sequence 51, Appl	789	6	2.0	199	4	US-09-252-991A-10266	Sequence 10266, A
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718	6	2.0	176	4	US-09-248-796A-23424	Sequence 23424, A	791	6	2.0	200	4	US-09-252-991A-20897	Sequence 20897, A
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721	6	2.0	177	4	US-09-902-540-13376	Sequence 13376, A	794	6	2.0	201	4	US-09-252-991A-33202	Sequence 33202, A
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724	6	2.0	178	4	US-09-252-991A-32741	Sequence 32741, A	797	6	2.0	202	4	US-09-710-279-1108	Sequence 1108, Ap
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727	6	2.0	179	3	US-09-283-471A-33	Sequence 33, Appl	800	6	2.0	203	3	US-09-299-041-8	Sequence 8, Appl1
728	6	2.0	179	4	US-09-270-767-32460	Sequence 32460, A	801	6	2.0	203	4	US-09-252-991A-20284	Sequence 20284, A
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731	6	2.0	181	4	US-09-252-991A-30481	Sequence 30481, A	804	6	2.0	203	4	US-09-543-681A-4741	Sequence 4741, Ap
732	6	2.0	181	4	US-09-328-352-7055	Sequence 7055, Ap	805	6	2.0	203	4	US-09-270-767-35326	Sequence 35326, A
733	6	2.0	181	4	US-09-489-039A-11004	Sequence 11004, A	806	6	2.0	203	4	US-09-270-767-50543	Sequence 50543, A
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736	6	2.0	182	4	US-09-252-991A-27971	Sequence 27971, A	809	6	2.0	204	4	US-09-489-039A-7474	Sequence 7474, Ap
737	6	2.0	182	4	US-09-252-991A-31478	Sequence 31478, A	810	6	2.0	205	4	US-09-252-991A-29378	Sequence 29378, A
738	6	2.0	182	4	US-09-543-681A-6272	Sequence 6272, Ap	811	6	2.0	205	4	US-09-270-767-43520	Sequence 43520, A
739	6	2.0	182	4	US-09-248-796A-17553	Sequence 17553, A	812	6	2.0	205	4	US-09-107-433-3118	Sequence 3118, Ap
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741	6	2.0	183	4	US-09-252-991A-22355	Sequence 22355, A	814	6	2.0	206	4	US-09-252-991A-26202	Sequence 26202, A
742	6	2.0	183	4	US-09-252-991A-32179	Sequence 32179, A	815	6	2.0	207	4	US-09-252-991A-33043	Sequence 33043, A
743	6	2.0	183	6	5168049-4	Patent No. 5168049	816	6	2.0	208	4	US-09-328-352-6009	Sequence 6009, Ap
744	6	2.0	183	6	5168049-4	Patent No. 5168049	817	6	2.0	208	4	US-09-134-000C-3698	Sequence 3698, Ap
745	6	2.0	184	3	US-08-759-628-10	Sequence 10, Appl	818	6	2.0	208	4	US-09-710-279-1084	Sequence 1084, Ap
746	6	2.0	184	4	US-09-252-991A-17955	Sequence 17955, A	819	6	2.0	208	4	US-09-949-016-7529	Sequence 7529, Ap
747	6	2.0	184	4	US-09-252-991A-20944	Sequence 20944, A	820	6	2.0	209	4	US-09-252-991A-16676	Sequence 16676, A
748	6	2.0	185	3	US-09-218-163-15	Sequence 15, Appl	821	6	2.0	209	4	US-09-248-796A-16078	Sequence 16078, A
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752	6	2.0	186	4	US-09-252-991A-27151	Sequence 27151, A	825	6	2.0	211	2	US-08-164-292B-2	Sequence 2, Appl1
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754	6	2.0	186	4	US-09-489-039A-11500	Sequence 11500, A	827	6	2.0	211	3	US-08-845-623-2	Sequence 2, Appl1
755	6	2.0	187	4	US-09-252-991A-18467	Sequence 18467, A	828	6	2.0	211	3	US-08-815-927-2	Sequence 2, Appl1
756	6	2.0	187	4	US-09-252-991A-21931	Sequence 21931, A	829	6	2.0	211	3	US-09-103-330-2	Sequence 2, Appl1
757	6	2.0	187	4	US-09-248-796A-16116	Sequence 16116, A	830	6	2.0	211	3	US-09-435-243-2	Sequence 2, Appl1

831	6	2.0	211	3	US-09-323-872A-12	Sequence 12, Appl	904	6	2.0	233	2	US-08-458-568A-4	Sequence 4, Appl
832	6	2.0	211	4	US-09-252-991A-24927	Sequence 24927, A	905	6	2.0	233	3	US-08-871-572B-8	Sequence 8, Appl
833	6	2.0	211	4	US-09-252-991A-26393	Sequence 26393, A	906	6	2.0	233	4	US-09-252-991A-22617	Sequence 22617, A
834	6	2.0	211	4	US-09-072-433-21	Sequence 21, Appl	907	6	2.0	233	4	US-09-252-991A-25021	Sequence 25021, A
835	6	2.0	211	4	US-09-394-142B-4	Sequence 4, Appl	908	6	2.0	233	4	US-09-252-991A-25399	Sequence 25399, A
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842	6	2.0	213	4	US-09-252-991A-24240	Sequence 24240, A	915	6	2.0	235	4	US-09-198-452A-930	Sequence 930, App
843	6	2.0	213	4	US-09-252-991A-27051	Sequence 27051, A	916	6	2.0	236	3	US-09-230-156-22	Sequence 22, Appl
844	6	2.0	213	4	US-09-248-796A-26548	Sequence 26548, A	917	6	2.0	236	4	US-09-252-991A-26394	Sequence 26394, A
845	6	2.0	214	4	US-09-252-991A-19407	Sequence 19407, A	918	6	2.0	236	4	US-09-902-540-10625	Sequence 10625, A
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847	6	2.0	214	4	US-09-252-991A-25326	Sequence 25326, A	920	6	2.0	237	4	US-09-499-227-13	Sequence 13, Appl
848	6	2.0	214	4	US-08-722-570-2	Sequence 2, Appl	921	6	2.0	237	4	US-09-252-991A-17927	Sequence 17927, A
849	6	2.0	214	4	US-08-932-411A-2	Sequence 2, Appl	922	6	2.0	237	4	US-09-252-991A-32341	Sequence 32341, A
850	6	2.0	214	4	US-09-758-282B-19	Sequence 19, Appl	923	6	2.0	238	4	US-09-140-749-51	Sequence 51, Appl
851	6	2.0	214	4	US-09-758-282B-19	Sequence 20, Appl	924	6	2.0	238	4	US-09-270-767-43802	Sequence 43802, A
852	6	2.0	214	4	US-09-577-304A-19	Sequence 19, Appl	925	6	2.0	239	4	US-09-252-991A-25790	Sequence 25790, A
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## ALIGNMENTS

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US-09-733-167A-6
; Sequence 6, Application US/09733167A
; Patent No. 6696547
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; APPLICANT: Peter, Marcus
; APPLICANT: Kramer, Peter
; TITLE OF INVENTION: Protein for Regulation of Apoptosis
; FILE REFERENCE: 4121-120
; CURRENT APPLICATION NUMBER: US/09/733,167A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/DE99/01712
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
; PRIOR FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising amino
; US-09-733-167A-6
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Best Local Similarity 100.0%; Pred. No. 0.00047;
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US-08-859-167-4
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; Sequence 4, Application US/08859167
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; Patent No. 6037461
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; GENERAL INFORMATION:
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; APPLICANT: Alnemri, Emad S.
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; APPLICANT: Fernandez-Alnemri, Teresa
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; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
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; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
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; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461r1s
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
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; COUNTRY: USA
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; APPLICATION NUMBER: US/08/859,167
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; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
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; NAME: Deluca, Mark
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; REGISTRATION NUMBER: 33,229
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; REFERENCE/DOCKET NUMBER: TJU-
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; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (215) 568-3100
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; TELEFAX: (215) 568-3439
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; INFORMATION FOR SEQ ID NO: 4:
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; TYPE: amino acid
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; TOPOLOGY: linear
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; MOLECULE TYPE: protein
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; US-08-859-167-4
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Best Local Similarity 100.0%; Pred. No. 0.0007;
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US-08-859-167-6
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; Sequence 6, Application US/08859167
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; Patent No. 6037461
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; GENERAL INFORMATION:
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; APPLICANT: Alnemri, Emad S.
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; APPLICANT: Fernandez-Alnemri, Teresa
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; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
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; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
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; NUMBER OF SEQUENCES: 17
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; CORRESPONDENCE ADDRESS:
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; ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461r1s
```

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; STREET: One Liberty Place, 46th floor
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; CITY: Philadelphia
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; STATE: PA
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; APPLICATION NUMBER: US/08/859,167
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; FILING DATE:
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; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
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```
; NAME: Deluca, Mark
```

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; REGISTRATION NUMBER: 33,229
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; REFERENCE/DOCKET NUMBER: TJU-
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-859-167-6

Query Match 4.3%; Score 13; DB 3; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
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DB 192 TCDIRLRVRAEYC 204

## RESULT 4

US-09-109-273-4  
Sequence 4, Application US/09109273  
Patent No. 6063760  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
TITLE OF INVENTION: OF MAKING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760rls  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/109,273  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,167  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-109-273-4

Query Match 4.3%; Score 13; DB 3; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
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DB 192 TCDIRLRVRAEYC 204

## RESULT 5

US-09-109-273-6  
Sequence 6, Application US/09109273  
Patent No. 6063760  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
TITLE OF INVENTION: OF MAKING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760rls  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS  
SOFTWARE: WordPerfect  
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FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,167  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-109-273-6

Query Match 4.3%; Score 13; DB 3; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
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DB 192 TCDIRLRVRAEYC 204

## RESULT 6

US-09-276-993-4  
Sequence 4, Application US/09276993  
Patent No. 6207801  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF  
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS  
TITLE OF INVENTION: OF MAKING THE SAME  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801rls  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-4

Query Match      4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
Db      192 TCDIRLRVRAEYC 204

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US-09-276-993-6
; Sequence 6, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-6

Query Match      4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
Db      192 TCDIRLRVRAEYC 204

RESULT 8
US-09-723-450-4
; Sequence 4, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF USING THE SAME, AND
; TITLE OF INVENTION: COMPOSITIONS FOR AND METHODS OF MAKING THE SAME
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751el Sequence
; US-09-723-450-4

Query Match      4.3%; Score 13; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
Db      192 TCDIRLRVRAEYC 204

RESULT 9
US-09-723-450-6
; Sequence 6, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF USING THE SAME, AND
; TITLE OF INVENTION: COMPOSITIONS FOR AND METHODS OF MAKING THE SAME
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: No. 6576751el Sequence  
US-09-723-450-6

Query Match 4.3%; Score 13; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
Db 192 TCDIRLRVRAEYC 204

RESULT 10  
US-09-733-167A-1  
Sequence 1, Application US/09733167A  
Patent No. 6696547  
GENERAL INFORMATION:  
APPLICANT: Peter, Marcus  
TITLE OF INVENTION: Protein for Regulation of Apoptosis  
FILE REFERENCE: 4121-120  
CURRENT APPLICATION NUMBER: US/09/733,167A  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: PCT/DE99/01712  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3  
PRIOR FILING DATE: 1998-06-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-733-167A-1

Query Match 4.3%; Score 13; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
Db 192 TCDIRLRVRAEYC 204

RESULT 11  
US-09-733-167A-3  
Sequence 3, Application US/09733167A  
Patent No. 6696547  
GENERAL INFORMATION:  
APPLICANT: Peter, Marcus  
APPLICANT: Kramer, Peter  
TITLE OF INVENTION: Protein for Regulation of Apoptosis  
FILE REFERENCE: 4121-120  
CURRENT APPLICATION NUMBER: US/09/733,167A  
PRIOR FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: PCT/DE99/01712  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3  
PRIOR FILING DATE: 1998-06-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 3  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-733-167A-3

Query Match 4.3%; Score 13; DB 4; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207  
Db 192 TCDIRLRVRAEYC 204

RESULT 12  
US-09-252-991A-30543  
Sequence 30543, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 30543  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30543

Query Match 3.0%; Score 9; DB 4; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 RRRRGAPA 177  
Db 5 RRRRGAPA 13

RESULT 13  
US-09-602-777A-230  
Sequence 230, Application US/09602777A  
Patent No. 6831165  
GENERAL INFORMATION:  
APPLICANT: Pompeius, Markus  
APPLICANT: Krogger, Burkhard  
APPLICANT: Schroder, Hartwig  
APPLICANT: Zelder, Oskar  
APPLICANT: Habenhauer, Gregor  
TITLE OF INVENTION: CORYNBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
FILE REFERENCE: BGI-128CP  
CURRENT APPLICATION NUMBER: US/09/602,777A  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 60/141031  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: DE 19931636.8  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: DE 19932125.6  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932126.4  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932127.2  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932128.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932129.9  
PRIOR FILING DATE: 1999-07-19  
PRIOR APPLICATION NUMBER: DE 19932226.0  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: DE 19932920.6  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932922.2  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932924.9  
PRIOR FILING DATE: 1999-07-14



PRIOR APPLICATION NUMBER: DE 19932928.1  
PRIOR FILING DATE: 1998-07-14  
PRIOR APPLICATION NUMBER: DE 19932930.3  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932933.8  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932935.4  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19932973.7  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933002.6  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933003.4  
PRIOR FILING DATE: 1998-07-14  
PRIOR APPLICATION NUMBER: DE 19933005.0  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19933006.9  
PRIOR FILING DATE: 1999-07-14  
PRIOR APPLICATION NUMBER: DE 19941378.9  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941379.7  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941390.8  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19941391.6  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: DE 19942088.2  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 442  
SEQ ID NO 230  
LENGTH: 336  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-602-777A-230

Query Match 3.0%; Score 9; DB 4; Length 336;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 EALREAVGR 290  
DB 58 EALREAVGR 66

RESULT 14  
US-09-252-991A-18973  
Sequence 18973, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 18973  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18973

Query Match 3.0%; Score 9; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 RRRGAPAP 179  
DB 119 RRRGAPAP 127

RESULT 15  
US-09-252-991A-25124  
Sequence 25124, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 25124  
LENGTH: 386  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-25124

Query Match 3.0%; Score 9; DB 4; Length 386;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRRGA 175  
DB 171 GARRRRRGA 179

Search completed: February 12, 2005, 16:39:45  
Job time : 35 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2005, 16:16:39 ; Search time 21 Seconds  
(without alignments)  
1388.270 Million cell updates/sec

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Title:      US-10-030-271-2
Perfect score: 1550
Sequence:   1 MALSGSTPAPCMEDECLDY.....LREAVGRVRLIVSYDEAD 303

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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*
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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	136	8.8	397	2	A33880	syndecan 2 - human
2	110	7.1	891	2	G64633	probable proline-γ
3	108.5	7.0	483	2	S36470	ε2 protein - human
4	108.5	7.0	3924	2	S37431	ankyrin 2, neuronal
5	108	7.0	581	2	E75383	conserved hypothe
6	106	6.8	6831	2	A88852	protein unc-22 (d
7	106	6.8	6839	2	S57242	twitchin (similar
8	106	6.8	7160	2	T27935	twitchin (similar
9	105.5	6.8	1571	2	T00062	hypothetical prot
10	103.5	6.7	658	2	T46359	hypothetical prot
11	103.5	6.7	1469	2	T09219	basal transcrip
12	103.5	6.7	1791	2	T02345	hypothetical prot
13	102.5	6.6	705	2	A35353	synapsin I splice
14	102.5	6.6	1106	2	J00045	hypothetical 119.5
15	101.5	6.5	274	2	A55335	myelin regulatory
16	101	6.5	241	2	T30761	hypothetical prot
17	101	6.5	494	2	G84386	hypothetical prot
18	100	6.5	414	2	C86301	arginine/serine-γ
19	100	6.5	1298	1	EDBEV5	immediate-early p
20	99.5	6.4	297	2	C87515	hypothetical prot
21	99.5	6.4	2248	2	A35938	profilaggrin - hu
22	99	6.4	1460	1	EDBEVF	immediate-early
23	98.5	6.4	335	2	T21503	hypothetical prot
24	98.5	6.4	706	2	B30411	synapsin Ia - bov
25	98.5	6.4	998	2	T35745	probable ATP-bind
26	98	6.3	498	1	W2WU5	ε2 protein - human
27	98	6.3	1557	2	T02859	ε2 probable serine/tr
28	98	6.3	1773	2	A81937	IgA-specific meta
29	98	6.3	1815	2	C81169	IgA-specific meta

30	97.5	6.3	351	2	B34768	ORF5 protein - Orf
31	97.5	6.3	433	2	S15647	KUP protein - huma
32	97.5	6.3	975	2	S35121	homeotic protein C
33	97	6.3	372	2	A41792	homeotic protein e
34	97.6	6.3	424	2	H87520	hypochelical proteo
35	97	6.3	900	2	S70630	xeroderma pigmento
36	96	6.2	221	2	A42701	splitting factor SP
37	96	6.2	221	2	A42701	PK26 protein - ch
38	96	6.2	279	2	H87917	protein F28D9.1 (I
39	96	6.2	454	2	T42680	hypochelical prote
40	96	6.2	461	2	A31237	alpha-2c-adeninegi
41	96	6.2	2786	1	UC4743	fatty-acid synthase
42	95.5	6.2	676	1	EDB823	immediate-early pr
43	95	6.1	187	2	T51584	splitting factor 9G
44	95	6.1	231	2	S40438	homeotic protein e
45	95	6.1	235	2	T30656	hypochelical prote

## ALIGNMENTS

## RESULT 1

syndecan 2 - human (fragment)  
N:Alternate names: cell surface-associated fibroglycan; heparan sulfate proteoglycan 1  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence, revision 31-Mar-1990 #text, change 05-Nov-1999  
C:Accession: A33880  
R:Maryann, P.; Zhang, J.; Cassiman, J.J.; Van den Berghe, H.; David, G.  
J. Biol. Chem. 264, 7017-7024, 1989  
A:Title: Partial primary structure of the 48- and 90-kilodalton core proteins of cell surface evidence for multiple distinct core proteins at the cell surface of human lung fibroblast  
;Reference number: A33880; MUID:89214123; PMID:2523388

		8.4%;	Score 136;	DB 2;	Length 397;	
		Best Local Similarity	26.1%;	Pred.	No. 0 0088;	
		Matches	71;	Conservative	32; Mismatches 100; Indels	50; Gaps 13;
QY	DEAPG--AAGLAR-----ARSGLELLERRCGCCGSNRLRGLQLURVLARDH	97	:   :	:   :	:   :	:
Dd	EEDGRARRRRRGAAAEPAVPLGRBALQIPPELQPRGRAPAALPL-----NF	64	:   :	:   :	:   :	:
QY	LPLHARKRRPVSPPE---RYSYGTSSSKRTGSCRRRRQSSSANSQQCGWETGPSPT	154	:   :	:   :	:   :	:
Dd	CSSLASQRISYSLKPETEPFHGGKVGAAMPQOSKTSFEQPERSITVSYG---VOKEP	121	:   :	:   :	:   :	:
QY	KRRRSNGSRSGGA--RRRRGAPAAPQOQSSEARS-SRGKYTCIDILRVR-ABEYCH	209	:   :	:   :	:   :	:
Dd	ERAIPRSSGAAGAAGGSRRRRRKRAPSP---EFESPSSLNNRCGTLIRLRKGLAERMWG	177	:   :	:   :	:   :	:
QY	G--PALTEGVASSRPPOALAROLDVFQAATAVLRSDLDGSVCDIKFSELSTYDAFMGDY	266	:   :	:   :	:   :	:
Dd	GFULPFLQAAAGS-----SRSLGNRRRAWTLL---TLGIIVAC-VSAESRAELTSDKMVT	227	:   :	:   :	:   :	:
QY	LSGALLQALRGVP	279	:   :	:   :	:   :	:
Dd	LDNSSIIEASGYV	240	:   :	:   :	:   :	:

RESULT 2  
J84693



F:727-759/Domain: ankyrin repeat homology <AN21>  
F:760-792/Domain: ankyrin repeat homology <AN22>  
F:793-825/Domain: ankyrin repeat homology <AN23>

Query Match 7.0%; Score 108.5; DB 2; Length 3924;

Best Local Similarity 25.1%; Pred. No. 9.5;  
Matches 48; Conservative 27; Mismatches 67; Indels 49; Gaps 9;

QY 48 LIDEAPGAAGGLARASGLLELEERRGGCGESNRLIGQLRVLAHDL----- 98  
DB 1724 LIEET--IGSIDKTKALQKVEDQKGR--SKLP-----IRVKGEDVPKKTTHRH 1773  
QY 99 ---LPHLAKRRRPPSP---ERYSYGTSSSSKRTGSCRRRQSSSSANSQGGWETGS 151  
DB 1774 PAAPSLKSEERHAPGSPSPKTERHS--TLSSSAKTE-----RHPPVSPSSKTEKHSPPS 1825  
QY 152 PPTKQRRGRGRRPGSGARRRRGAPAPQOQSEPPAPSSGKTCIRLRVRAEYCEHP 211  
DB 1826 PAKTERHS--PASSSSKTEKHSPPSPKTERHSPPSTKTE-----RHPP 1870  
QY 212 ALEQGVASRRP 222  
DB 1871 VSPSGKTDKRP 1881

## RESULT 5

E75383 conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C/Species: Deinococcus radiodurans  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #ext\_change 09-Jul-2004

C/Accession: E75383  
R/White, O.; Eichen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; NUID:20036896; PMID:10567266

A/Accession: E75383

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-581 <MHI>

A/Cross-references: UNIPROT:Q9RU45; GB:AE001998; GB:AE000513; NID:96459302; PIDN:AAPI110

A/Genetic source: strain R1

C/Genetics:

A:Gene: DR1549

A:Map position: 1

Query Match 7.0%; Score 108; DB 2; Length 581;

Best Local Similarity 25.9%; Pred. No. 1.5;  
Matches 67; Conservative 26; Mismatches 96; Indels 70; Gaps 13;

QY 18 LDYGMLSLHRMFVVGQLTECELELAFLL-----DEAPGAG---GLARRS--- 64  
DB 174 LYANMAG-QRVNVEVA-BOLRGAAALTTQQLRQOOSDALRGLQGEQTKLAELDRRT 231  
QY 65 -GLELLLELERRGGCGESNL-----RLIGQLRVLAHDLPHLARKR 107  
DB 232 RQADLAELQSAQ-GQAVAVRTQAQALTAQTIDSLVGNVRETR-----LEEER 284  
QY 108 RVSPSPRVSYSSTSSKRTGSCRRRQSSSSANSQGGWETGSPTKQRRSGRPSGC 167  
DB 285 RLLEER-----RRREAEARRIRAEQERARKE-----AEELAIRAEQE-- 323  
QY 168 ARRRRGAPAPQOQSEPPAPSSGKTCIRLRVRAEYCEHP 223  
DB 324 -RKAEAAAROKALAEKAAQAQAARAEKARAEKARAEKARAEKARAEKARAEKARAE 382  
QY 224 ALARQLDVGQATAVLRSR 242  
DB 383 AQAR-----AQAEAAARAEKARAEKARAEKARAEKARAEKARAEKARAEKARAE 396

## RESULT 6

A88852 protein unc-22 [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #ext\_change 09-Jul-2004

C/Accession: A88852  
R/Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A/Reference number: A75000; NUID:99069613; PMID:9851916

A/Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elc

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-6831 <STO>

A/Cross-references: UNIPROT:Q23550; GB:chr\_IV; PIDN:CAA98081.1; PID:93881830; GSPDB:GN000

A:Gene: unc-22

C/Genetics:

A:Map position: 4

C/Superfamily: twitchin, fibronectin type III repeat homology; immunoglobulin homology;

Query Match 6.8%; Score 106; DB 2; Length 6831;

Best Local Similarity 22.9%; Pred. No. 25;  
Matches 72; Conservative 37; Mismatches 131; Indels 74; Gaps 13;

QY 4 SGSTPAPCWEDECDLYYGMLSLHRMFVVGQLTECELELAFLLDEAPGAAGGLARAR 63  
DB 128 SASPTPAKMKMGVPLSMGL-YHALFSDLGQTYLCQLR-----RPPSSDA-GQYR 179  
QY 64 SGLELLLELERRGGCGESNRLIGQLRVLAHDLPHLARKR-----RRPV 110  
DB 180 CNI-----RNDQETN-----ANLALFEEDPDERGERKRTSPAPSSRGPGSRPS 227  
QY 111 SPERSYGTSSSSKRT-----EGSCRR--ROSSSSANSQGGWETG-----S 151  
DB 228 SPKSMKSRGPPKTKLPKREKSPSKLRSTPNEVVSSESRSRTDKMEVDQVS 287  
QY 152 PPTKQRRGRGRRPGSGARRRRGAPAPQOQSEPPAPSSGKTCIRLRVRAEYCE 208  
DB 288 GASKRRPDLPPPGDEKTLRAGSPSTRKASPPSPKSSAGAAAGTTGASAS 347  
QY 209 HEPALQGVAS-----RRPQALRQLDVFGQATAVLRSLRSLGVSVCIDIKFSELSYL 259  
DB 348 ATSATSAGSASDASDRDKYTRPPYVL-----EASRSGTRIGGSVVLVYQWQCHSST 399  
QY 260 DAFMGDIYLSGALLQ 273  
DB 400 IIEW--YRDGTLVR 411

## RESULT 7

S57242 twitchin [similarity] - Caenorhabditis elegans  
N/Alternate names: myosin-regulating protein  
N/Contains: protein kinase (EC 2.7.1.-)

C/Species: Caenorhabditis elegans

C/Date: 28-Oct-1995 #sequence\_revision 24-Oct-1997 #ext\_change 09-Jul-2004

C/Accession: S57242; S067971; S57218; T27934; T28030

R/Bentley, G.W.; V'Hernault, S.W.; Morris, M.B.

submitted to the EMBL Data Library, February 1993

A/Description: Additional sequence complexity within twitching of Caenorhabditis elegans

A/Reference number: S57242

A/Accession: S57242

A/Molecule type: DNA

A/Residues: 1-6839 <BEN1>

A/Cross-references: UNIPROT:Q23550; EMBL:L10351

A/Experimental source: var. Bristol

R/Bentley, G.

submitted to the EMBL Data Library, November 1989

A/Reference number: S07571

A/Accession: S07571

A/Molecule type: DNA

A/Residues: 792-6839 <BEN2>

A:Cross-references: EMBL:X15423; NID:G6897; PIDN:CAA33463.1; PID:G6898  
 A:Experimental source: var. Bristol  
 R:Beniam, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.  
 Nature 342, 43-50, 1969  
 A>Title: Sequence of an unusually large protein implicated in regulation of myosin activity  
 A:Reference number: S06797; MUID:90044042; PMID:281202  
 A:Accession: S06797  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 806-1175;1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693;5696-6359, 'I', 6  
 A:Cross-references: EMBL:X15423  
 A:Experimental source: var. Bristol  
 R:Beniam, G.M.; L'Hernault, S.W.; Morris, M.E.  
 Genetics 134, 1097-1104, 1993  
 A>Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded product  
 A:Reference number: S57218; MUID:93387664; PMID:8397135  
 A:Accession: S57218  
 A:Molecule type: DNA  
 A:Residues: 2-99;108-194, 'Q', 196-206;374-468;658-753 <BEN4>  
 A:Experimental source: var. Bristol  
 R:White, S.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z20442  
 A:Accession: T27934  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'MGIPGKKCKQ', 19-6839 <W1>  
 A:Cross-references: EMBL:Z73897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a  
 A:Experimental source: clone ZK617  
 R:Haris, B.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z20458  
 A:Accession: T28030  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'MGIPGKKCKQ', 19-6839 <W12>  
 A:Cross-references: EMBL:Z73899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a  
 A:Experimental source: clone ZK829  
 C:Comment: Lack of unc-22 leads to a constant twitching of the body muscles.  
 C:Genetics:  
 A:Gene: unc-22; CESP:ZK617.1a  
 A:Map position: 4  
 A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60  
 152/3; 6691/3; 6776/1; 6808/3  
 C:Superfamily: ATP; fibronectin type III repeat homology; immunoglobulin homology;  
 C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; setine/th  
 F:806-899,899-990,991-1083,1084-1175,1178-1273,1474-1567,1770-1864,2066-2159,2358-2450,2  
 96-5790,6263-6356,6386-6478,6541-6635,6649-6742,6745-6838/Region: motif 2 2259-2357,2451-2  
 F:1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2451-2  
 F:1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2451-2  
 F:5940-6197/Domain: protein kinase homology <KIN>  
 F:5948-5956/Region: protein kinase ATP-binding motif  
 F:5971/Active site: Lys #status predicted

Query Match 6.8%; Score 106; DB 2; Length 6839;  
 Best Local Similarity 22.9%; Pred. No. 25;  
 Matches 72; Conservative 37; Mismatches 131; Indels 74; Gaps 13;

QY 4 SGSTAPPCWEEDECDIYGMISLHMFEEVVGQLTCELELLAFLIDEAPGAGGLARAR 63  
 DB 136 SASITPVAKMKMDGVPISMGGL-YHAIFSDIGQTYLCOLEI-----RGPSSDA-GQYR 187  
 QY 64 SGLLELLLERRGCGESNLRLLGQLRVLARHDLPLHARR-----RRPV 110  
 DB 188 CNI-----RNDGFTN-----ANLALNFEEDPSEERERKRTASPRSPSGSRPS 235  
 QY 111 SPERYSTYSSSSKRT-----EGSCRR--RRSSSSANSQOGWETG-----S 151  
 DB 236 SPKSKMSKREGTPKTKLRGSPSKLARSSTSTPVNEEVSQSESRSRSTDKMEVDQVS 295  
 QY 152 PPTKQRRSRGRRSGGARRRRGAPR--AFQOQSEPARPSESGKTCIRLRVAEYCE 208  
 DB 296 GASKRRKPDGLPPGDEKTLRAGSPSTRKSPRSKASPTPRSKGSAGGASGTTGASAS 355

QY 209 HGPALEQGVAS-----RRPOLARQLDVFGQATAVLRSDGVCIDIKFSELSYL 259  
 DB 356 ATSATSGGSASSDASRDKTRPPYLV-----EASRSQTRIGSGSVLVEVQCHSST 407  
 QY 260 DAFWGDYLSGALLQ 273  
 DB 408 IIEW--YRDGTLVR 419

RESULT 8  
 127935  
 hypothetical protein ZK617.1b - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T27935; T28031  
 R:White, S.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z20442  
 A:Accession: T27935  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7160 <W1>  
 A:Cross-references: UNIPROT:Q23551; EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK  
 R:Haris, B.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z20458  
 A:Accession: T28031  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7160 <W12>  
 A:Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b  
 A:Experimental source: clone ZK829  
 C:Genetics:  
 A:Gene: CESP:ZK617.1b  
 A:Map position: 4  
 A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59  
 3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3  
 C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match 6.8%; Score 106; DB 2; Length 7160;  
 Best Local Similarity 22.9%; Pred. No. 27;  
 Matches 72; Conservative 37; Mismatches 131; Indels 74; Gaps 13;

QY 4 SGSTAPPCWEEDECDIYGMISLHMFEEVVGQLTCELELLAFLIDEAPGAGGLARAR 63  
 DB 128 SASITPVAKMKMDGVPISMGGL-YHAIFSDIGQTYLCOLEI-----RGPSSDA-GQYR 179  
 QY 64 SGLLELLLERRGCGESNLRLLGQLRVLARHDLPLHARR-----RRPV 110  
 DB 180 CNI-----RNDGFTN-----ANLALNFEEDPSEERERKRTASPRSPSGSRPS 227  
 QY 111 SPERYSTYSSSSKRT-----EGSCRR--RRSSSSANSQOGWETG-----S 151  
 DB 228 SPKSKMSKREGTPKTKLRGSPSKLARSSTSTPVNEEVSQSESRSRSTDKMEVDQVS 287  
 QY 152 PPTKQRRSRGRRSGGARRRRGAPR--AFQOQSEPARPSESGKTCIRLRVAEYCE 208  
 DB 288 GASKRRKPDGLPPGDEKTLRAGSPSTRKSPRSKASPTPRSKGSAGGASGTTGASAS 347  
 QY 209 HGPALEQGVAS-----RRPOLARQLDVFGQATAVLRSDGVCIDIKFSELSYL 259  
 DB 348 ATSATSGGSASSDASRDKTRPPYLV-----EASRSQTRIGSGSVLVEVQCHSST 399  
 QY 260 DAFWGDYLSGALLQ 273  
 DB 400 IIEW--YRDGTLVR 411

RESULT 9  
 120062  
 hypothetical protein KIAA0434 - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004  
C:Accession: T00062  
R:ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.;  
submitted to the EMBL Data Library, October 1997  
A:Description: Prediction of the coding sequences of unidentified human genes. VIII. The  
A:Reference number: Z14082  
A:Accession: T00062  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1571 <ISH>  
A:Cross-references: UNIPROT:O43161; EMBL:AB007894; NID:G2662148; PIDN:BA23707.1; PID:G2  
A:Experimental source: brain; clone H82165  
C:Genetics:  
A>Note: KIAA0434

Query Match 6.7%; Score 105.5; DB 2; Length 1571;  
Best Local Similarity 24.5%; Pred. No. 6.3;  
Matches 46; Conservative 25; Mismatches 70; Indels 47; Gaps 7;

QY 53 PGAGGLARARSGLELLELERRGCGESNLRLLGQ-----LRLVLAHDLPLHLA 103  
DB 1275 PHDEGGPGHNAAKE-----HHGHGHSGRHTGEPRRAAKPHAKDLGSHKAPRPH-S 1328  
QY 104 RKRRPVSPEYRYSTGSSSKRTGSCRRRQSS--SANSQCGWETGSPPTKQRSS 160  
DB 1329 QPSSAPAMPKKGQPGYSSAEXYOPS---RASSAVYHNASDKSGRQAHSGPALAQ--S 1382  
QY 161 RRRPBGARRRRGAPAAPOQSEPARPSEKVTCTDILRLRAEYCEHGPALGQVNR 220  
DB 1383 KAEPAQPOLGQRAAPGQSQSPS-----SRQIPGSAAR 1419  
QY 221 RPOALARQ 228  
DB 1420 QPQTQQQQ 1427

## RESULT 10

T46359  
hypothetical protein DKFZp434K1316.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46359  
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z23037  
A:Accession: T46359  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-658 <AAA>  
A:Cross-references: UNIPROT:Q9NTP9; EMBL:AL137291  
A:Experimental source: adult testis; clone DKFZp434K1316  
C:Genetics:  
A>Note: DKFZp434K1316.1

Query Match 6.7%; Score 103.5; DB 2; Length 658;  
Best Local Similarity 28.9%; Pred. No. 3.7;  
Matches 59; Conservative 18; Mismatches 74; Indels 53; Gaps 10;

QY 59 LARARSGLELLELERRGQ-----CGESNLRLLGQLRLVLAHDLPLHLARRRRPVSPE 113  
DB 21 LEOVSSGLHRLRLRFRFOAHWYDEGFARLNG--AGPGREAVLAALALRR---APE 73  
QY 114 RYSYGT-----SSSKRTGSCRRRROSSSANSQCGWETGSPPTKQRSSR 161  
DB 74 P-SAGTPEPMALALDLSPPALRLRWGRQARQ-Q-ELERRIQOHLEENSPRGYRRRAD 131  
QY 162 GRPSCGARRRRRG-----APAPQOQSEPAR-----PSSEGVTCIDILRLVAEYCE 208  
DB 132 GASGCGAQWGRPSPPSLSSLLPSSPCGRPAFPHCSLAPCE-----DYEE 178  
QY 209 HGPALEQGVASRRPQA-LARQUDV 231

DB 179 EGPELAPAEAGRPRAVLIRGLEV 202

## RESULT 11

T09219  
basal transcription factor SNAPc large chain SNAP190 - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 16-Aug-2004  
C:Accession: T09219  
R:Wong, M.W.; Henry, R.W.; Ma, B.; Kobayashi, R.; Klages, N.; Matchias, P.; Strublin, M.;  
Wol, Cell. Biol. 18, 368-377, 1998  
A:Title: The large subunit of basal transcription factor SNAPc is a Myb domain protein  
A:Reference number: Z16616; MUID:98078693; PMID:9418884  
A:Accession: T09219  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-1469 <WON>  
A:Cross-references: UNIPROT:Q9Y6P7; EMBL:AF032387; NID:G2641556; PIDN:AA02972.1; PID:G2  
A:Experimental source: tissue type fetal cell teratocarcinoma  
C:Genetics:  
A:Gene: SNAP190

C:Function:  
A:Description: transcription factor; required for transcription of snRNA genes  
C:Superfamily: myb DNA-binding repeat homology  
C:Keywords: DNA binding; RNA biosynthesis; transcription factor  
F:396-447/Domain: myb DNA-binding repeat homology <MYB>

Query Match 6.7%; Score 103.5; DB 2; Length 1469;  
Best Local Similarity 24.3%; Pred. No. 8.3;  
Matches 59; Conservative 32; Mismatches 75; Indels 77; Gaps 12;

QY 50 DEAPAGGLARARSGLELLELERRGCGESNLRLLGQLRLVLAHDL-----LP 100  
DB 429 EYFPRSAQCRDRLRLRLHPSLK-----GRNLKEEOLLEILIKYGVGHAKTASELP 484  
QY 101 H-----LARKRRPVSPEYRYSTGSSSKRTGSCRRRQSSSAN 141  
DB 485 HRSGGCLSKWKIMGKQGLRRRRRARHVSVMG--STSSGSSSGSSGSSSSSSSS 542  
QY 142 -----SQCGWENG--SP-----PTKQRSSRGPSGARRRRGAPAA--- 178  
DB 543 EDEPEQAQAGEGDRALLSPYMWPDMDLWVPA--RSTSGPMWCGAGAWLGCPLASLS 599  
QY 179 PQOQSEPARPSE-----GKVTCDILRLVRAEYCEHGPALGQVNR-----RPOAL 225  
DB 600 PPKSSASQCGSKKASTTAAAPGETSPVQVPARA---HGVPKSAQASHSADTRPAGA 655  
QY 226 ARQ 228  
DB 656 EKQ 658

## RESULT 12

T02345  
hypothetical protein KIAA0324 - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T02345  
R:Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saundere, E.; Robinson, D.;  
re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.  
submitted to the EMBL Data Library, March 1998  
A:Description: Sequencing of human chromosome 16p13.3.  
A:Reference number: Z14664

A:Accession: T02345  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1791 <RIC>  
A:Cross-references: UNIPROT:O60382; EMBL:AC004493; NID:G2996648; PIDN:AA08453.1; PID:G2  
C:Genetics:  
A:Map position: 16  
A:Introns: 1610/2; 1706/2  
A>Note: KIAA0324





Db	197	YSRKSRSRTRSRSRSTSKSRARSRKSKSSVSRSRSRSRSRSRSPPPVSKRESKR	256
Qy	185	-----PARPSEKVT	195
Db	257	SRKSPPKSPBEGVVS	273

Search completed: February 12, 2005, 16:30:28  
Job time : 24 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 12, 2005, 16:38:00 / Search time 15 Seconds  
(without alignments)  
755.515 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 303  
Sequence: 1 MALSGSTPAPCWEDECLDY.....LREAVGREAVRLVSYDEAD 303

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 147297 seqs, 37401721 residues

Word size : 0

Total number of hits satisfying chosen parameters: 147297

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/prodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.6	439	6	US-10-450-763-51705 Sequence 51705, A
2	8	2.6	439	6	US-10-450-763-54383 Sequence 54383, A
3	8	2.6	712	6	US-10-450-763-30700 Sequence 30700, A
4	8	2.6	805	6	US-10-450-763-54385 Sequence 54385, A
5	8	2.6	1066	6	US-10-450-763-54384 Sequence 54384, A
6	8	2.6	1089	6	US-10-450-763-53691 Sequence 53691, A
7	8	2.6	1125	6	US-10-450-763-51707 Sequence 51707, A
8	8	2.6	1127	6	US-10-489-448-2732 Sequence 2732, Ap
9	8	2.6	1131	6	US-10-450-763-51706 Sequence 51706, A
10	8	2.6	1142	6	US-10-450-763-54386 Sequence 54386, A
11	8	2.6	1292	6	US-10-489-448-997 Sequence 997, App
12	8	2.6	1388	6	US-10-450-763-51703 Sequence 51703, A
13	8	2.3	33	6	US-10-699-562-21 Sequence 21, App1
14	7	2.3	41	6	US-10-450-763-32943 Sequence 32943, A
15	7	2.3	64	6	US-10-450-763-52787 Sequence 52787, A
16	7	2.3	113	6	US-10-450-763-49753 Sequence 49753, A
17	7	2.3	122	7	US-11-031-175-10858 Sequence 10858, A
18	7	2.3	164	7	US-11-031-175-14156 Sequence 14156, A
19	7	2.3	164	7	US-11-031-175-15953 Sequence 15953, A
20	7	2.3	171	7	US-11-031-175-13213 Sequence 13213, A
21	7	2.3	225	7	US-11-027-399-3301 Sequence 3301, Ap
22	7	2.3	225	7	US-11-027-843-3301 Sequence 3301, Ap
23	7	2.3	225	7	US-11-027-878-3301 Sequence 3301, Ap
24	7	2.3	225	7	US-11-028-169-3301 Sequence 3301, Ap
25	7	2.3	225	7	US-11-028-204-3301 Sequence 3301, Ap

26	7	2.3	225	7	US-11-027-877-3301 Sequence 3301, Ap
27	7	2.3	225	7	US-11-027-879-3301 Sequence 3301, Ap
28	7	2.3	225	7	US-11-028-149-3301 Sequence 3301, Ap
29	7	2.3	225	7	US-11-027-802-3301 Sequence 3301, Ap
30	7	2.3	225	7	US-11-027-890-3301 Sequence 3301, Ap
31	7	2.3	225	7	US-11-027-892-3301 Sequence 3301, Ap
32	7	2.3	225	7	US-11-028-099-3301 Sequence 3301, Ap
33	7	2.3	225	7	US-11-028-197-3301 Sequence 3301, Ap
34	7	2.3	225	7	US-11-028-434-3301 Sequence 3301, Ap
35	7	2.3	225	7	US-11-028-050-3301 Sequence 3301, Ap
36	7	2.3	225	7	US-11-028-457-3301 Sequence 3301, Ap
37	7	2.3	225	7	US-11-027-891-3301 Sequence 3301, Ap
38	7	2.3	225	7	US-11-028-291-3301 Sequence 3301, Ap
39	7	2.3	225	7	US-11-028-455-3301 Sequence 3301, Ap
40	7	2.3	264	1	PCT-US04-17965-1054 Sequence 1054, Ap
41	7	2.3	264	1	PCT-US04-17965-2068 Sequence 2068, Ap
42	7	2.3	264	1	PCT-US04-17965-3604 Sequence 3604, Ap
43	7	2.3	294	8	US-60-643-717-7253 Sequence 7253, Ap
44	7	2.3	298	8	US-60-643-717-7823 Sequence 7823, Ap
45	7	2.3	300	7	US-11-031-175-14290 Sequence 14290, A
46	7	2.3	302	8	US-60-643-717-18643 Sequence 18643, A
47	7	2.3	355	7	US-11-031-175-15046 Sequence 15046, A
48	7	2.3	382	8	US-60-643-717-4153 Sequence 4153, Ap
49	7	2.3	382	8	US-60-643-717-14833 Sequence 14833, A
50	7	2.3	382	8	US-60-643-717-18949 Sequence 18949, A
51	7	2.3	386	8	US-60-643-717-12030 Sequence 12030, A
52	7	2.3	387	8	US-60-643-717-12515 Sequence 12515, A
53	7	2.3	403	7	US-11-031-175-11445 Sequence 11445, A
54	7	2.3	439	6	US-10-450-763-42544 Sequence 42544, A
55	7	2.3	505	6	US-10-450-763-34076 Sequence 34076, A
56	7	2.3	551	8	US-60-643-717-2548 Sequence 2548, Ap
57	7	2.3	551	8	US-60-643-717-6872 Sequence 6872, Ap
58	7	2.3	569	6	US-10-450-763-33416 Sequence 33416, A
59	7	2.3	574	6	US-10-450-763-33565 Sequence 33565, A
60	7	2.3	591	6	US-10-450-763-47629 Sequence 47629, A
61	7	2.3	602	8	US-60-643-717-11276 Sequence 11276, A
62	7	2.3	619	7	US-11-031-175-14059 Sequence 14059, A
63	7	2.3	684	6	US-10-450-763-44485 Sequence 44485, A
64	7	2.3	690	6	US-10-863-245A-2 Sequence 2, App1
65	7	2.3	690	6	US-10-863-245A-18 Sequence 18, App1
66	7	2.3	694	8	US-60-643-717-18622 Sequence 18622, A
67	7	2.3	710	6	US-10-450-763-50473 Sequence 50473, A
68	7	2.3	731	7	US-11-031-175-13763 Sequence 13763, A
69	7	2.3	731	8	US-60-643-717-12386 Sequence 12386, A
70	7	2.3	749	8	US-60-643-717-9435 Sequence 9435, Ap
71	7	2.3	752	6	US-10-450-763-58459 Sequence 58459, A
72	7	2.3	755	1	PCT-US04-17965-1405 Sequence 1405, Ap
73	7	2.3	775	8	US-60-643-717-5553 Sequence 5553, Ap
74	7	2.3	1035	6	US-10-450-763-35678 Sequence 35678, A
75	7	2.3	1037	7	US-11-031-175-9845 Sequence 9845, Ap
76	7	2.3	1099	7	US-11-033-545-5451 Sequence 5451, App
77	7	2.3	1100	7	US-11-033-545-344 Sequence 344, App
78	7	2.3	1524	6	US-10-450-763-60700 Sequence 60700, A
79	7	2.3	2108	8	US-60-643-717-5434 Sequence 5434, Ap
80	6	2.0	15	6	US-10-817-970-2016 Sequence 2016, Ap
81	6	2.0	19	6	US-10-699-567-11 Sequence 11, App1
82	6	2.0	22	6	US-10-699-565-9 Sequence 9, App1
83	6	2.0	28	6	US-10-450-763-49931 Sequence 49931, A
84	6	2.0	31	7	US-11-026-433-19 Sequence 19, App1
85	6	2.0	37	6	US-10-450-763-35382 Sequence 32582, A
86	6	2.0	40	7	US-11-042-241-236 Sequence 236, App
87	6	2.0	46	6	US-10-450-763-38359 Sequence 38359, A
88	6	2.0	50	6	US-10-450-763-44143 Sequence 44143, A
89	6	2.0	50	7	US-11-031-175-10534 Sequence 10534, A
90	6	2.0	51	6	US-10-699-566-22 Sequence 22, App1
91	6	2.0	54	6	US-10-450-763-47626 Sequence 47626, A
92	6	2.0	57	6	US-10-450-763-59101 Sequence 59101, A
93	6	2.0	62	6	US-10-450-763-55230 Sequence 52530, A
94	6	2.0	64	6	US-10-450-763-38358 Sequence 38358, A
95	6	2.0	65	6	US-10-450-763-33166 Sequence 33166, A
96	6	2.0	65	6	US-10-450-763-46258 Sequence 46258, A
97	6	2.0	65	6	US-10-450-763-54312 Sequence 54312, A
98	6	2.0	65	6	US-10-489-448-1889 Sequence 1289, Ap

99	6	2.0	US-10-450-763-50892	Sequence 50892, A	172	6	2.0	150	6	US-10-489-448-3360	Sequence 3360, Ap
100	6	2.0	US-10-450-763-56851	Sequence 56851, A	173	6	2.0	151	7	US-11-031-175-11681	Sequence 11681, A
101	6	2.0	US-11-031-175-13076	Sequence 13076, A	174	6	2.0	151	7	US-11-031-175-13473	Sequence 13473, A
102	6	2.0	US-10-450-763-54318	Sequence 54318, A	175	6	2.0	152	7	US-11-031-175-12154	Sequence 12154, A
103	6	2.0	US-11-032-643-42	Sequence 42, Appl	176	6	2.0	153	1	PCT-US04-43356-135	Sequence 135, App
104	6	2.0	US-11-033-490-42	Sequence 42, Appl	177	6	2.0	155	1	PCT-US04-43356-137	Sequence 137, App
105	6	2.0	US-10-450-763-56859	Sequence 56859, A	178	6	2.0	155	6	US-10-450-763-53914	Sequence 53914, A
106	6	2.0	US-10-450-763-49874	Sequence 49874, A	179	6	2.0	155	7	US-11-021-949-135	Sequence 135, App
107	6	2.0	US-10-450-763-46477	Sequence 46477, A	180	6	2.0	155	7	US-11-021-949-137	Sequence 137, App
108	6	2.0	US-11-031-175-15595	Sequence 15595, A	181	6	2.0	156	6	US-10-450-763-18290	Sequence 3890, Ap
109	6	2.0	PCT-US05-00040-7	Sequence 7, Appl1	182	6	2.0	156	8	US-60-643-717-4345	Sequence 4345, Ap
110	6	2.0	US-11-031-175-11751	Sequence 11751, A	183	6	2.0	158	8	US-60-643-717-6836	Sequence 6836, Ap
111	6	2.0	US-11-031-175-13717	Sequence 13717, A	184	6	2.0	159	7	US-11-031-175-10781	Sequence 10781, A
112	6	2.0	US-10-450-763-41733	Sequence 41733, A	185	6	2.0	160	6	US-10-450-763-44237	Sequence 44237, A
113	6	2.0	US-10-450-763-58648	Sequence 58648, A	186	6	2.0	160	7	US-11-031-175-12994	Sequence 12994, A
114	6	2.0	US-11-031-175-11177	Sequence 113177, A	187	6	2.0	160	7	US-11-031-175-15069	Sequence 15069, A
115	6	2.0	US-10-450-763-56812	Sequence 56812, A	188	6	2.0	164	6	US-10-450-763-10837	Sequence 30837, A
116	6	2.0	US-10-450-763-46990	Sequence 46990, A	189	6	2.0	164	6	US-10-489-448-2854	Sequence 2854, Ap
117	6	2.0	US-10-450-763-56868	Sequence 56868, A	190	6	2.0	165	6	US-10-450-763-53865	Sequence 53865, A
118	6	2.0	US-10-450-763-57565	Sequence 57565, A	191	6	2.0	168	7	US-11-031-175-12003	Sequence 12003, A
119	6	2.0	US-10-489-448-2863	Sequence 2863, Ap	192	6	2.0	168	8	US-60-643-717-6603	Sequence 2603, Ap
120	6	2.0	US-10-450-763-56849	Sequence 56849, A	193	6	2.0	168	8	US-60-643-717-6637	Sequence 8637, Ap
121	6	2.0	US-10-450-763-35724	Sequence 35724, A	194	6	2.0	170	6	US-10-450-763-54535	Sequence 54535, A
122	6	2.0	US-10-450-763-46475	Sequence 46475, A	195	6	2.0	175	6	US-60-643-717-10236	Sequence 10236, A
123	6	2.0	PCT-US04-43356-195	Sequence 46475, A	196	6	2.0	177	6	US-10-450-763-39793	Sequence 39793, A
124	6	2.0	PCT-US04-09510-1260	Sequence 195, App	197	6	2.0	177	7	US-11-031-175-13376	Sequence 13376, A
125	6	2.0	US-11-021-949-195	Sequence 1260, Ap	198	6	2.0	180	6	US-10-450-763-16969	Sequence 46969, A
126	6	2.0	PCT-US04-09510-1192	Sequence 1192, App	199	6	2.0	182	6	US-10-450-763-56901	Sequence 56901, A
127	6	2.0	PCT-US04-09510-1210	Sequence 1210, Ap	200	6	2.0	182	6	US-11-031-175-11219	Sequence 11219, A
128	6	2.0	PCT-US04-09510-1257	Sequence 1257, Ap	201	6	2.0	182	7	US-11-031-175-11219	Sequence 11219, A
129	6	2.0	PCT-US04-09510-1259	Sequence 1259, Ap	202	6	2.0	184	6	US-10-450-763-56222	Sequence 56222, A
130	6	2.0	PCT-US04-09510-1262	Sequence 1262, Ap	203	6	2.0	185	6	US-10-450-763-43248	Sequence 43248, A
131	6	2.0	US-10-450-763-56635	Sequence 56635, A	204	6	2.0	185	7	US-11-027-399-5249	Sequence 5249, Ap
132	6	2.0	US-10-489-448-3034	Sequence 3034, Ap	205	6	2.0	185	7	US-11-027-843-5249	Sequence 5249, Ap
133	6	2.0	US-11-031-175-12948	Sequence 12948, A	206	6	2.0	185	7	US-11-027-878-5249	Sequence 5249, Ap
134	6	2.0	US-10-450-763-59788	Sequence 59788, A	207	6	2.0	185	7	US-11-028-169-5249	Sequence 5249, Ap
135	6	2.0	US-10-450-763-45938	Sequence 45938, A	208	6	2.0	185	7	US-11-028-204-5249	Sequence 5249, Ap
136	6	2.0	US-11-031-175-16230	Sequence 16230, A	209	6	2.0	185	7	US-11-027-879-5249	Sequence 5249, Ap
137	6	2.0	US-10-450-763-56850	Sequence 56850, A	210	6	2.0	185	7	US-11-027-819-5249	Sequence 5249, Ap
138	6	2.0	US-10-450-763-56866	Sequence 56866, A	211	6	2.0	185	7	US-11-028-149-5249	Sequence 5249, Ap
139	6	2.0	US-10-489-448-1169	Sequence 1169, Ap	212	6	2.0	185	7	US-11-027-802-5249	Sequence 5249, Ap
140	6	2.0	US-10-450-763-56893	Sequence 56893, A	213	6	2.0	185	7	US-11-027-880-5249	Sequence 5249, Ap
141	6	2.0	US-10-450-763-30915	Sequence 30915, A	214	6	2.0	185	7	US-11-027-892-5249	Sequence 5249, Ap
142	6	2.0	US-10-450-763-33598	Sequence 33598, A	215	6	2.0	185	7	US-11-028-099-5249	Sequence 5249, Ap
143	6	2.0	US-10-450-763-48461	Sequence 48461, A	216	6	2.0	185	7	US-11-028-197-5249	Sequence 5249, Ap
144	6	2.0	US-10-450-763-41631	Sequence 41631, A	217	6	2.0	185	7	US-11-027-884-5249	Sequence 5249, Ap
145	6	2.0	US-10-450-763-31996	Sequence 31996, A	218	6	2.0	185	7	US-11-028-050-5249	Sequence 5249, Ap
146	6	2.0	US-10-450-763-32086	Sequence 32086, A	219	6	2.0	185	7	US-11-028-487-5249	Sequence 5249, Ap
147	6	2.0	US-10-450-763-50726	Sequence 50726, A	220	6	2.0	185	7	US-11-027-891-5249	Sequence 5249, Ap
148	6	2.0	US-10-450-763-47370	Sequence 47370, A	221	6	2.0	185	7	US-11-028-291-5249	Sequence 5249, Ap
149	6	2.0	US-11-031-175-11057	Sequence 11057, A	222	6	2.0	185	7	US-11-028-458-5249	Sequence 5249, Ap
150	6	2.0	US-10-450-763-56670	Sequence 56670, A	223	6	2.0	186	6	US-10-450-763-53866	Sequence 53866, A
151	6	2.0	US-10-450-763-56886	Sequence 56886, A	224	6	2.0	186	6	US-10-450-763-38643	Sequence 38643, A
152	6	2.0	US-10-450-763-56887	Sequence 56887, A	225	6	2.0	189	8	US-60-643-717-9578	Sequence 9578, Ap
153	6	2.0	US-11-031-175-12036	Sequence 12036, A	226	6	2.0	190	8	US-60-643-717-11429	Sequence 11429, A
154	6	2.0	US-10-489-448-3218	Sequence 3218, Ap	227	6	2.0	194	7	US-11-031-175-10363	Sequence 10363, Ap
155	6	2.0	US-10-450-763-49020	Sequence 49020, A	228	6	2.0	194	8	US-60-643-717-6493	Sequence 6493, Ap
156	6	2.0	US-10-450-763-33789	Sequence 33789, A	229	6	2.0	196	8	US-60-643-717-16741	Sequence 16741, A
157	6	2.0	US-10-489-448-1137	Sequence 1137, Ap	230	6	2.0	197	6	US-10-450-763-47420	Sequence 47420, Ap
158	6	2.0	US-10-450-763-48571	Sequence 48571, A	231	6	2.0	197	8	US-60-643-717-7170	Sequence 7170, Ap
159	6	2.0	US-10-450-763-51259	Sequence 51259, A	232	6	2.0	197	8	US-60-643-717-14429	Sequence 14429, A
160	6	2.0	US-10-450-763-46449	Sequence 46449, A	233	6	2.0	198	6	US-10-450-763-52565	Sequence 52565, A
161	6	2.0	US-10-450-763-49216	Sequence 49216, A	234	6	2.0	198	6	US-10-489-448-119	Sequence 1719, Ap
162	6	2.0	US-10-450-763-40374	Sequence 40374, A	235	6	2.0	198	8	US-60-643-717-18072	Sequence 18072, A
163	6	2.0	US-10-489-448-2880	Sequence 2880, Ap	236	6	2.0	199	8	US-60-643-717-6233	Sequence 6233, Ap
164	6	2.0	US-10-450-763-30551	Sequence 30551, A	237	6	2.0	200	8	US-60-643-717-6500	Sequence 6900, Ap
165	6	2.0	US-10-489-448-2810	Sequence 2810, Ap	238	6	2.0	202	7	US-11-031-175-15190	Sequence 10636, A
166	6	2.0	US-11-031-175-14536	Sequence 14536, A	239	6	2.0	202	7	US-60-643-717-930	Sequence 930, App
167	6	2.0	US-10-450-763-56857	Sequence 56857, A	240	6	2.0	203	6	US-10-489-448-2926	Sequence 2926, Ap
168	6	2.0	US-10-450-763-56857	Sequence 56857, A	241	6	2.0	205	6	US-10-450-763-33788	Sequence 33788, A
169	6	2.0	US-11-040-661-40	Sequence 40, Appl	242	6	2.0	205	6	US-60-643-717-4680	Sequence 4680, Ap
170	6	2.0	US-10-450-763-38063	Sequence 38063, A	243	6	2.0	207	6	US-10-450-763-50498	Sequence 50498, A
171	6	2.0			244	6	2.0				

245	6	2.0	207	8	US-60-643-717-14300	Sequence 14300, A	318	6	2.0	242	7	US-11-028-457-4354	Sequence 4354, Ap
246	6	2.0	211	6	US-11-031-175-15438	Sequence 15438, A	319	6	2.0	242	7	US-11-027-891-4354	Sequence 4354, Ap
247	6	2.0	213	7	US-10-450-763-44656	Sequence 44656, A	320	6	2.0	242	7	US-11-028-291-4354	Sequence 4354, Ap
248	6	2.0	215	6	US-10-450-763-56887	Sequence 56887, A	321	6	2.0	242	7	US-11-028-454-4354	Sequence 4354, Ap
249	6	2.0	217	6	US-11-031-175-12063	Sequence 12063, A	322	6	2.0	243	1	PCR-US04-43356-136	Sequence 136, App
250	6	2.0	217	8	US-60-643-717-10078	Sequence 10078, A	323	6	2.0	243	7	US-11-021-944-136	Sequence 136, App
251	6	2.0	217	8	US-60-643-717-17367	Sequence 17367, A	324	6	2.0	243	7	US-11-031-175-16197	Sequence 16197, A
252	6	2.0	218	6	US-10-450-763-58871	Sequence 58871, A	325	6	2.0	244	6	US-10-450-763-60492	Sequence 60492, A
253	6	2.0	218	7	US-11-047-224-10	Sequence 10, Appl	326	6	2.0	246	6	US-10-450-763-31092	Sequence 31092, A
254	6	2.0	223	6	US-10-489-448-3453	Sequence 3453, Ap	327	6	2.0	246	7	US-11-027-399-4242	Sequence 4242, Ap
255	6	2.0	223	7	US-11-031-175-14920	Sequence 14920, A	328	6	2.0	246	7	US-11-027-884-4242	Sequence 4242, Ap
256	6	2.0	224	6	US-10-450-763-48306	Sequence 48306, A	329	6	2.0	246	7	US-11-027-878-4242	Sequence 4242, Ap
257	6	2.0	224	7	US-11-031-175-12540	Sequence 12540, A	330	6	2.0	246	7	US-11-028-169-4242	Sequence 4242, Ap
258	6	2.0	225	7	US-11-031-175-12361	Sequence 12361, A	331	6	2.0	246	7	US-11-028-204-4242	Sequence 4242, Ap
259	6	2.0	225	7	US-11-031-175-12564	Sequence 12564, A	332	6	2.0	246	7	US-11-027-877-4242	Sequence 4242, Ap
260	6	2.0	225	7	US-11-031-175-12564	Sequence 12564, A	333	6	2.0	246	7	US-11-027-877-4242	Sequence 4242, Ap
261	6	2.0	226	6	US-10-450-763-53953	Sequence 53953, A	334	6	2.0	246	7	US-11-027-878-4242	Sequence 4242, Ap
262	6	2.0	226	6	US-10-450-763-58728	Sequence 58728, A	335	6	2.0	246	7	US-11-027-892-4242	Sequence 4242, Ap
263	6	2.0	228	6	US-10-489-448-2889	Sequence 2889, Ap	336	6	2.0	246	7	US-11-027-892-4242	Sequence 4242, Ap
264	6	2.0	229	6	US-10-450-763-35177	Sequence 35177, A	337	6	2.0	246	7	US-11-027-892-4242	Sequence 4242, Ap
265	6	2.0	229	6	US-10-450-763-53966	Sequence 53966, A	338	6	2.0	246	7	US-11-027-892-4242	Sequence 4242, Ap
266	6	2.0	230	6	US-10-450-763-41579	Sequence 41579, A	339	6	2.0	246	7	US-11-028-099-4242	Sequence 4242, Ap
267	6	2.0	230	6	US-10-450-763-54448	Sequence 54448, A	340	6	2.0	246	7	US-11-028-197-4242	Sequence 4242, Ap
268	6	2.0	231	6	US-10-450-763-35550	Sequence 35550, A	341	6	2.0	246	7	US-11-027-884-4242	Sequence 4242, Ap
269	6	2.0	233	7	US-11-031-175-11845	Sequence 11845, A	342	6	2.0	246	7	US-11-028-050-4242	Sequence 4242, Ap
270	6	2.0	233	7	US-11-031-175-16165	Sequence 16165, A	343	6	2.0	246	7	US-11-028-457-4242	Sequence 4242, Ap
271	6	2.0	233	8	US-60-643-717-4918	Sequence 4918, Ap	344	6	2.0	246	7	US-11-027-891-4242	Sequence 4242, Ap
272	6	2.0	234	7	US-11-031-175-14877	Sequence 14877, A	345	6	2.0	246	7	US-11-028-291-4242	Sequence 4242, Ap
273	6	2.0	234	8	US-60-643-717-2865	Sequence 2865, Ap	346	6	2.0	247	1	PCR-US04-42360-679	Sequence 679, App
274	6	2.0	234	8	US-60-643-717-2946	Sequence 2946, Ap	347	6	2.0	247	1	US-11-031-175-10732	Sequence 10732, A
275	6	2.0	234	8	US-60-643-717-3555	Sequence 3555, Ap	348	6	2.0	248	6	US-10-450-763-38064	Sequence 38064, A
276	6	2.0	235	6	US-10-489-448-1001	Sequence 1001, Ap	349	6	2.0	248	7	US-11-031-175-13538	Sequence 13538, A
277	6	2.0	236	6	US-10-450-763-53622	Sequence 53622, A	350	6	2.0	248	7	US-11-031-175-16714	Sequence 16714, A
278	6	2.0	236	6	US-10-450-763-57806	Sequence 57806, A	351	6	2.0	251	8	US-60-643-717-4830	Sequence 4830, Ap
279	6	2.0	236	6	US-11-031-175-10625	Sequence 10625, A	352	6	2.0	251	8	US-60-643-717-12695	Sequence 12695, A
280	6	2.0	239	1	PCR-US04-17965-842	Sequence 842, App	353	6	2.0	254	6	US-10-450-763-37316	Sequence 37316, A
281	6	2.0	239	6	US-10-450-763-54491	Sequence 54491, A	354	6	2.0	254	6	US-10-450-763-55437	Sequence 55437, A
282	6	2.0	240	7	US-11-027-399-2970	Sequence 2970, Ap	355	6	2.0	255	1	PCR-US04-17965-9016	Sequence 2016, Ap
283	6	2.0	240	7	US-11-027-843-2970	Sequence 2970, Ap	356	6	2.0	258	6	US-10-717-666A-59	Sequence 59, Appl
284	6	2.0	240	7	US-11-027-878-2970	Sequence 2970, Ap	357	6	2.0	259	6	US-10-450-763-38102	Sequence 38102, A
285	6	2.0	240	7	US-11-028-169-2970	Sequence 2970, Ap	358	6	2.0	259	7	US-11-031-175-12875	Sequence 12875, A
286	6	2.0	240	7	US-11-028-204-2970	Sequence 2970, Ap	359	6	2.0	262	8	US-60-643-717-13969	Sequence 13969, A
287	6	2.0	240	7	US-11-027-877-2970	Sequence 2970, Ap	360	6	2.0	263	6	US-10-450-763-34078	Sequence 34078, A
288	6	2.0	240	7	US-11-027-879-2970	Sequence 2970, Ap	361	6	2.0	263	7	US-11-031-175-15616	Sequence 15616, A
289	6	2.0	240	7	US-11-028-149-2970	Sequence 2970, Ap	362	6	2.0	264	7	US-11-027-399-3617	Sequence 3617, Ap
290	6	2.0	240	7	US-11-027-802-2970	Sequence 2970, Ap	363	6	2.0	264	7	US-11-027-843-3617	Sequence 3617, Ap
291	6	2.0	240	7	US-11-027-890-2970	Sequence 2970, Ap	364	6	2.0	264	7	US-11-027-878-3617	Sequence 3617, Ap
292	6	2.0	240	7	US-11-027-892-2970	Sequence 2970, Ap	365	6	2.0	264	7	US-11-028-169-3617	Sequence 3617, Ap
293	6	2.0	240	7	US-11-028-099-2970	Sequence 2970, Ap	366	6	2.0	264	7	US-11-028-204-3617	Sequence 3617, Ap
294	6	2.0	240	7	US-11-028-197-2970	Sequence 2970, Ap	367	6	2.0	264	7	US-11-027-887-3617	Sequence 3617, Ap
295	6	2.0	240	7	US-11-027-844-2970	Sequence 2970, Ap	368	6	2.0	264	7	US-11-027-879-3617	Sequence 3617, Ap
296	6	2.0	240	7	US-11-028-050-2970	Sequence 2970, Ap	369	6	2.0	264	7	US-11-028-149-3617	Sequence 3617, Ap
297	6	2.0	240	7	US-11-028-457-2970	Sequence 2970, Ap	370	6	2.0	264	7	US-11-027-880-3617	Sequence 3617, Ap
298	6	2.0	240	7	US-11-027-891-2970	Sequence 2970, Ap	371	6	2.0	264	7	US-11-027-892-3617	Sequence 3617, Ap
299	6	2.0	240	7	US-11-028-291-2970	Sequence 2970, Ap	372	6	2.0	264	7	US-11-027-899-3617	Sequence 3617, Ap
300	6	2.0	240	7	US-11-028-458-2970	Sequence 2970, Ap	373	6	2.0	264	7	US-11-028-099-3617	Sequence 3617, Ap
301	6	2.0	242	8	US-60-643-717-17851	Sequence 17851, A	374	6	2.0	264	7	US-11-028-197-3617	Sequence 3617, Ap
302	6	2.0	242	6	US-10-489-448-3475	Sequence 3475, Ap	375	6	2.0	264	7	US-11-027-884-3617	Sequence 3617, Ap
303	6	2.0	242	7	US-11-027-399-4354	Sequence 4354, Ap	376	6	2.0	264	7	US-11-027-884-3617	Sequence 3617, Ap
304	6	2.0	242	7	US-11-027-843-4354	Sequence 4354, Ap	377	6	2.0	264	7	US-11-028-050-3617	Sequence 3617, Ap
305	6	2.0	242	7	US-11-027-878-4354	Sequence 4354, Ap	378	6	2.0	264	7	US-11-027-881-3617	Sequence 3617, Ap
306	6	2.0	242	7	US-11-028-169-4354	Sequence 4354, Ap	379	6	2.0	264	7	US-11-027-891-3617	Sequence 3617, Ap
307	6	2.0	242	7	US-11-028-204-4354	Sequence 4354, Ap	380	6	2.0	264	7	US-11-028-291-3617	Sequence 3617, Ap
308	6	2.0	242	7	US-11-027-877-4354	Sequence 4354, Ap	381	6	2.0	264	7	US-11-028-459-3617	Sequence 3617, Ap
309	6	2.0	242	7	US-11-027-879-4354	Sequence 4354, Ap	382	6	2.0	267	8	US-60-643-717-6282	Sequence 6282, Ap
310	6	2.0	242	7	US-11-028-149-4354	Sequence 4354, Ap	383	6	2.0	269	7	US-11-031-175-12511	Sequence 12511, A
311	6	2.0	242	7	US-11-027-802-4354	Sequence 4354, Ap	384	6	2.0	270	6	US-10-450-763-38644	Sequence 38644, A
312	6	2.0	242	7	US-11-027-890-4354	Sequence 4354, Ap	385	6	2.0	270	6	US-10-450-763-54320	Sequence 54320, A
313	6	2.0	242	7	US-11-027-892-4354	Sequence 4354, Ap	386	6	2.0	270	7	US-10-489-448-3256	Sequence 3256, Ap
314	6	2.0	242	7	US-11-028-099-4354	Sequence 4354, Ap	387	6	2.0	272	6	US-11-031-175-13063	Sequence 13063, A
315	6	2.0	242	7	US-11-028-197-4354	Sequence 4354, Ap	388	6	2.0	272	7	US-10-489-448-1331	Sequence 1431, Ap
316	6	2.0	242	7	US-11-027-844-4354	Sequence 4354, Ap	389	6	2.0	274	6	US-11-031-175-15379	Sequence 15379, A
317	6	2.0	242	7	US-11-028-050-4354	Sequence 4354, Ap	390	6	2.0	275	1	PCR-US04-17965-847	Sequence 847, App

391	2.0	275	8	US-60-643-717-12609	Sequence 12609, A	464	2.0	304	1	PCT-US04-42360-448	Sequence 448, App
392	2.0	277	6	US-10-450-763-37953	Sequence 37953, A	465	2.0	304	7	US-11-031-175-14957	Sequence 14957, A
393	2.0	277	6	US-10-450-763-42217	Sequence 42217, A	466	2.0	305	6	US-10-450-763-44200	Sequence 34200, A
394	2.0	278	6	US-10-450-763-51810	Sequence 51810, A	467	2.0	305	6	US-10-450-763-40783	Sequence 40783, A
395	2.0	278	7	US-11-031-175-10783	Sequence 10783, A	468	2.0	305	6	US-10-450-763-57400	Sequence 57400, A
396	2.0	278	7	US-11-031-175-12602	Sequence 12602, A	469	2.0	307	6	US-10-450-763-55114	Sequence 55114, A
397	2.0	279	6	US-10-450-763-47976	Sequence 47976, A	470	2.0	307	8	US-60-643-717-2813	Sequence 2813, Ap
398	2.0	280	6	US-10-450-763-38441	Sequence 38441, A	471	2.0	308	7	US-11-031-175-15489	Sequence 15489, A
399	2.0	280	7	US-11-031-175-11498	Sequence 11498, A	472	2.0	309	8	US-60-643-717-15347	Sequence 15347, A
400	2.0	282	6	US-10-450-763-46262	Sequence 46262, A	473	2.0	310	7	US-10-489-448-1665	Sequence 1665, Ap
401	2.0	283	7	US-11-027-399-3190	Sequence 3190, Ap	474	2.0	310	7	US-11-031-175-15686	Sequence 15686, A
402	2.0	283	7	US-11-027-883-3190	Sequence 3190, Ap	475	2.0	313	7	US-11-023-805-4	Sequence 4, App11
403	2.0	283	7	US-11-027-878-3190	Sequence 3190, Ap	476	2.0	315	7	US-11-031-175-12484	Sequence 12484, A
404	2.0	283	7	US-11-028-169-3190	Sequence 3190, Ap	477	2.0	317	7	US-11-031-175-10998	Sequence 10988, A
405	2.0	283	7	US-11-028-204-3190	Sequence 3190, Ap	478	2.0	319	8	US-60-643-717-16444	Sequence 16444, A
406	2.0	283	7	US-11-027-877-3190	Sequence 3190, Ap	479	2.0	320	7	US-11-031-175-12125	Sequence 12125, A
407	2.0	283	7	US-11-027-879-3190	Sequence 3190, Ap	480	2.0	322	7	US-11-031-175-12207	Sequence 12207, A
408	2.0	283	7	US-11-028-149-3190	Sequence 3190, Ap	481	2.0	323	1	PCT-US04-30360-7	Sequence 7, App11
409	2.0	283	7	US-11-027-880-3190	Sequence 3190, Ap	482	2.0	328	6	US-10-450-763-40679	Sequence 40679, A
410	2.0	283	7	US-11-027-889-3190	Sequence 3190, Ap	483	2.0	328	6	US-10-450-763-55900	Sequence 55900, A
411	2.0	283	7	US-11-027-892-3190	Sequence 3190, Ap	484	2.0	328	6	US-10-489-448-1150	Sequence 1150, Ap
412	2.0	283	7	US-11-028-099-3190	Sequence 3190, Ap	485	2.0	330	1	PCT-US04-42360-2094	Sequence 2094, Ap
413	2.0	283	7	US-11-028-197-3190	Sequence 3190, Ap	486	2.0	332	6	US-10-450-763-33797	Sequence 33797, A
414	2.0	283	7	US-11-027-884-3190	Sequence 3190, Ap	487	2.0	332	6	US-10-450-763-37114	Sequence 37114, A
415	2.0	283	7	US-11-028-050-3190	Sequence 3190, Ap	488	2.0	332	6	US-60-643-717-17357	Sequence 17357, A
416	2.0	283	7	US-11-028-457-3190	Sequence 3190, Ap	489	2.0	333	6	US-10-450-763-50659	Sequence 50659, A
417	2.0	283	7	US-11-028-891-3190	Sequence 3190, Ap	490	2.0	333	7	US-11-031-175-10638	Sequence 10638, A
418	2.0	283	7	US-11-028-291-3190	Sequence 3190, Ap	491	2.0	333	7	US-11-047-224-8	Sequence 8, App11
419	2.0	283	7	US-11-031-175-14951	Sequence 14951, A	492	2.0	335	7	US-11-031-175-15208	Sequence 15208, A
420	2.0	283	7	US-11-028-458-3190	Sequence 3190, Ap	493	2.0	336	8	US-60-643-717-12181	Sequence 12181, A
421	2.0	284	6	US-10-450-763-57707	Sequence 57707, A	494	2.0	338	6	US-10-450-763-55341	Sequence 55341, A
422	2.0	287	6	US-10-450-763-55316	Sequence 55316, A	495	2.0	338	7	US-11-021-825-135	Sequence 13, App
423	2.0	288	6	US-11-031-175-10097	Sequence 10097, A	496	2.0	340	7	US-11-031-175-10905	Sequence 10905, A
424	2.0	289	6	US-10-450-763-41030	Sequence 41030, A	497	2.0	347	8	US-11-031-175-12586	Sequence 12586, A
425	2.0	289	8	US-60-643-717-6903	Sequence 6903, Ap	498	2.0	347	8	US-11-032-490-844	Sequence 44, App1
426	2.0	289	8	US-60-643-717-15213	Sequence 15213, A	499	2.0	345	7	US-11-032-643-84	Sequence 18557, A
427	2.0	290	6	US-10-450-763-46646	Sequence 46646, A	500	2.0	345	7	US-11-031-175-11383	Sequence 11383, A
428	2.0	291	6	US-10-450-763-57633	Sequence 57633, A	501	2.0	347	8	US-60-643-717-18557	Sequence 1716, Ap
429	2.0	292	7	US-11-027-399-4530	Sequence 4530, Ap	502	2.0	348	7	US-11-031-175-11715	Sequence 2027, Ap
430	2.0	292	7	US-11-027-843-4530	Sequence 4530, Ap	504	2.0	348	8	US-60-643-717-2027	Sequence 3417, Ap
431	2.0	292	7	US-11-027-878-4530	Sequence 4530, Ap	505	2.0	348	8	US-60-643-717-3417	Sequence 4094, Ap
432	2.0	292	7	US-11-028-169-4530	Sequence 4530, Ap	506	2.0	348	8	US-60-643-717-4094	Sequence 4679, Ap
433	2.0	292	7	US-11-028-204-4530	Sequence 4530, Ap	507	2.0	348	8	US-60-643-717-4679	Sequence 4927, Ap
434	2.0	292	7	US-11-027-877-4530	Sequence 4530, Ap	508	2.0	348	8	US-60-643-717-4927	Sequence 5923, Ap
435	2.0	292	7	US-11-027-879-4530	Sequence 4530, Ap	509	2.0	348	8	US-60-643-717-5923	Sequence 5928, Ap
436	2.0	292	7	US-11-028-149-4530	Sequence 4530, Ap	510	2.0	348	8	US-60-643-717-5928	Sequence 6593, Ap
437	2.0	292	7	US-11-028-149-4530	Sequence 4530, Ap	511	2.0	348	8	US-60-643-717-5928	Sequence 6598, Ap
438	2.0	292	7	US-11-027-802-4530	Sequence 4530, Ap	512	2.0	348	8	US-60-643-717-6598	Sequence 10962, A
439	2.0	292	7	US-11-027-890-4530	Sequence 4530, Ap	513	2.0	348	8	US-60-643-717-10962	Sequence 12834, A
440	2.0	292	7	US-11-027-892-4530	Sequence 4530, Ap	514	2.0	348	8	US-60-643-717-15834	Sequence 3385, Ap
441	2.0	292	7	US-11-028-099-4530	Sequence 4530, Ap	515	2.0	352	7	US-11-031-175-12834	Sequence 15411, A
442	2.0	292	7	US-11-028-197-4530	Sequence 4530, Ap	516	2.0	352	8	US-60-643-717-5385	Sequence 34005, A
443	2.0	292	7	US-11-027-844-4530	Sequence 4530, Ap	517	2.0	354	7	US-11-031-175-15411	Sequence 16622, A
444	2.0	292	7	US-11-028-050-4530	Sequence 4530, Ap	518	2.0	356	6	US-10-450-763-34005	Sequence 14419, A
445	2.0	292	7	US-11-028-457-4530	Sequence 4530, Ap	519	2.0	359	8	US-60-643-717-14419	Sequence 7014, Ap
446	2.0	292	7	US-11-027-891-4530	Sequence 4530, Ap	520	2.0	361	8	US-60-643-717-7014	Sequence 40366, A
447	2.0	292	7	US-11-028-291-4530	Sequence 4530, Ap	521	2.0	364	6	US-10-450-763-40366	Sequence 14265, A
448	2.0	292	7	US-11-031-175-13893	Sequence 13893, A	522	2.0	364	6	US-11-031-175-1265	Sequence 43483, A
449	2.0	292	7	US-11-028-458-4530	Sequence 4530, Ap	523	2.0	364	7	US-10-450-763-41483	Sequence 12925, A
450	2.0	294	8	US-60-643-717-3105	Sequence 3105, Ap	524	2.0	368	6	US-11-031-175-15682	Sequence 15682, A
451	2.0	294	8	US-60-643-717-6614	Sequence 6614, Ap	525	2.0	368	7	US-11-031-175-12925	Sequence 3568, Ap
452	2.0	294	8	US-60-643-717-15418	Sequence 15418, A	526	2.0	368	7	US-11-047-224-2	Sequence 15048, A
453	2.0	295	8	US-60-643-717-13568	Sequence 13568, Ap	527	2.0	368	8	US-60-643-717-13568	Sequence 15048, A
454	2.0	297	6	US-10-450-763-59513	Sequence 59513, A	528	2.0	368	8	US-60-643-717-15048	Sequence 850, App
455	2.0	297	8	US-60-643-717-14416	Sequence 14416, A	529	2.0	369	1	PCT-US04-42360-850	Sequence 9407, App
456	2.0	299	8	US-60-643-717-13515	Sequence 13515, A	530	2.0	370	1	PCT-US04-30360-101	Sequence 101, App
457	2.0	300	8	US-60-643-717-660	Sequence 660, App1	531	2.0	371	8	US-60-643-717-5901	Sequence 5901, Ap
458	2.0	300	6	PCT-US05-00638-87	Sequence 87, App1	532	2.0	371	8	US-60-643-717-11272	Sequence 11272, A
459	2.0	300	6	US-10-450-763-54319	Sequence 54319, A	533	2.0	373	6	US-10-450-763-46345	Sequence 46345, A
460	2.0	301	8	US-60-643-717-3038	Sequence 3038, Ap	534	2.0	373	6	US-60-643-717-6576	Sequence 6576, Ap
461	2.0	301	8	US-60-643-717-5654	Sequence 5654, Ap	535	2.0	373	8	US-60-643-717-7902	Sequence 7902, Ap
462	2.0	301	8	US-60-643-717-7902	Sequence 7902, Ap	536	2.0	373	8	US-60-643-717-17538	Sequence 17538, A
463	2.0	302	8	US-60-643-717-13840	Sequence 13840, A						

537	6	2.0	374	6	US-10-489-448-2999	Sequence 2999, Ap	610	6	2.0	426	7	US-11-031-175-10978	Sequence 10978, A
538	6	2.0	374	8	US-60-643-717-5932	Sequence 5932, Ap	611	6	2.0	429	8	US-60-643-717-5189	Sequence 5189, Ap
539	6	2.0	374	8	US-60-643-717-9485	Sequence 9485, Ap	612	6	2.0	434	6	US-10-450-763-32277	Sequence 32277, A
540	6	2.0	375	7	US-11-031-175-14394	Sequence 14394, A	613	6	2.0	434	7	US-11-031-175-10598	Sequence 10598, A
541	6	2.0	375	8	US-60-643-717-1707	Sequence 1707, Ap	614	6	2.0	434	8	US-11-031-175-10908	Sequence 10908, A
542	6	2.0	375	8	US-60-643-717-2794	Sequence 2794, Ap	615	6	2.0	437	7	US-60-643-717-19680	Sequence 19680, Ap
543	6	2.0	375	8	US-60-643-717-5930	Sequence 5930, Ap	616	6	2.0	437	8	US-60-643-717-14362	Sequence 14362, A
544	6	2.0	375	8	US-60-643-717-6601	Sequence 6601, Ap	617	6	2.0	442	8	US-60-643-717-6458	Sequence 6458, Ap
545	6	2.0	375	8	US-60-643-717-9511	Sequence 9511, Ap	618	6	2.0	446	7	US-11-031-175-13540	Sequence 13540, A
546	6	2.0	375	8	US-60-643-717-16384	Sequence 16384, A	619	6	2.0	447	7	US-11-031-175-14760	Sequence 14760, A
547	6	2.0	376	6	US-10-450-763-41149	Sequence 41149, A	620	6	2.0	448	8	US-60-643-717-14877	Sequence 14877, Ap
548	6	2.0	377	7	US-11-031-175-13599	Sequence 13599, A	621	6	2.0	449	6	US-10-450-763-31298	Sequence 31298, A
549	6	2.0	377	8	US-60-643-717-6577	Sequence 6577, Ap	622	6	2.0	452	7	US-11-031-175-9902	Sequence 9902, Ap
550	6	2.0	378	6	US-10-450-763-50320	Sequence 50320, A	623	6	2.0	452	8	US-60-643-717-6026	Sequence 6026, Ap
551	6	2.0	378	6	US-10-450-763-37352	Sequence 37352, Ap	624	6	2.0	453	6	US-10-450-763-45646	Sequence 45646, A
552	6	2.0	380	6	US-10-450-763-44602	Sequence 44602, A	625	6	2.0	453	6	US-10-450-763-47618	Sequence 47618, A
553	6	2.0	380	6	US-60-643-717-1824	Sequence 1824, Ap	626	6	2.0	453	6	US-10-450-763-58586	Sequence 58586, Ap
554	6	2.0	381	1	PCT-US03-35712-117	Sequence 117, App	627	6	2.0	455	8	US-60-643-717-2044	Sequence 2044, Ap
555	6	2.0	381	1	PCT-US04-42360-1613	Sequence 1613, Ap	628	6	2.0	455	6	US-10-489-448-1403	Sequence 1403, Ap
556	6	2.0	381	6	US-60-643-717-410	Sequence 410, App	629	6	2.0	455	6	US-10-489-448-1427	Sequence 1427, Ap
557	6	2.0	382	6	US-10-450-763-36402	Sequence 36402, A	630	6	2.0	455	7	US-11-027-897-3305	Sequence 3305, Ap
558	6	2.0	384	8	US-60-643-717-6210	Sequence 6210, Ap	631	6	2.0	455	7	US-11-027-843-3305	Sequence 3305, Ap
559	6	2.0	384	8	US-60-643-717-18207	Sequence 18207, A	632	6	2.0	455	7	US-11-027-878-3305	Sequence 3305, Ap
560	6	2.0	385	6	US-10-450-763-52155	Sequence 52155, A	633	6	2.0	455	7	US-11-028-169-3305	Sequence 3305, Ap
561	6	2.0	385	6	US-10-489-448-3232	Sequence 3232, Ap	634	6	2.0	455	7	US-11-028-204-3305	Sequence 3305, Ap
562	6	2.0	385	6	US-10-489-448-3233	Sequence 3233, Ap	635	6	2.0	455	7	US-11-027-879-3305	Sequence 3305, Ap
563	6	2.0	385	7	US-11-031-175-10094	Sequence 10094, A	636	6	2.0	455	7	US-11-027-879-3305	Sequence 3305, Ap
564	6	2.0	386	7	US-11-031-175-13651	Sequence 13651, A	637	6	2.0	455	7	US-11-028-149-3305	Sequence 3305, Ap
565	6	2.0	392	6	US-10-450-763-36946	Sequence 36946, A	638	6	2.0	455	7	US-11-027-802-3305	Sequence 3305, Ap
566	6	2.0	392	7	US-11-031-175-13511	Sequence 13511, A	639	6	2.0	455	7	US-11-027-899-3305	Sequence 3305, Ap
567	6	2.0	392	8	US-60-643-717-14734	Sequence 14734, A	640	6	2.0	455	7	US-11-027-899-3305	Sequence 3305, Ap
568	6	2.0	393	8	US-60-643-717-8850	Sequence 8850, Ap	641	6	2.0	455	7	US-11-028-099-3305	Sequence 3305, Ap
569	6	2.0	393	8	US-60-643-717-11131	Sequence 11131, A	642	6	2.0	455	7	US-11-028-197-3305	Sequence 3305, Ap
570	6	2.0	394	7	US-11-031-175-15751	Sequence 15751, A	643	6	2.0	455	7	US-11-027-854-3305	Sequence 3305, Ap
571	6	2.0	395	6	US-10-450-763-45735	Sequence 45735, A	644	6	2.0	455	7	US-11-028-050-3305	Sequence 3305, Ap
572	6	2.0	395	6	US-10-450-763-54072	Sequence 54072, A	645	6	2.0	455	7	US-11-027-897-3305	Sequence 3305, Ap
573	6	2.0	398	6	US-10-489-448-1694	Sequence 1694, Ap	646	6	2.0	455	7	US-11-028-891-3305	Sequence 3305, Ap
574	6	2.0	398	8	US-60-643-717-14646	Sequence 14646, Ap	647	6	2.0	455	7	US-11-028-291-3305	Sequence 3305, Ap
575	6	2.0	399	6	US-10-450-763-48134	Sequence 48134, A	648	6	2.0	455	7	US-11-028-458-3305	Sequence 3305, Ap
576	6	2.0	399	6	US-60-643-717-5245	Sequence 5245, Ap	649	6	2.0	458	6	US-10-450-763-40210	Sequence 40210, A
577	6	2.0	401	6	US-10-450-763-43518	Sequence 43518, A	650	6	2.0	459	1	PCT-US04-42360-50	Sequence 50, Appl
578	6	2.0	401	6	US-10-450-763-559473	Sequence 559473, A	651	6	2.0	460	7	US-11-031-175-15589	Sequence 15589, A
579	6	2.0	402	6	US-10-450-763-51116	Sequence 51116, A	652	6	2.0	461	8	US-60-643-717-12512	Sequence 12512, A
580	6	2.0	402	6	US-10-450-763-57402	Sequence 57402, A	653	6	2.0	462	7	US-11-031-175-16075	Sequence 16075, A
581	6	2.0	403	6	US-10-450-763-59076	Sequence 59076, A	654	6	2.0	463	6	US-10-450-763-57381	Sequence 57381, A
582	6	2.0	403	6	US-10-450-763-59076	Sequence 59076, A	655	6	2.0	464	6	US-10-450-763-52882	Sequence 52882, A
583	6	2.0	405	8	US-11-031-175-15722	Sequence 15722, A	656	6	2.0	464	6	US-60-643-717-6546	Sequence 6546, Ap
584	6	2.0	405	8	US-60-643-717-838	Sequence 838, App	657	6	2.0	465	8	US-60-643-717-6546	Sequence 6546, Ap
585	6	2.0	406	7	US-11-031-175-11121	Sequence 11121, A	658	6	2.0	466	8	US-60-643-717-15786	Sequence 15786, A
586	6	2.0	408	8	US-60-643-717-9181	Sequence 9181, Ap	659	6	2.0	466	8	US-60-643-717-18782	Sequence 18782, A
587	6	2.0	410	6	US-10-450-763-47658	Sequence 47658, A	660	6	2.0	466	8	PCT-US04-17965-2191	Sequence 2191, Ap
588	6	2.0	411	6	US-10-450-763-38787	Sequence 38787, A	661	6	2.0	470	1	US-10-450-763-49220	Sequence 49220, A
589	6	2.0	411	8	US-60-643-717-11943	Sequence 11943, A	662	6	2.0	471	6	US-11-031-175-11254	Sequence 11254, A
590	6	2.0	412	1	PCT-US04-42360-350	Sequence 350, App	663	6	2.0	472	6	US-11-027-399-3355	Sequence 3355, Ap
591	6	2.0	412	1	PCT-US04-42360-430	Sequence 430, App	664	6	2.0	472	6	US-10-450-763-33946	Sequence 33946, A
592	6	2.0	412	7	US-11-031-175-9713	Sequence 9713, Ap	665	6	2.0	472	6	US-10-450-763-56894	Sequence 56894, A
593	6	2.0	412	8	US-60-643-717-7960	Sequence 7960, Ap	666	6	2.0	473	6	US-10-450-763-35119	Sequence 35119, A
594	6	2.0	412	8	US-60-643-717-12491	Sequence 12491, A	667	6	2.0	473	6	US-60-643-717-706	Sequence 706, App
595	6	2.0	413	8	US-11-031-175-16100	Sequence 16100, A	668	6	2.0	476	7	US-11-028-11296	Sequence 11296, A
596	6	2.0	413	8	US-60-643-717-18360	Sequence 18360, A	669	6	2.0	476	8	US-60-643-717-1254	Sequence 1254, A
597	6	2.0	414	8	US-60-643-717-10629	Sequence 10629, A	670	6	2.0	477	7	US-11-027-879-3355	Sequence 3355, Ap
598	6	2.0	414	8	US-60-643-717-10629	Sequence 10629, A	671	6	2.0	477	7	US-11-027-884-3355	Sequence 3355, Ap
599	6	2.0	415	8	US-60-643-717-14045	Sequence 14045, A	672	6	2.0	477	7	US-11-027-897-3355	Sequence 3355, Ap
600	6	2.0	417	8	US-60-643-717-3162	Sequence 3162, Ap	673	6	2.0	477	7	US-11-027-897-3355	Sequence 3355, Ap
601	6	2.0	418	6	US-10-450-763-35046	Sequence 35046, A	674	6	2.0	477	7	US-11-028-169-3355	Sequence 3355, Ap
602	6	2.0	418	6	US-10-450-763-58869	Sequence 58869, A	675	6	2.0	477	7	US-11-027-879-3355	Sequence 3355, Ap
603	6	2.0	419	6	US-10-450-763-34474	Sequence 34474, A	676	6	2.0	477	7	US-11-027-879-3355	Sequence 3355, Ap
604	6	2.0	420	7	US-11-045-577-4	Sequence 4, Appl	677	6	2.0	477	7	US-11-028-149-3355	Sequence 3355, Ap
605	6	2.0	421	7	US-11-031-175-10569	Sequence 10569, A	678	6	2.0	477	7	US-11-027-899-3355	Sequence 3355, Ap
606	6	2.0	422	7	US-11-031-175-15849	Sequence 15849, A	679	6	2.0	477	7	US-11-027-899-3355	Sequence 3355, Ap
607	6	2.0	423	7	US-11-031-175-10934	Sequence 10934, A	680	6	2.0	477	7	US-11-027-899-3355	Sequence 3355, Ap
608	6	2.0	423	8	US-60-643-717-1518	Sequence 1518, Ap	681	6	2.0	477	7	US-11-028-099-3355	Sequence 3355, Ap
609	6	2.0	424	6	US-10-450-763-44494	Sequence 44494, A	682	6	2.0	477	7	US-11-028-197-3355	Sequence 3355, Ap



683	6	2.0	477	7	US-11-027-844-3555	Sequence 3555, Ap	756	6	2.0	539	8	US-60-643-717-575	Sequence 575, App
684	6	2.0	477	7	US-11-028-050-3555	Sequence 3555, Ap	757	6	2.0	542	8	US-60-643-717-3348	Sequence 3348, App
685	6	2.0	477	7	US-11-028-457-3555	Sequence 3555, Ap	758	6	2.0	543	1	PCT-US04-42360-347	Sequence 347, App
686	6	2.0	477	7	US-11-027-891-3555	Sequence 3555, Ap	759	6	2.0	543	1	PCT-US04-42360-2234	Sequence 2234, Ap
687	6	2.0	477	7	US-11-028-291-3555	Sequence 3555, Ap	760	6	2.0	543	6	US-10-875-518-1	Sequence 1, Appl1
688	6	2.0	477	7	US-11-031-175-15889	Sequence 15889, A	761	6	2.0	545	7	US-11-031-175-10533	Sequence 10533, A
689	6	2.0	477	7	US-11-028-458-3555	Sequence 3555, Ap	762	6	2.0	546	6	US-10-450-763-31111	Sequence 31111, A
690	6	2.0	478	6	US-10-450-763-30458	Sequence 30458, A	763	6	2.0	546	6	US-10-450-763-45232	Sequence 45232, A
691	6	2.0	478	6	US-10-450-763-30642	Sequence 30642, A	764	6	2.0	547	6	US-10-450-763-49217	Sequence 49217, A
692	6	2.0	478	6	US-11-031-175-11460	Sequence 11460, A	765	6	2.0	549	7	US-11-031-175-14387	Sequence 14387, A
693	6	2.0	478	6	US-60-643-717-5125	Sequence 5125, Ap	766	6	2.0	550	8	US-60-643-717-7000	Sequence 7000, Ap
694	6	2.0	482	7	US-11-031-175-16249	Sequence 16249, A	767	6	2.0	550	8	US-60-643-717-13768	Sequence 13768, Ap
695	6	2.0	483	6	US-10-450-763-52889	Sequence 52889, A	768	6	2.0	551	8	US-60-643-717-4563	Sequence 4563, Ap
696	6	2.0	485	6	US-10-450-763-49301	Sequence 49301, A	769	6	2.0	551	8	US-60-643-717-11068	Sequence 11068, A
697	6	2.0	485	8	US-60-643-717-8873	Sequence 8873, Ap	770	6	2.0	552	8	US-60-643-717-6008	Sequence 6008, Ap
698	6	2.0	486	1	PCT-US04-17965-1240	Sequence 1240, Ap	771	6	2.0	552	8	US-60-643-717-9253	Sequence 9253, Ap
699	6	2.0	486	6	US-10-450-763-36846	Sequence 36846, A	772	6	2.0	553	8	US-60-643-717-1772	Sequence 1772, Ap
700	6	2.0	486	6	US-10-450-763-52359	Sequence 52359, A	773	6	2.0	554	7	US-11-031-175-14972	Sequence 14972, Ap
701	6	2.0	488	6	US-10-450-763-58314	Sequence 58314, A	774	6	2.0	555	6	US-10-450-763-46906	Sequence 46906, A
702	6	2.0	489	8	US-60-643-717-14771	Sequence 14771, A	775	6	2.0	556	6	US-10-489-448-1453	Sequence 1453, Ap
703	6	2.0	490	7	US-11-031-175-16820	Sequence 16820, A	776	6	2.0	556	6	US-60-643-717-12725	Sequence 12725, A
704	6	2.0	490	8	US-60-643-717-1544	Sequence 1544, Ap	777	6	2.0	557	6	US-10-450-763-18664	Sequence 18664, A
705	6	2.0	491	7	US-11-031-175-15945	Sequence 15945, A	778	6	2.0	557	6	US-10-450-763-38551	Sequence 38551, A
706	6	2.0	493	6	US-10-450-763-51308	Sequence 51308, A	779	6	2.0	561	6	US-10-450-763-33378	Sequence 33378, A
707	6	2.0	494	6	US-11-031-175-11926	Sequence 11926, A	780	6	2.0	561	6	US-60-643-717-558	Sequence 558, App
708	6	2.0	495	8	US-60-643-717-16551	Sequence 16551, A	781	6	2.0	562	8	US-60-643-717-15103	Sequence 15103, A
709	6	2.0	500	8	US-60-643-717-15208	Sequence 15208, A	782	6	2.0	562	8	US-60-643-717-12802	Sequence 12802, A
710	6	2.0	500	8	US-60-643-717-15208	Sequence 15208, A	783	6	2.0	562	8	US-60-643-717-15117	Sequence 15117, A
711	6	2.0	501	8	US-60-643-717-17863	Sequence 17863, A	784	6	2.0	563	6	US-10-450-763-51307	Sequence 51307, A
712	6	2.0	501	1	PCT-US04-42360-328	Sequence 328, App	785	6	2.0	563	6	US-10-450-763-15113	Sequence 15113, A
713	6	2.0	503	1	PCT-US04-06979-599	Sequence 599, App	786	6	2.0	564	7	US-11-047-224-6	Sequence 6, Appl1
714	6	2.0	503	1	PCT-US04-06979-599	Sequence 599, App	787	6	2.0	567	7	US-11-031-175-11767	Sequence 11767, A
715	6	2.0	504	1	PCT-US04-42360-4263	Sequence 326, App	788	6	2.0	567	8	US-60-643-717-15245	Sequence 15245, A
716	6	2.0	504	6	US-10-450-763-45233	Sequence 45233, A	789	6	2.0	567	8	US-60-643-717-3138	Sequence 3138, Ap
717	6	2.0	506	6	US-60-643-717-4816	Sequence 4816, Ap	790	6	2.0	567	8	US-60-643-717-6863	Sequence 6863, Ap
718	6	2.0	507	6	US-10-450-763-33194	Sequence 33194, A	791	6	2.0	574	8	US-60-643-717-1898	Sequence 1898, Ap
719	6	2.0	507	6	US-10-450-763-50792	Sequence 50792, A	792	6	2.0	579	6	US-10-450-763-48241	Sequence 48241, A
720	6	2.0	507	6	US-10-489-448-2862	Sequence 2862, Ap	793	6	2.0	579	7	US-11-031-175-16017	Sequence 16017, A
721	6	2.0	511	8	US-60-643-717-10165	Sequence 10165, A	794	6	2.0	580	6	US-10-450-763-36598	Sequence 36598, A
722	6	2.0	512	8	US-60-643-717-338	Sequence 338, App	795	6	2.0	583	6	US-10-450-763-35175	Sequence 35175, A
723	6	2.0	512	8	US-60-643-717-7704	Sequence 7704, Ap	796	6	2.0	583	7	US-11-031-175-14031	Sequence 14031, A
724	6	2.0	512	8	US-60-643-717-14010	Sequence 14010, A	797	6	2.0	583	7	US-11-031-175-14460	Sequence 14460, A
725	6	2.0	512	8	US-60-643-717-16417	Sequence 16417, A	798	6	2.0	583	8	US-60-643-717-1848	Sequence 1848, A
726	6	2.0	514	6	US-10-450-763-41307	Sequence 41307, A	799	6	2.0	586	8	US-60-643-717-17736	Sequence 17736, A
727	6	2.0	514	6	US-10-450-763-51125	Sequence 51125, A	800	6	2.0	590	8	US-60-643-717-11727	Sequence 11727, A
728	6	2.0	515	8	US-60-643-717-14852	Sequence 14852, A	801	6	2.0	590	8	US-60-643-717-15184	Sequence 15184, A
729	6	2.0	515	1	PCT-US04-42360-2512	Sequence 2512, Ap	802	6	2.0	592	7	US-11-031-175-10635	Sequence 10635, A
730	6	2.0	517	7	US-11-031-175-10829	Sequence 10829, A	803	6	2.0	595	7	US-11-031-175-18334	Sequence 18334, A
731	6	2.0	517	8	US-60-643-717-17217	Sequence 17217, A	804	6	2.0	597	7	US-11-031-175-16436	Sequence 16436, A
732	6	2.0	518	6	US-10-450-763-34451	Sequence 34451, A	805	6	2.0	602	8	US-60-643-717-13112	Sequence 13112, A
733	6	2.0	518	6	US-10-450-763-52407	Sequence 52407, A	806	6	2.0	605	6	US-10-450-763-47185	Sequence 47185, A
734	6	2.0	520	8	US-60-643-717-3427	Sequence 3427, Ap	807	6	2.0	606	6	US-10-450-763-58585	Sequence 58585, A
735	6	2.0	522	8	US-60-643-717-15167	Sequence 15167, A	808	6	2.0	606	6	US-10-450-763-38590	Sequence 38590, A
736	6	2.0	526	6	US-10-450-763-48433	Sequence 48433, A	809	6	2.0	607	7	US-11-031-175-18935	Sequence 18935, A
737	6	2.0	526	8	US-60-643-717-1303	Sequence 1303, Ap	810	6	2.0	607	8	US-60-643-717-1414	Sequence 1414, Ap
738	6	2.0	527	8	US-60-643-717-16661	Sequence 16661, A	811	6	2.0	615	6	US-10-450-763-32948	Sequence 32948, A
739	6	2.0	528	8	US-60-643-717-638	Sequence 638, App	812	6	2.0	617	7	US-11-031-175-14297	Sequence 14297, A
740	6	2.0	528	8	US-60-643-717-1447	Sequence 1447, Ap	813	6	2.0	620	7	US-11-031-175-11179	Sequence 11179, A
741	6	2.0	528	8	US-60-643-717-4546	Sequence 4546, Ap	814	6	2.0	621	6	US-10-450-763-60658	Sequence 60658, A
742	6	2.0	528	8	US-60-643-717-12306	Sequence 12306, A	815	6	2.0	621	6	US-10-489-448-1744	Sequence 1744, Ap
743	6	2.0	528	8	US-60-643-717-13170	Sequence 13170, A	816	6	2.0	625	6	US-10-489-448-1613	Sequence 1613, Ap
744	6	2.0	528	8	US-60-643-717-13440	Sequence 13440, A	817	6	2.0	627	8	US-60-643-717-13548	Sequence 13548, A
745	6	2.0	529	8	US-60-643-717-945	Sequence 945, App	818	6	2.0	629	6	US-10-450-763-48138	Sequence 48138, A
746	6	2.0	529	8	US-60-643-717-12722	Sequence 12722, A	819	6	2.0	632	8	US-60-643-717-14510	Sequence 14510, A
747	6	2.0	530	8	US-10-450-763-60048	Sequence 60048, A	820	6	2.0	635	5	US-09-785-086C-6	Sequence 6, Appl1
748	6	2.0	531	8	US-60-643-717-10740	Sequence 10740, A	821	6	2.0	637	8	US-60-643-717-5269	Sequence 5269, Ap
749	6	2.0	533	8	US-60-643-717-5938	Sequence 5938, App	822	6	2.0	643	6	US-10-489-448-1613	Sequence 1613, Ap
750	6	2.0	534	7	US-11-031-175-13260	Sequence 13260, A	823	6	2.0	649	8	US-60-643-717-9713	Sequence 9713, Ap
751	6	2.0	535	6	US-10-450-763-33751	Sequence 33751, A	824	6	2.0	653	6	US-10-450-763-48711	Sequence 48711, A
752	6	2.0	537	6	US-10-450-763-41671	Sequence 41671, A	825	6	2.0	654	6	US-10-489-448-1529	Sequence 1529, Ap
753	6	2.0	539	6	US-10-450-763-59645	Sequence 59645, A	826	6	2.0	654	7	US-11-031-175-14501	Sequence 14501, A
754	6	2.0	539	6	US-10-489-448-3038	Sequence 3038, Ap	827	6	2.0	658	6	US-10-450-763-43779	Sequence 43779, A
755	6	2.0	539	7	US-11-031-175-11952	Sequence 11952, A	828	6	2.0	662	7	US-11-031-175-15594	Sequence 15594, A

829	6	2.0	667	6	US-10-450-763-59096	Sequence 59096, A	902	6	2.0	749	8	US-60-643-717-15068	Sequence 15068, A
830	6	2.0	667	6	US-10-852-335A-122	Sequence 122, App	903	6	2.0	755	8	US-60-643-717-11227	Sequence 11227, A
831	6	2.0	668	6	US-10-450-763-49321	Sequence 49321, A	904	6	2.0	759	6	US-10-450-763-56227	Sequence 56227, A
832	6	2.0	671	8	US-60-643-717-18137	Sequence 18137, A	905	6	2.0	759	6	US-10-450-763-60152	Sequence 60152, A
833	6	2.0	673	7	US-11-027-399-2860	Sequence 2860, Ap	906	6	2.0	762	6	US-10-450-763-55315	Sequence 55315, A
834	6	2.0	673	7	US-11-027-843-2860	Sequence 2860, Ap	907	6	2.0	765	6	US-10-450-763-58874	Sequence 58874, A
835	6	2.0	673	7	US-11-027-878-2860	Sequence 2860, Ap	908	6	2.0	767	8	US-60-643-717-5052	Sequence 5052, Ap
836	6	2.0	673	7	US-11-028-169-2860	Sequence 2860, Ap	909	6	2.0	772	1	PCT-US04-17965-1190	Sequence 1390, Ap
837	6	2.0	673	7	US-11-028-204-2860	Sequence 2860, Ap	910	6	2.0	772	8	US-60-643-717-12573	Sequence 12573, A
838	6	2.0	673	7	US-11-027-877-2860	Sequence 2860, Ap	911	6	2.0	773	8	US-60-643-717-1018	Sequence 1018, Ap
839	6	2.0	673	7	US-11-027-879-2860	Sequence 2860, Ap	912	6	2.0	774	8	US-60-643-717-2433	Sequence 2433, Ap
840	6	2.0	673	7	US-11-028-149-2860	Sequence 2860, Ap	913	6	2.0	777	6	US-10-489-448-1621	Sequence 1621, Ap
841	6	2.0	673	7	US-11-027-802-2860	Sequence 2860, Ap	914	6	2.0	783	7	US-11-031-175-11405	Sequence 11405, A
842	6	2.0	673	7	US-11-027-890-2860	Sequence 2860, Ap	915	6	2.0	784	8	US-60-643-717-5362	Sequence 5362, Ap
843	6	2.0	673	7	US-11-027-892-2860	Sequence 2860, Ap	916	6	2.0	784	7	US-11-031-175-16475	Sequence 16475, A
844	6	2.0	673	7	US-11-028-099-2860	Sequence 2860, Ap	917	6	2.0	802	6	US-10-450-763-54216	Sequence 54216, A
845	6	2.0	673	7	US-11-028-197-2860	Sequence 2860, Ap	918	6	2.0	802	7	US-11-031-175-14060	Sequence 14060, A
846	6	2.0	673	7	US-11-027-844-2860	Sequence 2860, Ap	919	6	2.0	804	6	US-10-450-763-45931	Sequence 45931, A
847	6	2.0	673	7	US-11-028-050-2860	Sequence 2860, Ap	920	6	2.0	805	6	US-10-489-448-1202	Sequence 1202, Ap
848	6	2.0	673	7	US-11-028-457-2860	Sequence 2860, Ap	921	6	2.0	819	6	US-10-450-763-49219	Sequence 49219, A
849	6	2.0	673	7	US-11-027-891-2860	Sequence 2860, Ap	922	6	2.0	819	8	US-60-643-717-16439	Sequence 16439, A
850	6	2.0	673	7	US-11-028-291-2860	Sequence 2860, Ap	923	6	2.0	820	6	US-10-450-763-47402	Sequence 47402, A
851	6	2.0	673	7	US-11-028-458-2860	Sequence 2860, Ap	924	6	2.0	821	6	US-10-489-448-1200	Sequence 1200, Ap
852	6	2.0	677	6	US-10-450-763-37731	Sequence 37731, A	925	6	2.0	828	7	US-11-031-175-10903	Sequence 10903, A
853	6	2.0	677	6	US-11-031-175-12985	Sequence 12985, A	926	6	2.0	830	8	US-60-643-717-9807	Sequence 9807, Ap
854	6	2.0	678	7	US-11-031-175-13408	Sequence 13408, A	927	6	2.0	831	5	US-09-684-305-5	Sequence 5, App1
855	6	2.0	680	6	US-10-450-763-60525	Sequence 60525, A	928	6	2.0	832	5	US-09-684-305-4	Sequence 4, App1
856	6	2.0	682	6	US-10-450-763-52417	Sequence 52417, A	929	6	2.0	833	5	US-09-684-305-8	Sequence 8, App1
857	6	2.0	683	6	US-10-717-665A-71	Sequence 71, App1	930	6	2.0	833	5	US-09-684-305-107	Sequence 107, App
858	6	2.0	684	1	PCT-US05-00638-125	Sequence 125, App	931	6	2.0	833	5	US-09-684-305-130	Sequence 130, App
859	6	2.0	684	7	US-11-027-399-5255	Sequence 5255, Ap	932	6	2.0	833	5	US-09-684-305-132	Sequence 132, App
860	6	2.0	684	7	US-11-027-843-5255	Sequence 5255, Ap	933	6	2.0	834	5	US-09-684-305-6	Sequence 6, App1
861	6	2.0	684	7	US-11-027-878-5255	Sequence 5255, Ap	934	6	2.0	834	5	US-09-684-305-160	Sequence 160, App
862	6	2.0	684	7	US-11-028-169-5255	Sequence 5255, Ap	935	6	2.0	836	5	US-09-684-305-162	Sequence 162, App
863	6	2.0	684	7	US-11-028-204-5255	Sequence 5255, Ap	936	6	2.0	836	5	US-09-684-305-164	Sequence 164, App
864	6	2.0	684	7	US-11-027-877-5255	Sequence 5255, Ap	937	6	2.0	836	6	US-10-450-763-31083	Sequence 31083, A
865	6	2.0	684	7	US-11-027-879-5255	Sequence 5255, Ap	938	6	2.0	836	6	US-10-875-094-8	Sequence 8, App1
866	6	2.0	684	7	US-11-028-149-5255	Sequence 5255, Ap	939	6	2.0	837	7	US-10-875-094-11	Sequence 11, App1
867	6	2.0	684	7	US-11-027-802-5255	Sequence 5255, Ap	940	6	2.0	837	7	US-11-025-607-317	Sequence 317, App
868	6	2.0	684	7	US-11-027-890-5255	Sequence 5255, Ap	941	6	2.0	837	7	US-11-033-545-380	Sequence 380, App
869	6	2.0	684	7	US-11-027-892-5255	Sequence 5255, Ap	942	6	2.0	840	6	US-10-450-763-39157	Sequence 39157, A
870	6	2.0	684	7	US-11-028-099-5255	Sequence 5255, Ap	943	6	2.0	842	6	US-10-875-094-15	Sequence 15, App1
871	6	2.0	684	7	US-11-028-197-5255	Sequence 5255, Ap	944	6	2.0	842	6	US-10-875-094-20	Sequence 20, App1
872	6	2.0	684	7	US-11-027-844-5255	Sequence 5255, Ap	945	6	2.0	842	6	US-10-875-094-23	Sequence 23, App1
873	6	2.0	684	7	US-11-028-050-5255	Sequence 5255, Ap	946	6	2.0	842	6	US-10-875-094-26	Sequence 26, App1
874	6	2.0	684	7	US-11-028-457-5255	Sequence 5255, Ap	947	6	2.0	847	6	US-10-850-763-47696	Sequence 47696, A
875	6	2.0	684	7	US-11-027-891-5255	Sequence 5255, Ap	948	6	2.0	849	6	US-10-931-719-10	Sequence 10, App1
876	6	2.0	684	7	US-11-028-291-5255	Sequence 5255, Ap	949	6	2.0	849	7	US-11-033-545-564	Sequence 564, App
877	6	2.0	684	7	US-11-028-458-5255	Sequence 5255, Ap	950	6	2.0	852	6	US-10-450-763-44045	Sequence 44045, A
878	6	2.0	686	6	US-10-450-763-37057	Sequence 37057, A	951	6	2.0	853	7	US-11-031-175-14044	Sequence 14044, A
879	6	2.0	686	6	US-10-450-763-47359	Sequence 47359, A	952	6	2.0	853	8	US-60-643-717-2104	Sequence 2104, Ap
880	6	2.0	686	6	US-10-450-763-38589	Sequence 38589, A	953	6	2.0	853	8	US-60-643-717-10173	Sequence 10173, A
881	6	2.0	686	6	US-10-489-448-1612	Sequence 1612, Ap	954	6	2.0	856	6	US-10-489-448-1220	Sequence 1220, Ap
882	6	2.0	687	1	PCT-US04-23166A-604	Sequence 604, App	955	6	2.0	862	1	PCT-US04-42360-1312	Sequence 1312, Ap
883	6	2.0	697	1	PCT-US04-23166A-748	Sequence 748, App	956	6	2.0	864	6	US-10-489-448-1042	Sequence 1042, Ap
884	6	2.0	699	7	US-11-025-607-12	Sequence 12, App1	957	6	2.0	868	6	US-10-450-763-54786	Sequence 54786, A
885	6	2.0	700	7	US-11-031-175-11872	Sequence 11872, A	958	6	2.0	876	8	US-60-643-717-765	Sequence 765, App
886	6	2.0	705	6	US-10-450-763-48643	Sequence 48643, A	959	6	2.0	886	6	US-10-450-763-34028	Sequence 34028, A
887	6	2.0	705	6	US-10-450-763-59189	Sequence 59189, A	960	6	2.0	891	5	US-09-785-085C-8	Sequence 8, App1
888	6	2.0	710	6	US-10-450-763-52854	Sequence 52854, A	961	6	2.0	894	6	US-10-485-555-16	Sequence 16, App1
889	6	2.0	724	6	US-10-450-763-50942	Sequence 50942, A	962	6	2.0	896	6	US-10-450-763-52997	Sequence 52997, A
890	6	2.0	725	6	US-10-450-763-48665	Sequence 48665, A	963	6	2.0	897	7	US-11-031-175-15636	Sequence 15636, A
891	6	2.0	725	6	US-10-450-763-58870	Sequence 58870, A	964	6	2.0	900	6	US-10-450-763-30870	Sequence 30870, A
892	6	2.0	726	8	US-60-643-717-17584	Sequence 17584, A	965	6	2.0	903	7	US-11-031-175-11595	Sequence 11595, A
893	6	2.0	728	6	US-10-450-763-33993	Sequence 33993, A	966	6	2.0	908	8	US-60-643-717-9942	Sequence 9942, Ap
894	6	2.0	731	6	US-10-852-335A-1204	Sequence 1094, App	967	6	2.0	908	8	US-60-643-717-9951	Sequence 9951, Ap
895	6	2.0	733	7	US-11-031-175-13857	Sequence 13857, A	968	6	2.0	909	6	US-10-936-061-80	Sequence 80, App1
896	6	2.0	745	5	US-09-785-085C-5	Sequence 5, App1	969	6	2.0	914	6	US-10-489-448-1914	Sequence 1914, Ap
897	6	2.0	745	7	US-11-031-175-10275	Sequence 10275, A	970	6	2.0	917	6	US-10-450-763-36655	Sequence 36655, A
898	6	2.0	748	6	US-10-937-758A-41	Sequence 10617, A	971	6	2.0	917	6	US-10-450-763-39139	Sequence 39139, A
899	6	2.0	748	7	US-11-031-175-10617	Sequence 10617, A	972	6	2.0	928	7	US-11-031-175-13048	Sequence 13048, A
900	6	2.0	749	8	US-60-643-717-2384	Sequence 2384, Ap	973	6	2.0	931	6	US-10-450-763-48926	Sequence 48926, A
901	6	2.0	749	8	US-60-643-717-7219	Sequence 7219, Ap	974	6	2.0				

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975 6 2.0 933 6 US-10-450-763-46103 Sequence 46103, A
976 6 2.0 943 6 US-10-450-763-41229 Sequence 41229, A
977 6 2.0 947 6 US-10-450-763-52541 Sequence 52541, A
978 6 2.0 950 8 US-60-643-717-15310 Sequence 15310, A
979 6 2.0 960 8 US-60-643-717-17814 Sequence 17814, A
980 6 2.0 963 6 US-10-489-448-1176 Sequence 1176, Ap
981 6 2.0 967 6 US-10-450-763-38693 Sequence 38693, A
982 6 2.0 978 1 PCT-US04-42360-364 Sequence 364, App
983 6 2.0 991 6 US-10-450-763-53804 Sequence 53804, A
984 6 2.0 993 6 US-11-033-545-332 Sequence 332, App
985 6 2.0 994 6 US-10-717-665A-38 Sequence 38, App1
986 6 2.0 1000 7 US-11-033-545-484 Sequence 484, App
987 6 2.0 1013 6 US-10-450-763-38471 Sequence 38471, A
988 6 2.0 1015 1 PCT-US05-00638-99 Sequence 99, App1
989 6 2.0 1016 6 US-10-450-763-39144 Sequence 39144, A
990 6 2.0 1016 6 US-10-852-335A-164 Sequence 164, App
991 6 2.0 1025 8 PCT-US04-42360-391 Sequence 391, App
992 6 2.0 1025 8 US-60-643-717-16057 Sequence 16057, A
993 6 2.0 1037 6 US-10-450-763-46107 Sequence 46107, A
994 6 2.0 1058 6 US-10-450-763-33212 Sequence 33212, A
995 6 2.0 1058 7 US-11-031-175-15976 Sequence 15976, A
996 6 2.0 1060 7 US-11-031-175-9866 Sequence 9866, Ap
997 6 2.0 1065 6 US-10-450-763-53805 Sequence 53805, A
998 6 2.0 1074 6 US-10-450-763-55007 Sequence 55007, A
999 6 2.0 1086 8 US-60-643-717-3535 Sequence 3535, Ap
1000 6 2.0 1090 6 US-10-450-763-56527 Sequence 56527, A

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## ALIGNMENTS

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RESULT 1
US-10-450-763-51705
; Sequence 51705, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51705
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (67)..(107)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00926G, p-value=2.950e-
; OTHER INFORMATION: 09, raw score of 12.21
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(117)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=7.7e-11, Pfam
; OTHER INFORMATION: score of 49.4
US-10-450-763-51705

```

```

Query Match 2.6%; Score 8; DB 6; Length 439;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 43 ELIAFLD 50
Db 122 ELIAFLD 129

```

```

RESULT 2
US-10-450-763-54383
; Sequence 54383, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54383
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (67)..(107)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00926G, p-value=2.950e-
; OTHER INFORMATION: 09, raw score of 12.21
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(117)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=7.7e-11, Pfam
; OTHER INFORMATION: score of 49.4
US-10-450-763-54383

```

```

Query Match 2.6%; Score 8; DB 6; Length 439;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 43 ELIAFLD 50
Db 122 ELIAFLD 129

```

```

RESULT 3
US-10-450-763-30700
; Sequence 30700, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 30700
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (287)..(305)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family 2 proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value-
; OTHER INFORMATION: 8.500e-20, raw score of 11.93

```

```
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (286)..(317)
/ OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases fam11 domain
/ OTHER INFORMATION: identified by Pfam, accession name UCH-1, E-value=9.8e-17, Pfam
/ OTHER INFORMATION: score of 69.0
US-10-450-763-30700
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 712;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 43 ELIAFLD 50
Db 380 ELIAFLD 387
```

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RESULT 4
US-10-450-763-54385
; Sequence 54385, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54385
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (552)..(570)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value=
; OTHER INFORMATION: 7.120e-18, raw score of 11.93
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (551)..(582)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases fam11 domain
; OTHER INFORMATION: identified by Pfam, accession name UCH-1, E-value=6.8e-13, Pfam
; OTHER INFORMATION: score of 56.3
US-10-450-763-54385
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 805;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 43 ELIAFLD 50
Db 645 ELIAFLD 652
```

```
RESULT 5
US-10-450-763-54384
; Sequence 54384, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
```

```
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 54384
/ LENGTH: 1066
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (622)..(640)
/ OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
/ OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value=
/ OTHER INFORMATION: 7.120e-18, raw score of 11.93
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (622)..(653)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases fam11 domain
; OTHER INFORMATION: identified by Pfam, accession name UCH-1, E-value=6.8e-13, Pfam
; OTHER INFORMATION: score of 56.3
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1066)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-54384
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 1066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 43 ELIAFLD 50
Db 715 ELIAFLD 722
```

```
RESULT 6
US-10-450-763-53691
; Sequence 53691, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53691
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
/ LOCATION: (994)..(1019)
/ OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
/ OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972D, p-value=
/ OTHER INFORMATION: 7.750e-19, raw score of 22.55
; FEATURE:
; NAME/KEY: DOMAIN
/ LOCATION: (991)..(1051)
/ OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
/ OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=1.1e-26, Pfam
/ OTHER INFORMATION: score of 102.0
US-10-450-763-53691
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```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 1089;
Matches 100.0%; Pred. No. 59;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELIAFLD 50  
|||||

Db 309 ELIAFLD 316

RESULT 7  
US-10-450-763-51707  
; Sequence 51707, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 51707  
; LENGTH: 1125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (254)..(1272)  
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins  
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value=  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1125)  
; OTHER INFORMATION: 7.120e-18, raw score of 11.93  
US-10-450-763-51707

Query Match 2.6%; Score 8; DB 6; Length 1125;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELIAFLD 50  
|||||

Db 347 ELIAFLD 354

RESULT 8  
US-10-489-448-2732  
; Sequence 2732, Application US/10489448  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyun  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ghosh, Malabika  
; APPLICANT: Wang, Dunru  
; APPLICANT: Ma, Yungang  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Weng, Gezhi  
; APPLICANT: Haley-Vicente, Dana  
; APPLICANT: Drmanac, Radoje T  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; FILE REFERENCE: 810CIP PCT  
; CURRENT APPLICATION NUMBER: US/10/489,448

CURRENT FILING DATE: 1004-03-10  
; PRIOR APPLICATION NUMBER: US 60/324,631  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/35017  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: US 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: PCT/US01/03800  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: US 09/515,126  
; PRIOR FILING DATE: 2000-02-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3476  
; SOFTWARE: pL\_genes Version 6.0  
; SEQ ID NO 2732  
; LENGTH: 1127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-489-448-2732

Query Match 2.6%; Score 8; DB 6; Length 1127;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELIAFLD 50  
|||||

Db 347 ELIAFLD 354

RESULT 9  
US-10-450-763-51706  
; Sequence 51706, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; PRIOR FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 51706  
; LENGTH: 1131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (66)..(113)  
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,  
; OTHER INFORMATION: accession number BL00226D, p-value=5.979e-24, raw score of 19.10  
US-10-450-763-51706

Query Match 2.6%; Score 8; DB 6; Length 1131;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELIAFLD 50  
|||||

Db 862 ELLAFLD 869

## RESULT 10

US-10-450-763-54386

Sequence 54386, Application US/10450763  
GENERAL INFORMATION:

APPLICANT: HySeq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 54386

LENGTH: 1142

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (76)..(123)

OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (1)..(121)

OTHER INFORMATION: Intermediate filament proteins domain identified by Pfam,

US-10-450-763-54386

## Query Match

Best Local Similarity 2.6%; Score 8; DB 6; Length 1142;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 873 ELLAFLD 880

## RESULT 11

US-10-489-448-997

Sequence 997, Application US/10489448  
GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Xue, Aidong J.

APPLICANT: Zhao, Qing A.

APPLICANT: Wang, Jian-Rui

APPLICANT: Wehrman, Tom

APPLICANT: Zhou, Ping

APPLICANT: Ghosh, Malabika

APPLICANT: Wang, Dunrui

APPLICANT: Ma, Yundong

APPLICANT: Asundi, Vinod

APPLICANT: Wang, Zhiwei

APPLICANT: Weng, Gezhi

APPLICANT: Haley-Vicente, Dana

APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: Novel Nucleic Acids and

FILE REFERENCE: 810CIP PCT

CURRENT APPLICATION NUMBER: US/10/489,448

CURRENT FILING DATE: 1004-03-10

PRIOR APPLICATION NUMBER: US 60/324,631

PRIOR FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: PCT/US00/35017  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: US 09/496,914  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: US 09/560,875  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: PCT/US01/03800  
PRIOR FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: US 09/515,126  
PRIOR FILING DATE: 2000-02-28  
Remaining Prior Application data removed - See File Wrapper or PAM.  
NUMBER OF SEQ ID NOS: 3476  
SOFTWARE: pt\_FL\_genes Version 6.0  
SEQ ID NO 997  
LENGTH: 1292  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-489-448-997

Query Match 2.6%; Score 8; DB 6; Length 1292;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 516 ELLAFLD 523

## RESULT 12

US-10-450-763-51703

Sequence 51703, Application US/10450763  
GENERAL INFORMATION:

APPLICANT: HySeq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 51703

LENGTH: 1388

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (1293)..(1318)

OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family 2 proteins

OTHER INFORMATION: domain identified by eMATRIX, accession number BI00972D, p-value=

OTHER INFORMATION: 7.750e-19, raw score of 22.55

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (1290)..(1350)

OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain

OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=1.1e-26, Pfam

US-10-450-763-51703

Query Match 2.6%; Score 8; DB 6; Length 1388;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ELAFLD 50  
Db 645 ELAFLD 652

RESULT 13  
US-10-699-562-21  
; Sequence 21, Application US/10699562  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: JIANG, Tao  
; APPLICANT: TSJEN, Roger Y.  
; TITLE OF INVENTION: PEPTIDES WHOSE UPTAKE BY CELLS IS  
; TITLE OF INVENTION: CONTROLABLE  
; FILE REFERENCE: 39754-0974A US  
; CURRENT APPLICATION NUMBER: US/10/699,562  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic polypeptide  
; NAME/KEY: UNSURE  
; LOCATION: 16, 32  
; OTHER INFORMATION: aminocaproic acid linker  
US-10-699-562-21

Query Match 2.3%; Score 7; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 GARRRR 173  
Db 24 GARRRR 30

RESULT 14  
US-10-450-763-32943  
; Sequence 32943, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hysq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 32943  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-450-763-32943

Query Match 2.3%; Score 7; DB 6; Length 41;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 RPSGAR 169  
Db 28 RPSGAR 34

RESULT 15  
US-10-450-763-52787  
; Sequence 52787, Application US/10450763  
; GENERAL INFORMATION:  
; APPLICANT: Hysq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 52787  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(64)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-52787

Query Match 2.3%; Score 7; DB 6; Length 64;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 SSANSQ 144  
Db 52 SSANSQ 58

Search completed: February 12, 2005, 16:43:14  
Job time : 26 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 12, 2005, 15:26:59 ; Search time 71 Seconds  
(without alignments)  
2185.352 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 1550

Sequence: 1 MALSGSTPAFCWEDECDLY.....LREAVGREAVRLVVSVDAD 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: uniprot\_03:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	99.5	326	1 DED2_HUMAN	Q8WKF8 homo sapien
2	1401	90.4	330	1 DED2_MOUSE	Q8WKF8 mus musculu
3	672.5	43.4	369	2 Q919M3	Q919M3 brachydanio
4	636.5	41.1	404	2 Q6DHM2	Q6DHM2 brachydanio
5	614.5	39.6	318	1 DED2_HUMAN	Q75618 homo sapien
6	610.5	39.4	318	1 DED2_MOUSE	Q922K0 ratcus norv
7	608.5	39.3	318	1 DED2_MOUSE	Q922K0 mus musculu
8	398	25.7	243	2 Q6GNZ8	Q6GNZ8 xenopus lae
9	349.5	22.5	244	2 Q6DHV2	Q6DHV2 brachydanio
10	253.5	16.4	168	2 Q8BRM9	Q8BRM9 mus musculu
11	116.5	7.5	531	2 Q7XU10	Q7XU10 oryza sativ
12	116	7.5	526	2 Q9ZRH9	Q9ZRH9 oryza sativ
13	115.5	7.5	476	2 Q6TRY3	Q6TRY3 human papil
14	115.5	7.5	5072	2 Q6UD66	Q6UD66 toxoplasma
15	114.5	7.4	381	2 Q73J76	Q73J76 mycobacteri
16	114.5	7.4	601	2 Q62185	Q62185 caenorhabdi
17	114	7.4	3084	2 Q8U211	Q8U211 pseudorhabdi
18	113.5	7.3	599	2 Q96NPI	Q96NPI homo sapien
19	113.5	7.3	725	1 ATU DROME	Q94546 drosophila
20	113.5	7.3	758	2 Q8N5H8	Q8N5H8 homo sapien
21	110.5	7.1	285	2 Q8LMS9	Q8LMS9 oryza sativ
22	110	7.1	878	2 Q8L7M3	Q8L7M3 arabidopsis
23	110	7.1	891	2 Q9ZM08	Q9ZM08 arabidopsis
24	110	7.1	894	2 Q9FYB2	Q9FYB2 arabidopsis
25	110	7.1	1310	2 Q9H7L6	Q9H7L6 homo sapien
26	109.5	7.1	1546	2 Q8TER5	Q8TER5 homo sapien
27	109.5	7.1	708	2 Q96JH4	Q96JH4 homo sapien
28	109.5	7.1	6620	2 Q96AA2	Q96AA2 homo sapien
29	109	7.0	1585	2 Q9UEM8	Q9UEM8 homo sapien
30	109	7.0	2303	2 Q9S596	Q9S596 homo sapien
31	108.5	7.0	374	2 Q9VHC0	Q9VHC0 drosophila

32	108.5	7.0	483	1 VE2 HPV14	P36783 human papil
33	108.5	7.0	3924	1 ANK2_HUMAN	Q01484 homo sapien
34	108	7.0	549	2 Q7XP77	Q7XP77 oryza sativ
35	108	7.0	581	2 Q9RU45	Q9RU45 deinococcus
36	107.5	6.9	220	2 Q6P366	Q6P366 xenopus tro
37	107.5	6.9	595	2 Q8S108	Q8S108 oryza sativ
38	107	6.9	323	2 Q7R429	Q7R429 giardia lam
39	106.5	6.9	231	2 Q8N922	Q8N922 homo sapien
40	106.5	6.9	238	2 Q6Y219	Q6Y219 oryza sativ
41	106.5	6.9	1040	2 Q8NHN2	Q8NHN2 homo sapien
42	106.5	6.9	2607	2 Q8BT18	Q8BT18 mus musculu
43	106	6.8	1469	2 Q6PD04	Q6PD04 mus musculu
44	106	6.8	6839	2 Q23550	Q23550 caenorhabdi
45	106	6.8	7158	2 Q23551	Q23551 caenorhabdi

## ALIGNMENTS

RESULT 1  
ID DED2\_HUMAN STANDARD; PRT; 326 AA.  
AC Q8WKF8; Q8NBR2; Q8NES1; Q8TRA8; Q96D35;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE DNA-binding death effector domain-containing protein 2 (DED-containing protein FLAME-3).  
GN Name=DED2; Synonym=FLAME3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND INTERACTION WITH CASP8.  
RX MEDLINE=21850646; PubMed=11741985; DOI=10.1074/jbc.M10749200;  
RA Roth M., Steiner-Liwen F., Pawlowski K., Godzik A., Reed J.C.;  
RT "Identification and characterization of DED2, a death effector domain-containing protein.";  
RT domain-containing protein.";  
RL J. Biol. Chem. 277:7501-7508(2002).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND INTERACTIONS WITH CASP8 AND GPR103.  
RX MEDLINE=21961615; PubMed=11965497; DOI=10.1038/ej/cdd/4401038;  
RA Zhan Y., Hegde R., Srinivasula S.M., Fernandes-Alnemri T., Alnemri E.S.;  
RT "Death effector domain-containing proteins DED and FLAME-3 form nuclear complexes with the TRIFC102 subunit of human transcription factor IIC.";  
RT Cell Death Differ. 9:439-447(2002).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=2220288; PubMed=12235123; DOI=10.1083/jcb.200112124;  
RA Lee J.C., Schickling O., Stegh A.H., Oshima R.G., Dinadate D., Cohen G.M., Peter M.R.;  
RT "DED regulates degradation of intermediate filaments during apoptosis.";  
RT J. Cell Biol. 158:1051-1066(2002).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX TISSUE=Testis; Carcinoma;  
RC PubMed=4702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa E., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T.,  
 RA Kusano Y., Kagehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
 RA Imase N., Mueshino K., Yuki H., Oshima A., Sasaki N., Aotake S.,  
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takekoshi M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Omori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Oktani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 RT cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Brain, and Lung;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Schetz T.E.,  
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carinci P., Prange C.,  
 RA Raha S.S., Loguettano N.J., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnanaprath P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Falley J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buterfield J.S.N., Krzywinski M.T., Skalska U., Smalish D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP INTERACTIONS WITH CASP8 AND CASP10.  
 RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;  
 RT Alciivar A., Hu S., Tang J., Yang X.,  
 RT "DEDD and DEDD2 associate with caspase-8/10 and signal cell death.";  
 RL Oncogene 22:291-297(2003).  
 CC -1- FUNCTION: May play a critical role in death receptor-induced  
 CC apoptosis and may target CASP8 and CASP10 to the nucleus. May  
 CC regulate degradation of intermediate filaments during apoptosis.  
 CC May play a role in the general transcription machinery in the  
 CC nucleus and might be an important regulator of the activity of  
 CC GTF3C3.  
 CC -1- SUBUNIT: Interacts with CASP8, CASP10 and GTF3C3. Homodimerizes  
 CC and heterodimerizes with DEDD.  
 CC -1- SUBCELLULAR LOCATION: Nuclear; accumulated in subnuclear  
 CC structures resembling nucleoli.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q8WXR8-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q8WXR8-2; Sequence=VSP\_010312;  
 CC -1- TISSUE SPECIFICITY: Expressed in most tissues. High levels were  
 CC found in liver, kidney, heart, ovary, spleen, testes, skeletal  
 CC muscle and peripheral blood leukocytes. Expression was absent or  
 CC low in colon and small intestine. Expression is relatively high in  
 CC the tumor cell lines chronic myelogenous leukemia K-562 and the  
 CC colorectal adenocarcinoma SW480. Expression is moderate in the

CC cervical carcinoma HeLa, the Burkitt's lymphoma Raji, the lung  
 CC carcinoma A549, and the melanoma G361. In contrast, two leukemia  
 CC cell lines, HL-60 (promyelocytic leukemia) and MOLT-4  
 CC (lymphoblastic leukemia), show relatively low levels.  
 CC -1- DOMAIN: Interacts with CASP8 and CASP10 are mediated by the DED  
 CC domain.  
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.  
 CC -1- CAUTION: Ref.5 (AAH13372) sequence differs from that shown due to  
 CC a frameshift in position 186.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC DR EMBL; AF443591; AAL48220.1; -;  
 CC DR EMBL; AF457575; AAM10835.1; -;  
 CC DR EMBL; AY125488; AAM95240.1; -;  
 CC DR EMBL; AK075328; BAC11551.1; -;  
 CC DR EMBL; BC013372; AAH13372.2; ALT\_FRAME.  
 CC DR EMBL; BC027930; AAH27930.1; -;  
 CC DR Genew; HGNC:24450; DEDD2.  
 CC DR H-InvDB; HIX0015171; -;  
 CC DR InterPro; IPR011029; DEATH\_like.  
 CC DR InterPro; IPR001875; DED.  
 CC DR Pfam; PF01335; DED, 1.  
 CC DR SMART; SM00031; DED, 1.  
 CC DR PROSITE; PS50168; DED, 1.  
 CC KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;  
 CC Transcription regulation.  
 CC FT DOMAIN 25 104  
 CC FT DOMAIN 104 109  
 CC FT DOMAIN 155 173  
 CC FT VASSPLIC 145 149  
 CC FT CONFLICT 27 27 Missing (in isoform 2).  
 CC FT CONFLICT 56 56 H -> N (in Ref. 2).  
 CC FT CONFLICT 79 79 A -> G (in Ref. 2).  
 CC FT CONFLICT 207 207 D -> G (in Ref. 4).  
 CC FT CONFLICT 207 207 C -> R (in Ref. 2).  
 CC FT CONFLICT 230 230 Missing (in Ref. 5; AAH13372).  
 CC SQ SEQUENCE 326 AA; 36178 MW; 3F7B0B307C870CD CRC64;  
 CC  
 CC Query Match 99.5%; Score 1543; DB 1; Length 326;  
 CC Best local similarity 99.7%; Pred. No. 6-5e-105;  
 CC Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC QY 1 MALGSGTPAPCWEDECDIYYGMLSLHMFPEVVGQULTECELELLAFLDEAPGAAGLA 60  
 CC DB 1 MALGSGTPAPCWEDECDIYYGMLSLHMFPEVVGQULTECELELLAFLDEAPGAAGLA 60  
 CC QY 61 PARSGLELLLEERRGCGESNRLRQLRVLARHDLPLHAKRRRPVSPERYSTGS 120  
 CC DB 61 PARSGLELLLEERRGCGESNRLRQLRVLARHDLPLHAKRRRPVSPERYSTGS 120  
 CC QY 121 SSSKRTSSCGRRSSSSANSOOGOWETGSPPTKRORSGRSGARRRRRGAAPAPQ 180  
 CC DB 121 SSSKRTSSCGRRSSSSANSOOGOWETGSPPTKRORSGRSGARRRRRGAAPAPQ 180  
 CC QY 121 SSSKRTSSCGRRSSSSANSOOGOWETGSPPTKRORSGRSGARRRRRGAAPAPQ 180  
 CC DB 121 SSSKRTSSCGRRSSSSANSOOGOWETGSPPTKRORSGRSGARRRRRGAAPAPQ 180  
 CC QY 181 QOSEPARSSSGKTYCDIRLVRARVEYCEHGALEOGVARRPQALARQLDVFGQATAVLR 240  
 CC DB 181 QOSEPARSSSGKTYCDIRLVRARVEYCEHGALEOGVARRPQALARQLDVFGQATAVLR 240  
 CC QY 241 SRDLSGVVCDIKFSELSTYDAFWGDIYSGALLQALRGVFLTEALREAVGRAVLLVSVD 300  
 CC DB 241 SRDLSGVVCDIKFSELSTYDAFWGDIYSGALLQALRGVFLTEALREAVGRAVLLVSVD 300  
 CC QY 301 EAD 303  
 CC DB 301 EAD 303  
 CC DB 301 EAD 303

RESULT 2	DEDD_MOUSE	STANDARD;	PRT;	330 AA.
ID	DEDD_MOUSE			
AC	Q8QZV0; Q8QZV1;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	DNA-binding death effector domain-containing protein 2 (DEDD-containing protein FLAME-3).			
GN	Name=Dedd2; Synonyms=Flame3;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
PN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	STRAIN=C57BL/6J;			
RX	MEDLINE=11961615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;			
RA	Zhan Y., Hegde B., Srinivasula S.M., Fernandes-Alnemri T.,			
RA	Alnemri B.S.;			
RT	"Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the Ffl1C102 subunit of human transcription factor TIFC."			
RL	Cell Death Differ. 9:439-447(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	PubMed=12527898; DOI=10.1038/sj.onc.1206099;			
RA	Alcivar A., Hu S., Tang J., Yang X.;			
RT	"DEDD and DEDD2 associate with caspase-8/10 and signal cell death."			
RN	Oncogene 22:291-297(2003).			
RP	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISUS=Retina;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,			
RA	Klauniger R.D., Collins P.S., Wagner L., Shermen C.W., Schuler G.D.,			
RA	Altshuler S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan E., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.J.,			
RA	Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Boak S.A., McEwan P.J., McKernan K.D., Malek J.A., Gamarallene P.H.,			
RA	Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Huilyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Whaley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalhus D.E.,			
RA	Gemeich A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-1- FUNCTION: May play a critical role in death receptor-induced			
CC	apoptosis and may target Casp8 and Casp10 to the nucleus. May			
CC	regulate degradation of intermediate filaments during apoptosis.			
CC	May play a role in the general transcription machinery in the			
CC	nucleus and might be an important regulator of the activity of			
CC	GTP33.			
CC	-1- SUBUNIT: Interacts with CASP8, CASP10 and GTP33. Homodimerizes			
CC	and heterodimerizes with DEDD (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear, accumulated in subnuclear			
CC	structures resembling nucleoli (By similarity).			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	IsoId=Q8QZV0-1; Sequence=Displayed;			
CC	Name=2;			
CC	IsoId=Q8QZV0-2; Sequence=VSP_010313, VSP_010314;			
CC	Note=No experimental confirmation available;			

CC	-1- TISSUE SPECIFICITY: Expression is high in liver, heart, kidney,
CC	and testis but low in brain, spleen, lung, and skeleton muscle.
CC	-1- DOMAIN: Interactions with Casp8 and Casp10 are mediated by the DED
CC	domain (by similarity).
CC	-1- SIMILARITY: Contains 1 death effector (DED) domain.
CC	-----
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AF545756; AAM10836.1; -
DR	EMBL; AF543541; AAM33179.1; -
DR	EMBL; BC037043; AAM37043.1; -
DR	MGI; MGI:1914629; 2410050B1IRK.
DR	InterPro; IPR011029; DEATH_1like.
DR	InterPro; IPR001875; DED.
DR	Pfam; PF01335; DED.1.
DR	SMART; SM00031; DED.1.
DR	PROSITE; PS50168; DED.1.
KW	Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
KW	Transcription regulation.
FT	DOMAIN 25 104 DED.
FT	DOMAIN 104 109 Nuclear localization signal (Potential).
FT	DOMAIN 156 174 Bipartite nuclear localization signal (Potential).
FT	VARSPLIC 1 171 Missing (in isoform 2).
FT	VARSPLIC 172 200 /FtId=VSP_010313.
FT	VARSPPLIC 172 200 RRRAGLASOOHQHGLGRPSSEGGKYTC -> MGKQARG
FT	VARSPPLIC 172 200 EVTCPRPTAPAMOSMDSIS (in isoform 2).
FT	VARSPPLIC 172 200 /FtId=VSP_010314.
FT	VARSPPLIC 172 200 /FtId=VSP_010314.
SO	SEQUENCE 330 AA; 36786 MW; 889BC4F5E01304B0 CRC64;
QY	Query Match 90.4%; Score 1401; DB 1; Length 330;
QY	Best Local Similarity 91.5%; Pred. No. 1.6e-94;
QY	Matches 281; Conservative 5; Mismatches 17; Indels 4; Gaps 2;
Db	1 MALSGSPAPQWEDDECLDYGYGMLSHRMFVVGQGLTECELELLAFLLDEAPGAAGLA 60
Db	1 MALSGSPAPQWEDDECLDYGYGMLSHRMFVVGQGLTECELELLAFLLDEAPGAAGLA 60
QY	61 PARSGELLELEERRQGCGESNRLQLQLRVLRHDLPLHARKRRRPVSPERYSYGT -119
Db	61 PARSGELLELEERRQGCGESNRLQLQLRVLRHDLPLHARKRRRPVSPERYSYGT -119
QY	120 SSSSKRTREGSCRRRRSSSSANSQCGQWEGSPPTKORSPRRGPGGARRRRGAPAP 179
Db	121 SSSSKRTREGSCRRRRSSSSANSQCGQWEGSPPTKORSPRRGPGGARRRRGAPAP 180
QY	180 ---QOQSEPPAPSPSEKAVTCDIRLVAEYCEHHPALCEGVASRRPOLARQLDVFQAT 236
Db	181 QOQHQHGLRLRPSSEKAVTCDIRLVAEYCEHHPALCEGVASRRPOLARQLDVFQAT 240
QY	237 AVLRSRDLGSVCDIKFSELSYLDAPFTGYLSGALLQALNGVFTALREAVGEBAYRL 296
Db	241 AVLRSRDLGSVCDIKFSELSYLDAPFTGYLSGALLQALNGVFTALREAVGEBAYRL 300
QY	297 VSVDEAD 303
Db	301 VSVDEAD 307
RESULT 3	
ID	Q919M3 PRELIMINARY; PRT; 369 AA.
AC	Q919M3;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Deddl.

GN Name=dedit;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20373792; PubMed=10917738;  
 RA Inohara N., Nunez G.;  
 RT "Genes with homology to mammalian apoptosis regulators identified in  
 RT zebrafish."  
 RL Cell Death Differ. 7:509-510(2000).  
 DR EMBL; AF232226; AAF66963.1; -  
 DR ZFIN; ZDB-GENE-000616-2; deddi.  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR Pfam; PF01335; DED; 1.  
 DR PROSITE; PS50168; DED; 1.  
 SQ SEQUENCE 369 AA; 42244 MW; 7380929B17EEC247 CRC64;  
 Query Match 43.4%; Score 672.5; DB 2; Length 369;  
 Best Local Similarity 45.6%; Pred. No. 3.5e-41;  
 Matches 156; Conservative 36; Mismatches 91; Indels 59; Gaps 7;  
 QY 12 WEDECDLYTGMLSHRMFEVVGQLTE-CELELLAFILDER-----P 53  
 DB 13 WEETECISLYETTLSHETFEIVGSQLTETCGE-VAFILDETPYPKHAPLDPGEWTEJLP 71  
 QY 54 GAAG-----GLARSGLELLELERRGCGESNRL 85  
 DB 72 GPDSFPQANTCPRLKXWQKQPOKEGCSIASRRKPSGVYELLERLRRGTLSDANLRP 131  
 QY 86 LGOLLRLVLRHDLPLHARKRRRPVSPERSYSGTSSSKRTGSCRRRRQSSSSANSQOG 145  
 DB 132 LLQLLRLTRHDVLPFVSGQKRRRTVSPEKQIDPEVDFRQDREVSNTNIPSFENTODH 191  
 QY 146 QWETGS---PPTKQRRSRGRPSGAGARRRRRGAAPAOQOSEPARPSSEGVTCIDILR 201  
 DB 192 HMRASGSSMTSASSNRRRRGRGHMSRSKR--GPEIOPSTP-----NKVTDILRR 243  
 QY 202 VRAECERGPALGEGVARRPQALARQLDFGQATVLRSDLSGVCDIKFSELSYDA 261  
 DB 244 VRAEISEHSALRGFPSPDKPPLRQPELFRASULTRRLGSLIVCDIKSKLTINDT 303  
 QY 262 FWGDYLSGALLQALRGVFLTEALREAVGREAVRLIVSDEAD 303  
 DB 304 FWPDMYSGALLKALKGVFITDILRAAGQGVRLIVSVDQYD 345  
 RESULT 4  
 Q6DHN2 PRELIMINARY; PRT; 404 AA.  
 AC Q6DHN2;  
 DT 25-OCT-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 GN Zgc:92202.  
 GN Name=zgc:92202;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins B.S., Wagner L., Scheimen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stedileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toehiyuki S., Gancini P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Guneratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,  
 RA Kiryavinski M.I., Skalska U., Smalins D.B., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RA Strausberg R.;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC075935; AAH75935.1; -  
 DR GO; GO:0005515; F:protein binding; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR011029; DEATH\_like.  
 DR InterPro; IPR01875; DED.  
 DR Pfam; PF01335; DED; 1.  
 DR SMART; SM00031; DED; 1.  
 DR PROSITE; PS50168; DED; 1.  
 SQ SEQUENCE 404 AA; 44888 MW; 3C949DB83B07B81A CRC64;  
 Query Match 41.1%; Score 636.5; DB 2; Length 404;  
 Best Local Similarity 44.2%; Pred. No. 1.7e-38;  
 Matches 142; Conservative 58; Mismatches 78; Indels 43; Gaps 9;  
 QY 4 SCSIPAPC-----WEDECDLYTGMLSHRMFEVVGQLTECELELLAF-----LDEAP 53  
 DB 77 SSTRFPAPSGVPEWPEEAVDAVGLYLMHMFIVGQLTRVVRVLSFVVDVIBDY- 135  
 QY 54 GAAGLARARSGLELLELERRGCGESNRLGLQLLRVLRHDLPLHARKRRRPVSPE 113  
 DB 136 ERGGI---RSGRPLALERQGRCDENFHVQLLITRHDLPVYTRKQOTVCPD 191  
 QY 114 RYSYGTSSSKRTGSCRRRRQSSSSANSQOG--QWETG-----SPTKQ---RSRG 162  
 DB 192 -----PVDKYLETSVRYVSPRGTDAGQGTTHRRGPPPLCCPSPGQVCEPRAKP 244  
 QY 163 RPSGAGARRRRGAPAPAOQOSEPARPSSEGVTCIDILRVRAEYCEHGPALGQVASRRP 222  
 DB 245 APPPSRRKRKRSHTADCR-----KOTCDILRVRAEYCOHESALQGVNFSNKQ 294  
 QY 223 QALARQLDFGQATVLRSDLSGVCDIKFSELSYDAFWGDYLSGALLQALRGVFLTE 282  
 DB 295 EALERQFERFQANTLRSRLGSLTCDIKFSELSYDAFWRDYINGSLRLALKGVFITD 354  
 QY 283 ALREAVGREAVRLIVSDEAD 303  
 DB 355 SLKQAVGHEALIKLVNVDDEED 375  
 RESULT 5  
 DEDD HUMAN  
 ID DEDD HUMAN STANDARD; PRT; 318 AA.  
 AC 075618; 060737;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Death effector domain-containing protein (Death effector domain-  
 GN containing testicular molecule) (DEDDpro) (FLDBD-1) (KE05).  
 GN Name=DEDD; Synonyms=DEDDPRO, DEDT;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=98447599; PubMed=9774341; DOI=10.1093/emboj/17.20.5974;  
 RA Steegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhansel C.,  
 RA Hofmann T.G., Grumet I., Krammer P.H., Peter M.B.;  
 RT "DEDD, a novel death effector domain-containing protein, targeted to  
 RT the nucleus.";  
 RL EMBO J. 17:5974-5986(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.  
 RC TISSUE=Testis;  
 RX MEDLINE=99049260; PubMed=9832420; DOI=10.1210/en.139.12.4839;  
 RA Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Haneh A.J.W.;  
 RT "DEPT, a novel death effector domain-containing molecule predominantly  
 RT expressed in testicular germ cells.";  
 RL Endocrinology 139:4839-4848(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Pan G.;  
 RT "PRD-1, a novel molecule with a DED-like domain.";  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Thome M., Techopp J.;  
 RT "DEDP1, a novel DED-containing protein.";  
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Dendritic cell;  
 RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;  
 RT "A novel gene from human dendritic cell.";  
 RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Bone marrow, and Placenta;  
 RX MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Kleiner S.F., Collins P.S., Wagner L., Shemen C.M., Schler G.D.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tashiro S., Carninci P., Prange C.,  
 RA Rabe S.S., Loughran N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP FUNCTION, AND INTERACTIONS WITH KRT8, KRT18 AND CASP3.  
 RX MEDLINE=22202088; PubMed=12235123; DOI=10.1083/jcb.200112124;  
 RA Lee J.C., Schickling O., Steegh A.H., Oshima R.G., Dinadale D.,  
 RA Cohen G.M., Peter M.B.;  
 RT "DEDD regulates degradation of intermediate filaments during  
 RT apoptosis.";  
 RL J. Cell Biol. 158:1051-1066(2002).  
 RN [8]  
 RP INTERACTION WITH GTP33.  
 RX MEDLINE=23961615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;  
 RA Zhan Y., Hsueh R., Srinivasula S.M., Fernandes-Alnemri T.,  
 RA Alnemri E.S.;  
 RT "Death effector domain-containing proteins DEDD and FLAME-3 form  
 RT nuclear complexes with the TPSTC102 subunit of human transcription

RT factor IIC.";  
 RL Cell Death Differ. 9:439-447(2002).  
 RN [9]  
 RP INTERACTIONS WITH CASP8 AND CASP10.  
 RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;  
 RA Alcivar A., Hu S., Tang J., Yang X.;  
 RT "DEDD and DEDD2 associate with caspase-8/10 and signal cell death.";  
 RL Oncogene 22:291-297(2003).  
 CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain  
 CC substrates and facilitates their ordered degradation during  
 CC apoptosis. May also play a role in mediating CASP3 cleavage of  
 CC KRT18. Regulates degradation of intermediate filaments during  
 CC apoptosis. May play a role in the general transcription machinery  
 CC in the nucleus and might be an important regulator of the activity  
 CC of GTP33. Inhibits DNA transcription in vitro (By similarity).  
 CC -1- SUBUNIT: Interacts with CASP8, CASP10, KRT8, KRT18, CASP3 and  
 CC FADD. Homodimerizes and heterodimerizes with DEDD2.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus  
 CC during CD95-mediated apoptosis where it is localized in the  
 CC nucleoli (By similarity). Following apoptosis induction, the mono  
 CC and/or dimerization form increases and forms filamentous  
 CC structures that colocalize with KRT8 and KRT18 intermediate  
 CC filament network in simple epithelial cells.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Name=1;  
 CC IsoId=075618-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=075618-2; Sequence=VSP\_003846;  
 CC Note=No experimental confirmation available;  
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in  
 CC testis.  
 CC -1- PTM: Exists predominantly in a mono- or dimerized form.  
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF088326; AAC3105.1; -  
 DR EMBL: AF100341; AAD16414.1; -  
 DR EMBL: AF043733; AAC60280.1; -  
 DR EMBL: AJ010973; CA009445.1; -  
 DR EMBL: AF064605; AAC17110.3; -  
 DR EMBL: BC016724; AAH16724.1; -  
 DR EMBL: BC013910; AAH13910.1; -  
 DR Genew: HGNC:2755; DEDD.  
 DR H-InvS: HIX0001231; -.  
 DR MIM: 606841; -.  
 DR GO: GO:0005737; C:cytoplasm; ISS.  
 DR GO: GO:0005730; C:nucleolus; ISS.  
 DR GO: GO:0005677; C:DNA binding; ISS.  
 DR GO: GO:0006917; P:induction of apoptosis; ISS.  
 DR GO: GO:0006625; P:induction of apoptosis via death domain rec. .; TAS.  
 DR GO: GO:0016481; P:negative regulation of transcription; ISS.  
 DR GO: GO:0007283; P:spermatogenesis; TAS.  
 DR InterPro: IPR011029; DEATH\_like.  
 DR InterPro: IPR001875; DED.  
 DR Pfam: PF01335; DED; 1.  
 DR SMART: SM00031; DED; 1.  
 DR PROSITE: PS50168; DED; 1.  
 KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;  
 KW Repressor; Transcription regulation.  
 FT DOMAIN 25 103 DED.  
 FT VARSPLC 194 194 D -> GERIQFQKRSRLREGYKELGHWAVAYAIQY (in  
 FT isoform 2).  
 FT /FTId=VSP\_003846.  
 FT P -> L (in Ref. 5).  
 FT SEQUENCE 318 AA; 36794 MW; FFD5FP9B61F6BB6 CRC64;

Query Match	39.6%	Score 614.5	DB 1.5	Length 318
Beet Local Similarity	44.9%	Pred. No. 5.1e-37		
Matches 135	Conservative 54	Mismatches 91	Indels 21	Gaps 6
QY	12	WEDECDLDYVGMISLHMEFVVGQULTECEBLAFL-LDEAPGAAGLAPARSGLELL	70	
DB	12	WPEHGEQEGHGLVSLHMFMDLVGTHLTHRDVAVLSPLFDVIDIDHBERGL-IRNGRDFLL	69	
QY	71	ELERRGGCGESNLRLGLQLRLANHDLPLHARRRRPVSV---ERYSTGS---SSSK	124	
DB	70	ALERRGRDESNFRVQLRLRIITHRDLFPYTLKRRRAVCPDLVDKYLEEYSIRVYTR	129	
QY	125	RTEGSCRRROSSSSANSQOQG--WETGSPPTKQGRSRSGARRRRCGAPAPQOQ	182	
DB	130	ALSDPEPPPPQDSKTVPPHYVYVCCPTSGPQMCSSKRAAGKATLSGQRKR-----	180	
QY	183	SEPARPSSEKATCDIRLRVRAEYCEHGEHALBOGVASRRPQALARQLDVFGQATAVLSR	242	
DB	181	KSVTPDREKQCTDIRLRVRAEYCOHETALQGVNPSNKODPLERQFERFNQNTILIKR	239	
QY	243	DLGSVVCIKPSLSYLDLFMDYLSGALLQALRGVFLTEALREANGRAVLLVSVDRA	302	
DB	240	DLGSIICIKPSFLTYLDAFMWDYINGSLLEALKGVITDLSKQAVGHAIRKLNVADDE	299	
QY	303			
DB	300	D 300		
RESULT 6				
DEDD RAT				
ID	DEDD RAT	STANDARD;	PRT;	318 AA.
AC	092230;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Death effector domain-containing protein (Death effector domain-			
DE	containing testicular molecule).			
GN	Name=Dedd; Synonyms=Defc;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RM	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.			
RC	TISSUE=Testis;			
RC	MEDLINE=99049260; PubMed=9832420; DOI=10.1210/en.139.12.4839;			
RA	Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Hsieh A.U.W.;			
RT	"DEPT, a novel death effector domain-containing molecule predominantly			
RT	expressed in testicular germ cells.";			
RL	Endocrinology 139:4839-4848(1998).			
CC	-FUNCTION: A scaffold protein that directs CASP3 to certain			
CC	substrates and facilitates their ordered degradation during			
CC	apoptosis. May also play a role in mediating CASP3 cleavage of			
CC	KR18. Regulates degradation of intermediate filaments during			
CC	apoptosis. May play a role in the general transcription machinery			
CC	in the nucleus and might be an important regulator of the activity			
CC	of GTF3C3. Inhibits DNA transcription in vitro (By similarity).			
CC	-SUBUNIT: Interacts with CASB8, CASP10, KR18, KR18, CASP3 and			
CC	PADL. Homodimerizes and heterodimerizes with DEDD2 (By			
CC	similarity).			
CC	-SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus			
CC	during C95-mediated apoptosis where it is localized in the			
CC	nucleoli. Following apoptosis induction, the mono and/or			
CC	dibiquitination form increases and forms filamentous structures			
CC	that colocalize with KR18 and KR18 intermediate filament network			
CC	in simple epithelial cells (By similarity).			
CC	-TISSUE SPECIFICITY: Widely expressed with highest levels in			
CC	testis. Within the testis, highly expressed in germ cells but not			
CC	expressed in Sertoli cells.			
CC	-DEVELOPMENTAL STAGE: First detected in 20-day-old animals. Reaches			
CC	a peak at 30 days.			

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length	DB 4	Length	DB 5	Length	DB 6	Length	DB 7	Length	DB 8	Length	DB 9	Length	DB 10	Length	DB 11	Length	DB 12	Length	DB 13	Length	DB 14	Length	DB 15	Length	DB 16	Length	DB 17	Length	DB 18	Length	DB 19	Length	DB 20	Length	DB 21	Length	DB 22	Length	DB 23	Length	DB 24	Length	DB 25	Length	DB 26	Length	DB 27	Length	DB 28	Length	DB 29	Length	DB 30	Length	DB 31	Length	DB 32	Length	DB 33	Length	DB 34	Length	DB 35	Length	DB 36	Length	DB 37	Length	DB 38	Length	DB 39	Length	DB 40	Length	DB 41	Length	DB 42	Length	DB 43	Length	DB 44	Length	DB 45	Length	DB 46	Length	DB 47	Length	DB 48	Length	DB 49	Length	DB 50	Length	DB 51	Length	DB 52	Length	DB 53	Length	DB 54	Length	DB 55	Length	DB 56	Length	DB 57	Length	DB 58	Length	DB 59	Length	DB 60	Length	DB 61	Length	DB 62	Length	DB 63	Length	DB 64	Length	DB 65	Length	DB 66	Length	DB 67	Length	DB 68	Length	DB 69	Length	DB 70	Length	DB 71	Length	DB 72	Length	DB 73	Length	DB 74	Length	DB 75	Length	DB 76	Length	DB 77	Length	DB 78	Length	DB 79	Length	DB 80	Length	DB 81	Length	DB 82	Length	DB 83	Length	DB 84	Length	DB 85	Length	DB 86	Length	DB 87	Length	DB 88	Length	DB 89	Length	DB 90	Length	DB 91	Length	DB 92	Length	DB 93	Length	DB 94	Length	DB 95	Length	DB 96	Length	DB 97	Length	DB 98	Length	DB 99	Length	DB 100	Length	DB 101	Length	DB 102	Length	DB 103	Length	DB 104	Length	DB 105	Length	DB 106	Length	DB 107	Length	DB 108	Length	DB 109	Length	DB 110	Length	DB 111	Length	DB 112	Length	DB 113	Length	DB 114	Length	DB 115	Length	DB 116	Length	DB 117	Length	DB 118	Length	DB 119	Length	DB 120	Length	DB 121	Length	DB 122	Length	DB 123	Length	DB 124	Length	DB 125	Length	DB 126	Length	DB 127	Length	DB 128	Length	DB 129	Length	DB 130	Length	DB 131	Length	DB 132	Length	DB 133	Length	DB 134	Length	DB 135	Length	DB 136	Length	DB 137	Length	DB 138	Length	DB 139	Length	DB 140	Length	DB 141	Length	DB 142	Length	DB 143	Length	DB 144	Length	DB 145	Length	DB 146	Length	DB 147	Length	DB 148	Length	DB 149	Length	DB 150	Length	DB 151	Length	DB 152	Length	DB 153	Length	DB 154	Length	DB 155	Length	DB 156	Length	DB 157	Length	DB 158	Length	DB 159	Length	DB 160	Length	DB 161	Length	DB 162	Length	DB 163	Length	DB 164	Length	DB 165	Length	DB 166	Length	DB 167	Length	DB 168	Length	DB 169	Length	DB 170	Length	DB 171	Length	DB 172	Length	DB 173	Length	DB 174	Length	DB 175	Length	DB 176	Length	DB 177	Length	DB 178	Length	DB 179	Length	DB 180	Length	DB 181	Length	DB 182	Length	DB 183	Length	DB 184	Length	DB 185	Length	DB 186	Length	DB 187	Length	DB 188	Length	DB 189	Length	DB 190	Length	DB 191	Length	DB 192	Length	DB 193	Length	DB 194	Length	DB 195	Length	DB 196	Length	DB 197	Length	DB 198	Length	DB 199	Length	DB 200	Length	DB 201	Length	DB 202	Length	DB 203	Length	DB 204	Length	DB 205	Length	DB 206	Length	DB 207	Length	DB 208	Length	DB 209	Length	DB 210	Length	DB 211	Length	DB 212	Length	DB 213	Length	DB 214	Length	DB 215	Length	DB 216	Length	DB 217	Length	DB 218	Length	DB 219	Length	DB 220	Length	DB 221	Length	DB 222	Length	DB 223	Length	DB 224	Length	DB 225	Length	DB 226	Length	DB 227	Length	DB 228	Length	DB 229	Length	DB 230	Length	DB 231	Length	DB 232
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RA Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhansel C.,  
 RA Hofmann T.G., Grummt I., Krammer P.H., Peter M.E.;  
 RA "DEBD, a novel death effector domain containing protein, targeted to  
 RA the nucleolus";  
 RA EMBO J. 17:5974-5986(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP Thome M., Tschopp J.;  
 RT "DEBPRO1, a novel DED-containing protein";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP STRAINFEV/N-3; TISSUE=Colon, and Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain  
 CC substrates and facilitates their ordered degradation during  
 CC apoptosis. May also play a role in mediating CASP3 cleavage of  
 CC KRT18. Regulates degradation of intermediate filaments during  
 CC apoptosis. May play a role in the general transcription machinery  
 CC in the nucleus and might be an important regulator of the activity  
 CC of GTF3C3 (By similarity). Inhibits DNA transcription in vitro.  
 CC -1- SUBUNIT: Interacts with CASP8, CASP10, KRT8, KRT18, CASP3 and  
 CC FADD. Homodimerizes and heterodimerizes with DEBD2 (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus  
 CC during CD95-mediated apoptosis where it is localized in the  
 CC nucleolus. Following apoptosis induction, the mono and/or  
 CC dimerization form increases and forms filamentous structures  
 CC that colocalize with KRT8 and KRT18 intermediate filament network  
 CC in simple epithelial cells (By similarity).  
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.  
 CC -1- PTM: Exists predominantly in a mono- or dimerized form.  
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL, AJ011386; CA009604.1; -  
 DR EMBL, AF100342; AAD16415.1; -  
 DR EMBL, BC023668; AAH23668.1; -  
 DR EMBL, BC054445; AAH54445.1; -  
 DR MGD, MGI:133874; Dded.  
 DR GO, GO:0005737; Cytoplasm; IDA.  
 DR GO, GO:0005730; C:nucleolus; IDA.  
 DR GO, GO:0003677; F:DNA binding; IDA.  
 DR GO, GO:0006917; P:induction of apoptosis; IDA.  
 DR GO, GO:0016481; P:negative regulation of transcription; IDA.  
 DR InterPro, IPR01029; DEATH\_1like.

DR InterPro, IPR01875; DED.  
 DR Pfam, PF01335; DED; 1.  
 DR SMART, SM00031; DED; 1.  
 DR PROSITE, PS0168; DED; 1.  
 KW Apoptosis; DNA-binding; Nuclear protein; Repressor;  
 KW Transcription regulation.  
 FT DOMAIN 25 103 DED.  
 FT CONFLICT 237 237 K -> N (in Ref. 2).  
 FT CONFLICT 316 316 A -> V (in Ref. 3; AAH54445).  
 SQ SEQUENCE 318 AA, 36805 MW, C9A31DPC4C0E57CA CRG64;  
 Query Match 39.3%; Score 608.5; DB 1; Length 318;  
 Best Local Similarity 43.5%; Pred. No. 1.4e-36;  
 Matches 111; Conservative 56; Mismatches 93; Indels 21; Gaps 5;  
 QY 12 WEDECDLYYGMGLSLHMFVYVGGQTECELEAFVLDAPGAAGGLARARGALL 70  
 DB 12 WPEERGBQHGGLYSIHRMFDIVGTHLTHRDVLSFLFDVIDDHERGL-IRNGDFLL 69  
 QY 71 EERRGQGESNRLILGQLRLVLRHDLPLHARRRRPVSP---ERYSGTSSSKATE 127  
 DB 70 ALERGRCDSESPROYQLRLITRHDLPVTLKRAVCDVDYKLESTIRYVTR 129  
 QY 128 GSCRRRGSSSANSQCGMETGSPPTK-----RGRSRGSPGARRRRGAPAPQOO 182  
 DB 130 ALSDEPRPOPSKTVPHYPVCCPTSGSCMSKRPARGRTTIGSRKR----- 180  
 QY 183 SEPAPSSSGKTCYDILRVAREYCEHGPALFQGVASRRPQALQADYFGQATVLR 242  
 DB 181 -KSVPDPPEKQTCYIRLRVAREYCOHETALQGVNSKQDPLERGFERNANTLKSR 239  
 QY 243 DGSAVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVLVSD 302  
 DB 240 DLSGIIICDKFELTYLDAPFMDYINGSLLEKGVFTITSLKQAVGHAITLVNVD 299  
 QY 303 D 303  
 DB 300 D 300  
 RESULT 8  
 Q6GNZ8 PRELIMINARY; PRT; 243 AA.  
 AC Q6GNZ8;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DE MGC80767 protein.  
 OS Name=MGC80767;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Spleen.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Buterfield Y.S., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,



RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=2341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg K.L., Wagner U., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC073351; AAH73351.1;  
 DR GO: GO:0005515; F:protein binding; IEA.  
 DR GO: GO:0042981; F:regulation of apoptosis; IEA.  
 DR InterPro: IPR011029; DEATH\_like.  
 DR InterPro: IPR001875; DED.  
 DR Pfam: PF01335; DED; 1.  
 DR PROSITE: PS50168; DED; 1.  
 SQ SEQUENCE 243 AA; 27767 MW; 57A2E89CEPD3E0BC CRC64;

Query Match 25.7%; Score 398; DB 2; Length 243;  
 Best Local Similarity 40.2%; Pred. No. 2.5e-21;  
 Matches 92; Conservative 31; Mismatches 52; Indels 54; Gaps 5;  
 QY 12 WEDECDLYYGMGLSHRMFEVVGQLTCECELELAFLDEA-----PG 54  
 DB 13 WEDECDLYYGMGLSHRMFEVVGQLTCECELELAFLDEA-----PG 72  
 QY 53 ---PGA-----GLARASGLLELLERRGCGESNRLRL 89  
 DB 73 EAMPASALLSAMQRRNRGRTLNLDSPDLARPKGTLELLELRGCGESNRLRL 132  
 QY 90 LRLVLAARDLLPHLAKRRRPVSPERYSGTSSSKRTGSCRRRROSSANSQCGQ 147  
 DB 133 LRLVLAARDLLPHLAKRRRPVSPERYSGTSSSKRTGSCRRRROSSANSQCGQ 187  
 QY 148 EFGSGPTKQRQRSGRPSGAGARRRRGAPAPQCGSEPARPSSEGVKTC 196  
 DB 188 EFGSGPTKQRQRSGRPSGAGARRRRGAPAPQCGSEPARPSSEGVKTC 231

RESULT 9  
 O6DHV2 PRELIMINARY; PRT; 244 AA.  
 AC O6DHV2; 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Dedd1 protein.  
 GN Name=Dedd1;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OK NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnaa.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins R.S., Wagner L., Shennan C.M., Schler G.D.,  
 RA Altshuler S.F., Zedberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Baka S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Roha S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RA Strausberg R.;  
 RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC075865; AAH75865.1;  
 DR GO: GO:0005515; F:protein binding; IEA.  
 DR GO: GO:0042981; F:regulation of apoptosis; IEA.  
 DR InterPro: IPR011029; DEATH\_like.  
 DR InterPro: IPR001875; DED.  
 DR Pfam: PF01335; DED; 1.  
 DR PROSITE: PS50168; DED; 1.  
 SQ SEQUENCE 244 AA; 28051 MW; 043225A5A5D79527 CRC64;

Query Match 22.5%; Score 349.5; DB 2; Length 244;  
 Best Local Similarity 37.6%; Pred. No. 9e-18;  
 Matches 88; Conservative 20; Mismatches 69; Indels 57; Gaps 5;  
 QY 12 WEDECDLYYGMGLSHRMFEVVGQLTCECELELAFLDEA-----PG 54  
 DB 13 WEDECDLYYGMGLSHRMFEVVGQLTCECELELAFLDEA-----PG 72  
 QY 55 AAG-----GLARASGLLELLERRGCGESNRLRL 86  
 DB 73 PDGSPQANTPCPRLLKSWQMOPQKGCISARRPKSGVELELLERRGCGESNRLRL 132  
 QY 87 GOLRLVLAARDLLPHLAKRRRPVSPERYSGTSSSKRTGSCRRRROSSANSQCGQ 146  
 DB 133 LQLRLVLAARDLLPHLAKRRRPVSPERYSGTSSSKRTGSCRRRROSSANSQCGQ 192  
 QY 147 WETGS-----PTKQRQRSGRPSGAGARRRRGAPAPQCGSEPARPSSEGVKTC 196  
 DB 193 WRAGSGSMTASASRRRRKRGHMSRKR--GPEIIGPGRP-----NKVTC 238

RESULT 10  
 O8BRM9 PRELIMINARY; PRT; 168 AA.  
 AC O8BRM9; 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)  
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched-  
 DE library, clone:AB31049M19 product:similar to death effector domain-  
 DE containing and DNA-binding protein 2, full insert sequence.  
 GN Name=Dedd2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OK NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cortex;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RX Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/9r.152600;
RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Hatada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa K., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1157-1171(2000).
RN
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirotsu T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Muraoka M., Nakamura M.,
RA Nihei K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK043908; BAC31699.1; -.
DR MGD: MGI:1914629; Decd42.
DR GO: GO:0042981; P:regulation of apoptosis; TAS.
DR KW DNA-binding.
SQ SEQUENCE 168 AA; 17242 MW; F75D71DC489D2425 CRC64;

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Query Match 16.4%; Score 253.5; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 6.1e-11;
Matches 60; Conservative 4; Mismatches 18; Indels 23; Gaps 4;

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QY 163 RPSG-----GARRRRGAPAP-----QQQSE-----ARPSSEKVTCDIRLRYA 204
DB 38 QPSGSGGCGA-----ALPVPSSGGEGALQPRSSSTSSSTRSWAPPSSEKATCDIRLRYA 92
QY 205 EYCEGPALEGGVARRRPPQALARQLDVGQATVATRSRDLSGVC 249
DB 93 EYCEGPALEGGVARRRPPQALARQLDVGQATVATVAVKPGGLCWC 137

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RESULT 11
Q7XU10 PRELIMINARY; PRT; 531 AA.
ID Q7XU10

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AC Q7XU10;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE OSUNBA0091D06.5 protein.
GN Name=OSUNBA0091D06.5;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN
[1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Peng Q., Zhang Y., Hao P., Wang S., Pu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL: AL606459; CADD41631.1; -.
DR Gramene; Q7XU10; -.
DR InterPro; IPR008552; DUF834.
DR Pfam; PF05754; DUF834; 1.
SQ SEQUENCE 531 AA; 56907 MW; AC26AB4A6459B71D CRC64;

```

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Query Match 7.5%; Score 116.5; DB 2; Length 531;
Best Local Similarity 27.5%; Pred. No. 2.5;
Matches 49; Conservative 18; Mismatches 72; Indels 39; Gaps 6;

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```

QY 53 PGAGGLARARSGELILLETERRGQC---GESNRLTLGQLRLVLRH--DLPLRLARKR 107
DB 250 PRTATGAAGARHGSTLAQGTARAGAAATRGDGR-----RQLTRAKAAHAREGRGAARGR 305
QY 108 RPSV---DERYSYGTSSSSKRTGSCRRRRQ-----SSSSANSQ 143
DB 306 GPAAHHRRHRRGHGVRSAATAATRSDDHRRPQVARTPGRRPTKGRKRREGSAHNDARR 365
QY 144 QGQMTGSPPTKGRGRSGRRGARRRRGAPAPPOOQSEARRPSSEKATCDIRLR 201
DB 366 RGRGRQGTAVTGLAKTTRRSSGDGRRSRGWRAPRSATB-----EGCAPADFRRR 417

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RESULT 12
Q9ZRH9 PRELIMINARY; PRT; 526 AA.
AC Q9ZRH9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Early embryogenesis protein.
GN Name=Q9ZRH9;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN
[1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Peng Q., Zhang Y., Hao P., Wang S., Pu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL: AL606459; CADD41631.1; -.
DR Gramene; Q7XU10; -.
DR InterPro; IPR008552; DUF834.
DR Pfam; PF05754; DUF834; 1.
SQ SEQUENCE 531 AA; 56907 MW; AC26AB4A6459B71D CRC64;

```

```

Query Match 7.5%; Score 116.5; DB 2; Length 531;
Best Local Similarity 27.5%; Pred. No. 2.5;
Matches 49; Conservative 18; Mismatches 72; Indels 39; Gaps 6;

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DR InterPro: IPR011051; RmlC like cupin.
DR InterPro: IPR006044; Seedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
SQ SEQUENCE 526 AA; 58770 MW; BC23C0F9D1711F9B CRC64;

Query Match 7.5%; Score 116; DB 2; Length 526;
Best Local Similarity 30.6%; Pred. No. 2.6;
Matches 38; Conservative 18; Mismatches 38; Indels 30; Gaps 4;

QY 100 PHLARKRRPVSPRYSTSSS-----KTEGSCRRRSSSSANSQCGQW 147
D 114 PAARRTTRPRRRRRRTTSAAVAVMRRDGRARERRRRRRPAAASSPSATS 173
QY 148 ETGSPPTKRRRRSGRRS---CGARR---RRGAPAPQOQSEPARPS----- 189
D 174 TRGSPSPARRRRGRRRAVLGPQRRRLPARRHLSRRRQORQPARFVLQAFRLAGGAR 233
QY 190 SEGK 193
D 234 SEGR 237

RESULT 13
O6TVJ3 PRELIMINARY; PRT; 476 AA.
AC O6TVJ3.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E2.
OS Human papillomavirus type 93.
OC Virusae; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=247268;
RN [1]
RP SEQUENCE FROM N.A.
RA Forslund O., Ly H., Higgins G., Hunziker A., deVilliers E.-M.;
RL Submitted (Sep-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY382778; AAQ88283.1; -.
DR HSSP; P17383; IAVG.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006275; P:regulation of DNA replication; IEA.
DR GO; GO:0006345; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR00427; E2_C.
DR InterPro; IPR001866; E2_N.
DR InterPro; IPR009021; Viral_DNA_bd.
DR Pfam; PF00511; PPV_E2_C; 1.
DR Pfam; PF00508; PPV_E2_N; 1.
DR ProDom; PD000672; E2_C; 1.
DR ProDom; PD000678; E2_N; 1.
SQ SEQUENCE 476 AA; 53928 MW; E6C199408892C93F CRC64;

Query Match 7.5%; Score 115.5; DB 2; Length 476;
Best Local Similarity 25.3%; Pred. No. 2.6;
Matches 44; Conservative 27; Mismatches 76; Indels 27; Gaps 4;

QY 91 RYLAHDLPLHARRRPVSPRYSTSSSKRTGSCRRRSSSSANSQCGQW 150
D 246 RYVGRRESPTSSSKRRSSSRKQKGRSRRSRTTSSQSRSGRRSGRGRT 305
QY 151 SPPTKRRRRSGRRPSG-----GARRRRGAPAP-----QOQSEPARPSSEKVT- 195
D 306 RRGKHTTKRGGRGGRKDRGRSRRSSSSPTTCTRSASQTRSKOSKCARPDGISTP 365
QY 196 CDIRLRVRAVEYCEHGPALGQVARRPQALARQLDVFGQATAVLSRDLGTVVC 249
D 366 GIVGKSV-----QTVSGNTGTLGLLEBARPPVILIRGEANTVKC 407

RESULT 14
O6JD66
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```
ID O6JD66 PRELIMINARY; PRT; 5072 AA.
AC O6JD66;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Eukaryotic initiation factor-2 alpha kinase-A.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OC NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14989696;
RA Sullivan W.J. Jr., Nazareian J., Bhatti M.M., Wek R.C.;
RT "Parasite-specific eIF2 (eukaryotic initiation factor-2) kinase
required for stress-induced translation control."
RL Biochem. J. 380:523-531(2004).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY518936; AAS48463.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0003743; F:translation initiation factor activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR Pfam; PF00069; Kinase; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; initiation factor; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 5072 AA; 541692 MW; 00FD7BD9B848E58 CRC64;

Query Match 7.5%; Score 115.5; DB 2; Length 5072;
Best Local Similarity 25.9%; Pred. No. 42;
Matches 68; Conservative 22; Mismatches 92; Indels 81; Gaps 12;

QY 61 PARSGLELLERNGCGESNRLGLQLVLAHDLPLAKRRRPVS---PERYS 116
D 4319 RRRSLPLSL-----SCGSRSSRE-----ERQULERRRRPRTSRYSYA 4357
QY 117 YGTSSSSKRTG-----SCRRRSSSSANSQCGQWETGSPPTKRRRRSGRPSG 167
D 4358 GREGRSRPTDGMWAKETLRKSARGRRSSSYSEKTDLRSGWCPCKQSVAPHSPT 4417
QY 168 ARRRRGAPAPQOQ---SEPARPS-----SEKVTCDIRLRVRAVEYCEHGPALGQVA 218
D 4418 AKRRAFSTIPALKEREHEHEEFPSWPFQEDSDSLTGKMIK---ESNDH-----AAR 4468
QY 219 SRRPQALARQLDVFGQATAVLSRDLGVCIDIKFSELSYDAPFGDVLGSA---LLQA 274
D 4469 ARAHRLCCSDGSFSDACTYTRNGS-----AFWG---AGAEAPRSIQV 4510
QY 275 LRGVFL-----TEALREAVGR 290
D 4511 SGGCTCRMTSGEETGPREASGR 4533

RESULT 15
O73TU6 PRELIMINARY; PRT; 381 AA.
ID O73TU6
AC O73TU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein
GN Ordered locus names=MAP3722;
OS Mycobacterium paratuberculosis.
```

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxId=1770;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K10;  
 RA Li U., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.,  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE017240; AAS06272.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 381 AA; 41951 MW; 987D2F6155BF5E8 CRC64;

Query Match 7.4%; Score 114.5; DB 2; Length 381;  
 Best Local Similarity 31.4%; Pred. No. 2.3;  
 Matches 58; Conservative 14; Mismatches 58; Indels 55; Gaps 11;  
 QY 53 PGAAGGLAPARSGL-ELLLELERRGCGGSNRLGQLRLVLRKHDLPHLAKRRPV 111  
 DB 25 PQAAGRRAARVALGDPADRRRG--GEPG-----HHALPH--RMRAVRG 67  
 QY 112 PERVSYGTSSSKRTGSCRRRRSSSSANSOQGWETGSPPTKQRGRGRPGGARR 171  
 DB 68 PGRRGSGT-----RRDPRLARRGRSAALASPARG-----APNRARRACRP---RRR 112  
 QY 172 RRG--APAAPQOQ-----SEPARPSSEKVTCDIRLRVRAEYCEHGPALEQVASRRP 222  
 DB 113 CRGPDAPAGPRHRVRPRPATREAAARAAG-----RARRPHC---PADGDDLQRGR 159  
 QY 223 QALAR 227  
 DB 160 LGRAR 164

Search completed: February 12, 2005, 16:29:59  
 Job time : 76 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 11:02:37 / Search time 2501 Seconds  
(without alignments)  
13834.635 Million cell updates/sec

Title: US-10-030-271-1

Perfect score: 909

Sequence: 1 atggcgcataccggtcgac.....tcagtcgtgagtgagtcgac 909

Scoring table: IDENTITY\_NTC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	907.4	99.8	1053	3	CR604307 full-length
2	907.4	99.8	1860	3	CR593642 full-length
3	907.4	99.8	1866	3	CR619301 full-length
4	907.4	99.8	1894	3	CR625070 full-length
5	847.2	93.2	1046	5	EX342837 EX342837
6	822.8	90.5	1021	5	EX384448 EX384448
7	802	88.2	1091	5	EX374729 EX374729
8	773.6	85.1	951	5	EX375652 EX375652
9	760.4	83.7	800	4	EX375652 EX375652
10	738.4	81.2	837	4	EX375652 EX375652
11	727.4	80.0	1089	5	EX375652 EX375652
12	711.2	78.0	820	5	EX375652 EX375652
13	704.2	77.5	1090	5	EX375652 EX375652
14	680.8	74.9	872	4	EX375652 EX375652
15	678.8	74.7	874	1	EX375652 EX375652
16	653	71.8	924	5	EX375652 EX375652
17	639.6	70.4	931	5	EX375652 EX375652
18	624.2	68.7	718	4	EX375652 EX375652
19	607.8	66.9	1042	5	EX375652 EX375652
20	605	66.6	926	4	EX375652 EX375652
21	596.4	65.3	1641	3	EX375652 EX375652
22	593.2	65.3	1025	6	EX375652 EX375652
23	588.8	64.6	4598	4	EX375652 EX375652
24	586.8	64.6	878	4	EX375652 EX375652

25	582.8	64.1	905	4	BI910528
26	582.8	64.1	927	4	BG251151
27	582.8	64.1	947	4	BI910416
28	582.8	64.1	1586	3	CR590827
29	582.4	64.1	1131	2	BI907024
30	582.4	64.1	1131	2	BE907425
31	582.4	64.1	1510	3	CR599685
32	582.4	64.1	1510	3	BM908148
33	581.4	63.9	655	7	CK429257
34	581.2	63.9	1051	5	BO073197
35	581.2	63.9	1161	5	BU902131
36	580.8	63.9	644	7	CR373290
37	579.6	63.8	678	7	CR373294
38	579.6	63.8	783	5	BU602002
39	577.4	63.5	826	6	CB991766
40	574	63.1	938	5	BU507654
41	572.4	63.0	671	7	CR373287
42	570.6	62.8	780	6	CB994488
43	570.4	62.8	931	5	EX381775
44	569.4	62.6	993	4	BM559141
45	562.8	61.9	1017	3	AK011713

#### ALIGNMENTS

RESULT 1  
LOCUS CR604307 1053 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CS0DL006YL09 of B cells (Ramos cell line)  
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR604307.1 GI:50485114  
VERSION HRC; CNGSLT\_CDNA.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue

REFERENCE  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr

COMMENT  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of invitrogen.  
FEATURES  
source location/Qualifiers  
1..1053  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cfeature="CS0DL006YL09"  
/cfeature type="B cells (Ramos cell line) Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

#### ORIGIN

Query Match 99.8%; Score 907.4; DB 3; Length 1053;  
Best Local Similarity 99.8%; Pred. No. 2.9e-189;  
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGCTGACCCCGGCGCTGCTGGAGAGATAGCGCTGACTAC 60  
DB 99 ATGGCGCTATCCGGCTGACCCCGGCGCTGCTGGAGAGATAGCGCTGACTAC 158

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QY 61 TACGGATCTGTGCTTACCGTATGTTGAGGTGTGTGGCGGCACTGACCGAGTGC 120
DB 159 TACGGATCTGTGCTTACCGTATGTTGAGGTGTGTGGCGGCACTGACCGAGTGC 218
QY 121 GAGCTGAGACTCTGTGCTTGTGCTGAGTGAAGGCTCTGTGGCGGCGGCACTGAGCC 180
DB 219 GAGCTGAGACTCTGTGCTTGTGCTGAGTGAAGGCTCTGTGGCGGCGGCACTGAGCC 278
QY 181 CGGGCCCGCAGCGGCTTAGAGCTCTGTGAGTGTGAGCGCGCGGCACTGAGCGGCGAG 240
DB 279 CGGGCCCGCAGCGGCTTAGAGCTCTGTGAGTGTGAGCGCGCGGCACTGAGCGGCGAG 338
QY 241 AGCAACTGTGGCTGTGTGGGCACTCTGTGGCTGTGGCGGCGGCACTGAGCGGCGAG 300
DB 339 AGCAACTGTGGCTGTGTGGGCACTCTGTGGCTGTGGCGGCGGCACTGAGCGGCGAG 398
QY 301 CAGCTGGCGGCAAGCGGCGGCGGCACTGTGCTGAGAAAGCTATGATGAGCACTTCC 360
DB 399 CAGCTGGCGGCAAGCGGCGGCGGCACTGTGCTGAGAAAGCTATGATGAGCACTTCC 458
QY 361 AGCTCTTCAAGAGAGCAGAGGGTAGCTGCTGCGCTGCGGCACTGAGCACTTCTGCA 420
DB 459 AGCTCTTCAAGAGAGCAGAGGGTAGCTGCTGCGCTGCGGCACTGAGCACTTCTGCA 518
QY 421 AATTCTCAGCAGGCTCAGTGGAGACAGGCTCCCCCAACCAAGCGGCGAGCT 480
DB 519 AATTCTCAGCAGGCTCAGTGGAGACAGGCTCCCCCAACCAAGCGGCGAGCT 578
QY 481 CGGGGCGGCGGCGGCTGAGTGTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 579 CGGGGCGGCGGCGGCTGAGTGTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 638
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DB 639 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAAGGCAAAAGTGAAGCTGTGACATCCGCTC 698
QY 601 CGGGTTCAGCAGAGTATCTGCGAGCATGTGGGCTGAGCGAGGCGGCTGAGATCCGCG 660
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QY 781 GCTTCTGTGGGCGGCTAATCTGAGTGTGCGGCTGTGCGGCGGCGGCGGCGGCGGCGG 840
DB 879 GCTTCTGTGGGCGGCTAATCTGAGTGTGCGGCTGTGCGGCGGCGGCGGCGGCGGCGG 938
QY 841 ACTGAGGCGGCTGAGAGGCTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900
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QY 901 GAGGCTGAC 909
DB 999 GAGGCTGAC 1007

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REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1. (bases 1 to 1860)
Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@life.techn.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1860)
Genoscope.
Direct Submission
Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: sequefgenoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK010YK16"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Best Local Similarity 99.9%; Pred. No. 3e-189;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGCGCTATCGGAGTCAGCCCGGCGGCTGCTGAGAGAGATGCTGAGTAC 60
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QY 61 TACGGATCTGTGCTTACCGTATGTTGAGGTGTGTGGCGGCAACTGACCGAGTGC 120
DB 121 TACGGATCTGTGCTTACCGTATGTTGAGGTGTGTGGCGGCAACTGACCGAGTGC 190
QY 121 GAGCTGAGACTCTGTGCTTCTGTGATGATAGCTCTGTGGCGGCGGCGGCGGCTTACCC 180
DB 191 GAGCTGAGACTCTGTGCTTCTGTGATGATAGCTCTGTGGCGGCGGCGGCGGCTTACCC 250
QY 181 CGGGCCCGCAGGCGGCTGAGACTCTGTGAGTGTGAGCGGCGGCGGCGGCGGCGGCGG 240
DB 251 CGGGCCCGCAGGCGGCTGAGACTCTGTGAGTGTGAGCGGCGGCGGCGGCGGCGGCGG 310
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DB 311 AGCAACTGTGCGGCTGTGGGCACTCTGTGCGGCTGTGCGGCGGCGGCGGCGGCGGCGG 370
QY 301 CACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 371 CACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 430
QY 361 AGCTCTTCAAGAGAGCAGAGGTAAGTGTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 420
DB 431 AGCTCTTCAAGAGAGCAGAGGTAAGTGTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGG 490
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DB 491 AATTCTCAGCAGGCTCAGTGGAGAGCAGGCTCCCCCAACCAAGCGGCGAGCGGAGT 550
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DB 551 CGGGGCGGCGGCGGCTGAGTGTGCGGAGAGCGGCGGCGGAGAGAGGCGGCGGCGGCGG 610
QY 541 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAGAGCAAAAGTGAAGCTGTGACATCCGCTC 600
DB 611 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAGAGCAAAAGTGAAGCTGTGACATCCGCTC 670

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RESULT 2
LOCUS CR53642 1860 bp mRNA linear HTC 21-JUN-2004
DEFINITION full-length cDNA clone CSODK010YK16 of Hela cells Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR53642
VERSION CR53642.1 GI:50474449
KEYWORDS HTC; cDNA;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE 1 (bases 1 to 1894)  
 AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.  
 JOURNAL Full-length cDNA libraries and normalization  
 REMARK Unpublished  
 Contact : Feng Liang Email : fliang@life.techn.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue  
 Redwood City, CA 94063  
 2 (bases 1 to 1894)  
 REFERENCE Genoscope.  
 AUTHORS Direct Submissions  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.

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 source Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /clone="CS00C001YCI8"  
 /issue\_type="Neuroblastoma Cot 25-normalized"  
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ORIGIN  
 Query Match 99.8%; Score 907.4; DB 3; Length 1894;  
 Best Local Similarity 99.9%; Pred. No. 3e-189; 1; Indels 0; Gaps 0;  
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGCGCTATCCGGGTGACACCCGCGCCCGTGTGGAGAGAGATGCTGACACTAC 60  
 89 ATGGCGCTATCCGGGTGACACCCGCGCCCGTGTGGAGAGAGATGCTGACACTAC 148  
 61 TACGGAGATCTGCTTACACCTGATGTTGAGAGTGTGGGCGGCACTGACCCAGATC 120  
 149 TACGGAGATCTGCTTACACCTGATGTTGAGAGTGTGGGCGGCACTGACCCAGATC 208  
 121 GAGCTGAGACTCTGCTGCTTCTGCTGATGATGAGAGCTCTGGGCGGCGGAGAGCTTAC 180  
 209 GAGCTGAGACTCTGCTGCTTCTGCTGATGATGAGAGCTCTGGGCGGCGGAGAGCTTAC 268  
 181 CGGGCCCGGAGCGGCTTACAGCTCTGCTGATGATGAGAGCTCTGGGCGGCGGAGAGCT 240  
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 329 AGCAACCTGCGGCTGCTGGGCGCACTCTGCGGTGCTGCGGCGGCGGAGAGCTTAC 388  
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 389 CACTGTCGCGGAGCGGCGGCGGCGGAGTGTCTCCAGAAAGCTATAGTATGACCACTCC 448  
 361 AGCTTTTCAAAAGAGACAGAGGGTACCTGCTGCGGAGTCAAGCACTTCTGCA 420  
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 509 AATTCTTCAACAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 568  
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 569 CGGGCGGCGGAGCGGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628  
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 629 CAGCACTCAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 688  
 601 CGGGTTTCAAGAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

DB 689 CGGGTTTCAAGAGAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 748  
 661 CGGGCCCGGAGCGGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
 749 CGGGCCCGGAGCGGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808  
 721 TCAAGGAG 780  
 809 TCAAGGAG 868  
 781 GCTTCTGAGGAG 840  
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 901 GAGGCTGAC 909  
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RESULT 5  
 LOCUS BX342837 1046 bp mRNA linear EST 07-APR-2004  
 DEFINITION BX342837 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
 Homo sapiens cDNA clone CS00D1006Y109.5-PRIME, mRNA sequence.  
 ACCESSION BX342837  
 VERSION BX342837.2 GI:46266793  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1046)  
 AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.  
 JOURNAL Full-length cDNA libraries and normalization  
 COMMENT Unpublished (2001)  
 On May 1, 2003 this sequence version replaced gi:30313128.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 9074.r

For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?e=CS00D1006Y109.5-PRIME.9074.r.  
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 source Location/Qualifiers  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN  
 Query Match 93.2%; Score 847.2; DB 5; Length 1046;  
 Best Local Similarity 98.1%; Pred. No. 5.2e-176;  
 Matches 888; Conservative 9; Mismatches 3; Indels 5; Gaps 4;

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QY 1 ATGGCGCTATCCGGGTGACACCCCGCCCGTGTGGAGAGATGATGCTGACTAC 60
DB 99 ATGGCGCTATCCGGGTGACACCCCGCCCGTGTGGAGAGATGATGCTGACTAC 158
QY 61 TACGGGATGCTGTGCTTCAACCTATGTTGAGTGTGGCGGCACTGACCGAGTGC 120
DB 159 TACGGGATGCTGTGCTTCAACCTATGTTGAGTGTGGCGGCACTGACCGAGTGC 218
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DB 219 GAGCTGAGAGTCTGTGCTTCTGTGATGATGAGCTCTGTGGCGCCGCGGAGCTTAC 277
QY 181 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGATGAGCGCGCGGAGCTGCGGAG 240
DB 278 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGATGAGCGCGCGGAGCTGCGGAG 337
QY 241 AGCAACCTGCGGTGTGTGGGGCAATCTCTGCGGTGTGTGGCGCGGAGCTGCGG 300
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QY 301 CACCTGAGCGGAGCGGCGGCGGAGCTCTCAAGAGCTATGATGAGCACTTCC 360
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QY 361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 456 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 515
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DB 516 AATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 575
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DB 756 CGGCCCCAGGCGGTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 815
QY 721 TCAAGGAGAGCTGTGCTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 816 TCAAGGAGAGCTGTGCTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 875
QY 781 GCTTTCTT-GGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
DB 876 GCTTTCTTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 935
QY 840 GACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
DB 936 GACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 994
QY 900 TGAGG 904
DB 995 TGAGS 999

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RESULT 6
LOCUS BX384448 1021 bp mRNA linear EST 23-APR-2004
DEFINITION BX384448 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
ACCESSION BX384448
VERSION BX384448.2 GI:46557783
KEYWORDS EST.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1021)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30440338.
Contract: Genoscope
Genoscope - Centre National de Sequenage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9074.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DK010BF08QPlc=9074.f.
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Location/Qualifiers
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/cell_line="HELA CELLS COT 25-NORMALIZED"
/clone_lib="Homo sapiens, HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match 90.5%; Score 822.8; DB 5; Length 1021;
Best Local Similarity 97.0%; Pred. No. 1,2e-170;
Matches 877; Conservative 12; Mismatches 9; Indels 6; Gaps 5;
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DB 71 ATGGCGCTATCCGGGTGACACCCCGCCCGTGTGGAGAGATGATGCTGACTAC 130
QY 61 TACGGGATGCTGTGCTTCAACCTATGTTGAGTGTGGCGGCACTGACCGAGTGC 120
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QY 121 GAGCTGAGAGTCTGTGCTTCTGTGATGATGAGCTCTGTGGCGCCGCGGAGCTTAC 180
DB 191 GAGCTGAGAGTCTGTGCTTCTGTGATGATGAGCTCTGTGGCGCCGCGGAGCTTAC 249
QY 181 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGATGAGCGCGCGGAGCTGCGGAG 240
DB 250 CGGGCCCGGAGCGGCTTGAAGCTCTGTGATGATGAGCGCGCGGAGCTGCGGAG 309
QY 241 AGCAACCTGCGGTGTGTGGGGCAATCTCTGCGGTGTGTGGCGCGGAGCTGCGG 300
DB 310 AGCAACCTGCGGTGTGTGGGGCAATCTCTGCGGTGTGTGGCGCGGAGCTGCGG 369
QY 301 CACCTGAGCGGAGCGGCGGCGGAGCTCTCAAGAGCTATGATGAGCACTTCC 360
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QY 361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 428 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
QY 420 AATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
DB 488 AATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
QY 480 TCGGGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539

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Db      548 TCGGGGCCCCCGAGGTGTGTGTCAGAGCGCGCGGAGAGGGGCCCGACCGCCACCCCA 607
Qy      540 GGAAGAGTGAAGCCCGCCAGACCTTCTCTGAAGGCAAGTGAAGTGAACATCCGGCT 599
Db      608 GCGAGGTGAAGCCCGCCAGACCTTCTCTGAAGGCAAGTGAAGTGAACATCCGGCT 667
Qy      600 CGGGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 659
Db      668 CGGGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 727
Qy      660 GCGGCCCCCAGGCTGTGCGCGGCACTGGAGCTGTGTTGGGAGGCGCAGTGTGCG 719
Db      728 GCGGCCCCCAGGCTGTGCGCGGCACTGGAGCTGTGTTGGGAGGCGCAGTGTGCG 787
Qy      720 CTCAGAGGAGCTGGGCTGTGTTGTGATCAATCAAGTTCAGAGCTCTCTATCTGA 779
Db      788 CTCAGAGGAGCTGGGCTGTGTTGTGATCAATCAAGTTCAGAGCTCTCTATCTGA 847
Qy      780 CGCTTCTGGGCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 839
Db      848 CGCTTCTGGGCGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 906
Qy      840 GACTGAGGCTTCGAGAGGCTGTGCGCGGCGGAGCTGTGTTGGGAGGCGCAGTGTGCG 899
Db      907 GACTGAGGCTTCGAGAGGCTGTGCGCGGCGGAGCTGTGTTGGGAGGCGCAGTGTGCG 965
Qy      900 TGAG 903
Db      966 TRAG 969

RESULT 7
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LOCUS      BX374729 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION      BX374729 cDNA clone CS0DC001Y18 5-PRIME, mRNA sequence.
ACCESSION      BX374729
VERSION      BX374729.2 GI:46557336
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Li,W.B., Gruber,C., Jessee,J. and Polyes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30438519.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9074.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DC001B090P1&c=9074.r.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/issue="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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FEATURES
source

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## ORIGIN

Query Match 88.2%; Score 802; DB 5; Length 1091;  
 Best Local Similarity 96.8%; Pred. No. 4,7e-166;  
 Matches 881; Conservative 10; Mismatches 11; Indels 8; Gaps 7;

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Qy      1 ATGGCGCTATCCGGGTGACACCCGCGCCCGTGTGAGAGAGATGATGCTTGAATAC 60
Db      89 ATGGCGCTATCCGGGTGACACCCGCGCCCGTGTGAGAGAGATGATGCTTGAATAC 148
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Db      209 GAGCTGAGAGCTCTGAGCTTCTGCTGATGAGAGTCTCTGAGCGCCGCGAGGCTTAC 267
Qy      181 CGGGCCCCGAGCGGCTTGAAGCTCTGCTGAGAGTGAAGCGCGCGGAGCTGCGCGAG 240
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Qy      241 AGCAACCTGCGGCTGCTGAGGAGTCTCTGAGAGTGAAGCGCGCGGAGCTGCGCGAG 300
Db      328 AGCAACCTGCGGCTGCTGAGGAGTCTCTGAGAGTGAAGCGCGCGGAGCTGCGCGAG 387
Qy      301 CACTTGAGCGGAGAGCGGCGCGGAGTGTCTCCAGAACGCTATAGTATGAGCACTTC 360
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Qy      421 AATTCTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 480
Db      506 AATTCTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 565
Qy      481 CGGGCCCCGAGCGGCTGAGTGTGTCAGAGCGGCGCGGAGAGAGGAGCGCCAGCCG 540
Db      566 CGGGCCCCGAGCGGCTGAGTGTGTCAGAGCGGCGCGGAGAGAGGAGCGCCAGCCG 624
Qy      541 CAGCAGTGAAGCCCGCCAGACCTTCTCTGAAGCAAGTGAAGTGAAGTGAAGTGAAG 600
Db      625 CAGCAGTGAAGCCCGCCAGACCTTCTCTGAAGCAAGTGAAGTGAAGTGAAGTGAAG 684
Qy      601 CGGGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 660
Db      685 CGGGTTCAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 744
Qy      661 CGGCCCCAGGCGCTGCGCGGCGGAGCTGACGTGTTGGGAGGCGCAGTGTGCGCG 720
Db      745 CGGCCCCAGGCGCTGCGCGGCGGAGCTGACGTGTTGGGAGGCGCAGTGTGCGCG 802
Qy      721 TCAAGGAGCTGGGCTGTGTTGTGATCAATCAAGTTCAGAGCTCTCTATCTGAGC 780
Db      803 TCAAGGAGCTGGGCTGTGTTGTGATCAATCAAGTTCAGAGCTCTCTATCTGAGC 862
Qy      781 GCCTTCT-GGGGGAGTACTGAGTGGGCGCTGAGAGGCGCTGAGGCGGCGGTGTTCT 839
Db      863 GCCTTCTGGGGGAGTACTGAGTGGGCGCTGAGAGGCGCTGAGGCGGCGGTGTTCT 922
Qy      840 GACTGAGGCTTCGAGAGGCTGTGCGCGGAGGCTGTTCCGCTGTGCTGAGTGTGA 899
Db      923 GACTGAGGCTTCGAGAGGCTGTGCGCGGAGGCTGTTCCGCTGTGCTGAGTGTGA 981
Qy      900 TGAGGCTGAC 909
Db      982 TGAGGCTGAC 991

RESULT 8
BX375652

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LOCUS      BX375652      951 bp      mRNA      linear      EST 26-APR-2004
DEFINITION BX375652 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC015YJ24 5-PRIME, mRNA sequence.
ACCESSION  BX375652
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 951)
            Li, W.-B., Gruber, C., Jesses, J., and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            On May 8, 2003 this sequence version replaced gi:30448429.
COMMENT    Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
            Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            9074.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdnas=CS0DC015DE120P1&c=9074.r.

FEATURES             source
     source
     1..951
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="CS0DC015YJ24"
     /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
     /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
     /note="1st strand cDNA was primed with a NotI-oligo(dT)
     primer. Five prime end enriched, double-strand cDNA was
     digested with Not I and cloned into the Not I and EcoR V
     sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      85.1%; Score 773.6; DB 5; Length 951;
Best Local Similarity 98.0%; Pred. No. 8.3e-160;
Matches 833; Conservative 2; Mismatches 8; Indels 7; Gaps 5;

QY      1 ATGGCGCTATCCGGGTGACACCCCGCCCGTGTGGAGAGAGATGAGTGCCTTGACTAC 60
DB      76 ATGGCGCTATCCGGGTGACACCCCGCCCGTGTGGAGAGAGATGAGTGCCTTGACTAC 135
QY      61 TAGCGGATGCTGTGCTTCAACCGATGATGAGGTGGGCGGCAACTGACCGAGTGC 120
DB      136 TAGCGGATGCTGTGCTTCAACCGATGATGAGGTGGGCGGCAACTGACCGAGTGC 195
QY      121 GAGCTGAGAGTCTCTGAGCTTCTGCTGATGAGGCTCTTGCGCGCGCGAGGCTTAC 180
DB      196 GAGCTGAGAGTCTCTGAGCTTCTGCTGATGAGGCTCTTGCGCGCGCGAGGCTTAC 254
QY      181 CGGGCCCGGAGCGGCTTGAAGCTCTGCTGAGAGCTGAGAGCGCCCGGCGAGTGGCGAG 240
DB      255 CGGGCCCGGAGCGGCTTGAAGCTCTGCTGAGAGCTGAGAGCGCCCGGCGAGTGGCGAG 314
QY      241 AGCAACTGCGGCTGCTGGGGCAACTCTGCGGCTGCTGGCGCGCAAGCACTGCTGCGG 300
DB      315 AGCAACTGCGGCTGCTGGGGCAACTCTGCGGCTGCTGGCGCGCAAGCACTGCTGCGG 374
QY      301 CACCTGCGCGCAAGCGCGCGCGCAAGTGTCTCCAGAACGCTATAGCTATGCACTTCC 360
DB      375 CACCTGCGCGCAAGCGCGCGCGCAAGTGTCTCCAGAACGCTATAGCTATGCACTTCC 432
QY      361 AGCTCTTCAAGAGAGAGAGAGAGTACCTGCTGCGCGCTGCGGAGTCAAGAGTTTTCGA 420
DB      433 AGCTCTTCAAGAGAGAGAGAGAGTACCTGCTGCGCGCTGCGGAGTCAAGAGTTTTCGA 492

RESULT  9
BG685173
LOCUS      BG685173      800 bp      mRNA      linear      EST 01-MAY-2001
DEFINITION BG685173 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764639 5',
            mRNA sequence.
ACCESSION  BG685173
VERSION    BG685173.1 GI:13916570
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 800)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LNCM622 row: d column: 16
            High quality sequence stop: 794.
            Location/Qualifiers
            1..800
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4764639"
            /tissue_type="primary B-cells from tonsils (cell line)"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 48"
            /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
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QY 421 AATTCTCAGCAGGGTCAGTGGGAGCAGAGTCCCCCAACCAAGCGGACGGCGAGT 480

Db 460 AATTCTCAGCAGGGTCAGTGGGAGCAGAGTCCCCCAACCAAGCGGACGGCGAGT 518

QY 481 CGGGGCGGGCCAGTGTGTGTCCAGACGGCGCGGAGAGGGGGCCCAAGCGCA -CCCA 539

Db 519 CGGGGCGGG - CCAGTGTGTGTCCAGACGGCGGGGAGAGGGGGCCCAAGCGCA 577

QY 540 GCAGGAGTCAGAGCCCCCGCAGACTTCTCTGAAGGCAAGTGACTGTGACTCCGGCT 599

Db 578 GCAGGAGTCAGAGCCCCCGCAGACTTCTCTGAAGGCAAGTGACTGTGACTCCGGCT 637

QY 600 CCGGGTTGAGCAGAGTACTCGGAGCA -TGGGCGAGCCCTTGAGAGAGGGCGT -GGCATCC 657

Db 638 CCGGGTTGAGCAGAGTACTCGGAGCATTTGGGCGAGCCCTTGAGAGAGGGCGCTGGGCATCC 697

QY 658 CGGCGGGCCCAAGCCACTGGCGCGGAGCTGACGTGTTTGGGCAAGCCAGCGAGTGTG 717

Db 698 CGGCGGGCCCAAGCCACTGGCGCGGAGCTGACGTGTTTGGGCAAGCCAGCGAGTGTG 757

QY 718 CGCTCAAGGAGACTTGGGCTCTGTGTGTTGTGACATCAAGTTCTCAGAGCTCTCTATGTG 777

Db 758 CGCTCAAGGAGACTTGGGCTCTGTGTGTTGTGACATCAAGTTCTCAGAGCTCTCTATGTG 817

QY 778 GACGCTTCTGGGCGGACTA 797

Db 818 GACGCTTCTGGGCGGACTA 837

RESULT 11	
BM925969	
LOCUS	BM925969
DEFINITION	1089 bp mRNA linear EST 12-MAR-2002
	AGENCOURT_6649774 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5764272
	5', mRNA sequence.

ACCESSION	BM925969	GI:1937636
VERSION	BM925969.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 1089)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

**FEATURES**  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.jnl.gov>  
 Plate: ILNL12817 row: h column: 01  
 High quality sequence start: 14  
 High quality sequence stop: 586  
 Location/Qualifiers

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/lab_host="DH10B"
/clone_11b="NH MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber

```

ORIGIN  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

Query Match	80.0%;	Score 727.4;	DB 5;	Length 1089;
Best Local Similarity	95.7%;	Pred. No. 1.2e-14;		
Matches 780; Conservative	0;	Mismatches 31;	Indels 4;	Gaps 3;

OY	1	TTGCGCATATCCGGGTGACCCCGGCCCGTGGAGAGAGATGATGCTGTGATAC	60
Db	71	ATGCGCTATCCGGGTGACCCCGGCCCGTGGAGAGAGATGATGCTGTGATAC	130
OY	61	TACGGAGTCTGTGCTTCAACCGTATGTTGAGGTGTTGGCGGGCAACTGACCGAGTGC	120
Db	131	TACGGAGTCTGTGCTTCAACCGTATGTTGAGGTGTTGGCGGGCAACTGACCGAGTGC	190
OY	121	GAGCTGGAAGCTCTTGGGCTTTCTGTCTGGATGAGGCTCTGGCGCGCGGAGGCTTAGCC	180
Db	191	GAGCTGGAAGCTCTTGGGCTTTCTGTCTGGATGAGGCTCTGGCGCGCGGAGGCTTAGCC	250
OY	181	CGGGCCCGCAGCGGCTTAGAGCTCTGTGAGCTTGAGCGCCCGCGGCAAGTGGCGGAG	240
Db	251	CGGGCCCGCAGCGGCTTAGAGCTCTGTGAGCTTGAGCGCCCGCGGCAAGTGGCGGAG	310
OY	241	AGCAACCTGCGGCTGTGGGGCAACTCTCTGCGGTGGCTGGCCGCACAGACTTGTCTCG	300
Db	311	AGCAACCTGCGGCTGTGGGGCAACTCTCTGCGGTGGCTGGCCGCACAGACTTGTCTCG	370
OY	301	CACCTGGCGGCAAGCGGCGCGCGGCGCAAGTCTCAGAAAGCTTAGCTTAGGCACTCC	360
Db	371	CACCTGGCGGCAAGCGGCGCGCGGCGCAAGTCTCAGAAAGCTTAGCTTAGGCACTCC	430
OY	361	AGCTCTTCAAGAAGAGAGAGAGGAGTAGCTGCGCGTGGCGGCAAGTGAAGTCTTGCA	420
Db	431	AGCTCTTCAAGAAGAGAGAGGAGTAGCTGCGCGTGGCGGCAAGTGAAGTCTTGCA	490
OY	421	AATTTCTAGCAGGGGTCAAGTGGAGACAGAGCTCCCCCACAACAGCGGACGGCGGAGT	480
Db	491	AATTTCTAGCAGGGGTCAAGTGGAGACAGAGCTCCCCCACAACAGCGGACGGCGGAGT	550
OY	481	CGGGGCGGGCCCAATGATGTTGGTCCAGACCGCGGGGAGAGGGGGCCAGCGGCACTCCAG	540
Db	551	CGGGGCGGGCCCAATGATGTTGGTCCAGACCGCGGGGAGAGGGGGCCAGCGGCACTCCAG	610
OY	541	CAGCAGTCAGAGCCCGGCAAGCTTCTCTTGAAAGCAAAAGTGAACCTGTGACATCCGGCTC	600
Db	611	CAGCAGTCAGAGCCCGGCAAGCTTCTCTTGAAAGCAAAAGTGAACCTGTGACATCCGGCTC	670
OY	601	CGGGTTGAGCAGAGTACTGCGAGCAITGGGCGACGCTTGGAGCAGAGGGGTGGATCCGG	660
Db	671	CGGGTTGAGCAGAGTACTGCGAGCAITGGGCGACGCTTGGAGCAGAGGGGTGGATCCGG	730
OY	661	CGGGCCCAAGGGGCTGGGGCGGCACTGGAGAG - TGTTTTGGGAGGCGAACCGGAGTG - CTGC	718
Db	731	GGGGCCCAAGGGGCTGGGGCGGCACTGGAGAGCTGTGGGGAGGCGAACCGGAGTGCTGC	790
OY	719	GCTCAAGGGAAGCTGGGCT - CTGTGTGTTTGGACATCAAGTTCTTCAGAGCTCTCTATCT	776
Db	791	GCTCAAGGGAAGCTGGGGTCTCTGGGCTTGGGCACTAAGTTCTTCAAGCTCTCAAAATT	850
OY	777	GGAGCGCTTCTGGGCGCACTACTGAGTGGCGCC	811
Db	851	GGAACTCTTCTGGGCGCACTACTGAACTGGCCGC	885

RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
BP158001	BP158001	BP158001 full-length enriched swine CDNA library, adult spleen Sus scrofa cDNA clone SPL010019D2 5', mRNA sequence.	BP158001	BP158001.1	GI:40407474
				EST.	



SOURCE	Sus scrofa (pig)
ORGANISM	Sus scrofa
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE	1 (bases 1 to 820)
AUTHORS	Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinaka,H., Okumura,N., Hamashima,N. and Awata,T.
TITLE	PEEB (pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
JOURNAL	Nucleic Acids Res. 32 (1), D484-D488 (2004)
COMMENT	Contact: Hirohide Uenishi

Email: huenhish@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and SRAFF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13  
and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

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FEATURES
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/db_xref="taxon:9823"
/clone="SPR01001SD12"
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/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
spleen"

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## ORIGIN

Query Match	78.2%	Score 711.2;	DB 5	Length 820;
Best Local Similarity	92.6%	Pred. No. 4.5e-146;		
Matches 759;	Conservative 0;	Mismatches 58;	Indels 3;	Gaps 1;

[illegible]

OY	521	AGGCCCCAGCCGACCCACAGAGAGTCAAGGCCCGACGACTTTCCTGAAAGCAAG	580
Db	481	GGGGCCAGCCGACACCCAGCAAGCAAGAGCCAGCCAGGCCACTTCAGAAAGCAAG	540
OY	581	TGACCTTGACATCCGAGCTCCGAGGTTCAGACAGAGTACTGCAGCATGGCCAGCTTGG	640
Db	541	TGACCTTGATATCCGAGCTCAGGGTCAGAGCAGAGTACTGTGAGATGGGCCAGCTTGG	600
OY	641	AGCAGGGCGTGGCATCCCGCGGCCCCACAGGCGCTGGCCGCGCACTGATGTTTGGGC	700
Db	601	AGCAGGGCGTGGCATCCCGCGGCCCCACAGGCACTGGCCGCGCAGCTGATGTTTGGGC	660
OY	701	AGGCAACCGCAGTGTCTGGCTCAAGAGCACTGGGCTCTGTGGTTTGTACATCAAGTTCT	760
Db	661	AGGCTTACAGCAGTGTCTGGCTCAGAGGACCTGGGCTCTGTGGTTCATCAAGTTCT	720
OY	761	CAGAGCTCTCTATCTGGAGGCTTCTTGGGGGGACTACCTAGTAGGCGCCCTGGCTGCAGG	820
Db	721	CAGAGCTCTCTATCTGGAGGCTTCTTGGGGTGTACTACCTAGTAGGGGCGCTGGCTGCAGG	780
OY	821	CCCTGCGGGGCGTGTCTCTGACTAGAGCCCTGCAGAGAGC	860
Db	781	CCCTGCGGGGCGTGTCTCTGACTAGAGCTCTGCAGAGAGC	820

RESULT 13	
LOCUS	BM920838
DEFINITION	BM920838 1090 bp mRNA linear EST 12-MAR-2002
ACCESSION	AGNCNCOURT 6706034 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752092
VERSION	5', mRNA sequence.
KEYWORDS	BM920838 BM920838.1 GI:19371217
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 1090)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: cgabds-rc@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
plate: LLAM12785 row: 1 column: 13  
High quality sequence stop: 625.  
location/label: 625

**Sou**

## Source

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/clone_1lb="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

```

### Query Match

77.5%; Score 704.2; DB 5; Length 1090,

Best Local Similarity 95.5%; Pred. No. 1.6e-144;  
Matches 780; Conservative 0; Mismatches 28; Indels 9; Gaps 5;

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QY 1 ATGGCGCTATCCGGGTGACCCCGGCGCGCTGCTGGAGAGAGATGAGTGCCTGAGACTAC 60
Db 102 ATGGCGCTATCCGGGTGACCCCGGCGCGCTGCTGGAGAGAGATGAGTGCCTGAGACTAC 161
QY 61 TACGGAGATGCTGTGCTTCAACCTATGATGAGTGTGGCGGCACTGACCGAGTGC 120
Db 162 TACGGAGATGCTGTGCTTCAACCTATGATGAGTGTGGCGGCACTGACCGAGTGC 221
QY 121 GAGCTGAGAGCTTCTGCTTCTGCTGATGAGGCTCTTGCGCGCGCGGAGGCTTACCC 180
Db 222 GAGCTGAGAGCTTCTGCTTCTGCTGATGAGGCTCTTGCGCGCGCGGAGGCTTACCC 281
QY 181 CGGGCCCGCAGCGGGCTGAGAGCTCTGCTGAGAGTGAAGCGCGCGGCACTGGCGGAG 240
Db 282 CGGGCCCGCAGCGGGCTGAGAGCTCTGCTGAGAGTGAAGCGCGCGGCACTGGAGCAG 341
QY 241 AGCAACCTGCGGCTGTGGGCAACTCTCTGCGCGCTGTGGCGCGCACTGCTGCTGCG 300
Db 342 AGCAACCTGCGGCTGTGGGCAACTCTCTGCGCGCTGTGGCGCGCACTGCTGCTGCG 401
QY 301 CACCTGGCGCGCAAGCGCGCGCGCACTGTCTCCAGAACCTATAGCTATGCACTTCC 360
Db 402 CACCTGGCGCGCAAGCGCGCGCGCACTGTCTCCAGAACCTATAGCTATGCACTTCC 461
QY 361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 462 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 521
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Db 522 AATTCTAGAGAGAGTCAAGTGGAGAGAGAGTCTCCCGCCCAACAAGCGGCAAGCGGAGT 581
QY 481 CGGGCGCGCGCGCACTGTGTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 582 CGGGCGCGCGCGCACTGTGTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 641
QY 541 CAGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 642 CAGCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
QY 601 CGGGTTCAGAGAGAGTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
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QY 661 CGGGCCCAAGCGGCTGTGGCGCGCACTGTGTTT--GGGCAAGGCCACCGCACTGTG- 717
Db 762 CGGGCCCAAGCGGCTGTGGCGCGCACTGTGTTTGGGCAAGGCCACCGCACTGTG- 821
QY 718 CGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 771
Db 822 CGGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
QY 772 TATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808
Db 882 ATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
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RESULT 14  
B1523561 872 bp mRNA linear EST 29-AUG-2001  
LOCUS 60317585.F1 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5240077 5',  
DEFINITION mRNA sequence.  
ACCESSION B1523561  
VERSION B1523561.1 GI:15348353  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 872)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.lnl.gov>  
Plate: L1M1605 row: f column: 14  
High quality sequence start: 28  
High quality sequence stop: 805.  
Location/Qualifiers

#### FEATURES

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/clone\_lib="NIH\_MGC\_121"  
/note="Organ: brain; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3  
fetal brains, female age 20 weeks, female age 24 weeks,  
and male age 26 weeks. Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
0.7-3.5 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 017. Note:  
this is a NIH\_MGC Library."

#### ORIGIN

Query Match 74.9%; Score 680.8; DB 4; Length 872;  
Best Local Similarity 98.8%; Pred. No. 2.2e-139;  
Matches 759; Conservative 0; Mismatches 2; Indels 7; Gaps 7;

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QY 1 ATGGCGCTATCCGGGTGACCCCGGCGCGCTGCTGGAGAGAGATGAGTGCCTGAGACTAC 60
Db 108 ATGGCGCTATCCGGGTGACCCCGGCGCGCTGCTGGAGAGAGATGAGTGCCTGAGACTAC 167
QY 61 TACGGAGATGCTGTGCTTCAACCTATGATGAGTGTGGCGGCACTGACCGAGTGC 120
Db 168 TACGGAGATGCTGTGCTTCAACCTATGATGAGTGTGGCGGCACTGACCGAGTGC 227
QY 121 GAGCTGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 228 GAGCTGAGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
QY 181 CGGGCCCGCAGCGGCTGTGAGAGCTTCTGCTGAGAGTGAAGCGCGCGGCACTGTGCGGAG 240
Db 288 CGGGCCCGCAGCGGCTGTGAGAGCTTCTGCTGAGAGTGAAGCGCGCGGCACTGTGCGGAG 347
QY 241 AGCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299
Db 348 AGCAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 407
QY 300 GCACTGTGGC--GCGCAAGCGGCGCGGCACTGTCTCCAGAACGCTATAGCTATG--GCACC 357
Db 408 GCACTGTGGC--GCGCAAGCGGCGCGGCACTGTCTCCAGAACGCTATAGCTATG--GCACC 467
QY 358 TCCAGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Db 468 TCCAGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 527
QY 418 GCAAAATTCTAGAGAGAGTCAAGTGGAGAGAGAGTCTCCCGCC--AACCAAGGAGAGCGGCG 476
Db 528 GCAAAATTCTAGAGAGAGTCAAGTGGAGAGAGAGTCTCCCGCC--AACCAAGGAGAGCGGCG 587
QY 477 GAGTGGGAGCGGCGCAAGTGTGTGTCAGACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 536
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Db 588 GAGTCGGGGCCGCGCCAGTGTGTGCGCAGACGGGCGGAGAGAGGGGCCCGACCGCA-C 646

QY 537 CCAGCAGAGTCCAGAGCCCGCCAGACCTTCTCTGAAAGCAAGTGAATCTGTGACATCCG 596

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QY 597 GCTCCGGGTTCCAGCAGAGTACTGCGAGCATGGGCGCCCTTGGAGAGAGGGCCGTGGATC 656

Db 706 GCTCCGGGTTCCAGCAGAGTACTGCGAGCATGGGCGCCCTTGGAGAGAGGGCCGTGGATC 765

QY 657 CCGGCGGCGCCGAGCGCTGCGCGCGCAGCTGAGAGTGTGGGCGAGGCCAAGCGAGTGT 716

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Db 826 GGGCTCAAGGAGCTGGGCTCTGTGTGTGTGTGACATCAAGTCTCAGA 872

## RESULT 15

AL519410

LOCUS

DEFINITION AL519410 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens

ACCESSION AL519410

VERSION AL519410.3 GI:45694960

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 874) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jeejee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:31037757.

Contact: Genoscope

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Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Left strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

9074.1

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?cs=CSDB004CC050P1&c=9074.1.

Location/Qualifiers

1. 874

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSDB004YF09"

/issue\_type="NEUROBLASTOMA COT 10-NORMALIZED"

/clone\_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"

/note="Left strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 74.7%; Score 678.8; DB 1; Length 874;

Best Local Similarity 89.8%; Pred. No. 6.1e-119;

Matches 750; Conservative 36; Mismatches 42; Indels 7; Gaps 6;

QY 1 ATGAGCGTATCCGGGATGAGCCCGCGGCTGGGAGAGATGAGTGGCTGGACTAC 60

Db 43 ATGAGCGTATCCGGGATGAGCCCGCGGCTGGGAGAGATGAGTGGCTGGACTAC 102

QY 61 TACGGGATGCTGCTGCTTCAACCGTATGAGAGTGGTGGCGGCAACTGACGATGC 120

Db 103 TACGGGATGCTGCTGCTTCAACCGTATGAGAGTGGTGGCGGCAACTGACGATGC 162

QY 121 GAGCTGAGCTCTCTGCTTCTTCTGCTGATGAGGCTTCTGCGCCCGCGAGGCTTAGCC 180

Db 163 GAGCTGAGCTCTCTGCTTCTTCTGCTGATGAGGCTTCTGCGCCCGCGAGGCTTAGCC 221

QY 181 CGGGCCCGGAGCGGCGCTAGAGCTCTGCTGAGGCTTCTGAGGCGGCGGCGGCGGCGG 239

Db 222 CGGGCCCGGAGCGGCGCTAGAGCTCTGCTGAGGCTTCTGAGGCGGCGGCGGCGGCGG 281

QY 240 GAGCAACTGCGGCTGCTGGGCACTCTGCGCGTCTGCGCGGCGGCGGCGGCGGCGG 299

Db 282 GAGCAACTGCGGCTGCTGGGCACTCTGCGCGTCTGCGCGGCGGCGGCGGCGGCGG 341

QY 300 GCACTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 359

Db 342 GCACTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 400

QY 360 CAGCTCTTCAAG 419

Db 401 CAGCTCTTCAAG 460

QY 420 AAATTTCTAG-CAGGCTAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478

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QY 599 TCCGGGTTCCAGCAGAGTACTGAGCAGATGAGGCGAGCTTGGAGCAGGCGTGGCATCC 658

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QY 659 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 718

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